

5	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460.1 tubulin	3.5
	413786	AW613780	Hs.13500	ESTs	3.5
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	3.5
	439904	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004 Homo	3.5
	449909	AA004681	Hs.59432	ESTs	3.5
10	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	3.5
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.5
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
15	453916	AW974874	Hs.75212	ornithine decarboxylase 1	3.5
	430200	BE613337	Hs.234896	geminin	3.4
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	3.4
	423645	AI215632	Hs.147487	ESTs	3.4
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate synthase	3.4
20	434966	AA657494		gb:nt66104.s1 NCL_CGAP_Pr3 Homo sapiens	3.4
	404571			NM_015902: Homo sapiens progesterone induce	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
	436374	AA400709	Hs.96716	ESTs, Weakly similar to T17210 hypothel	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
25	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.4
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.4
	402031			ENSP00000251056*: Plasma membrane calcium	3.4
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	449603	AI655662	Hs.197698	ESTs	3.4
30	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	3.4
	436805	AA731533	Hs.270751	ESTs	3.4
	437367	AA749316	Hs.271879	ESTs, Moderately similar to ALU1_HUMAN A	3.4
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.4
	430144	AI732722	Hs.187694	ERGL protein; ERGIC-53-like protein	3.4
35	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.4
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (3.4
	439375	AA689526	Hs.344249	steroid dehydrogenase homolog	3.4
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
40	408267	AW380525	Hs.343564	tubulin-specific chaperone e	3.4
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.4
	422564	AI148006	Hs.222120	ESTs	3.4
	424842	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	3.4
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	3.4
45	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	436137	AI056769	Hs.133512	ESTs	3.4
	440348	AW015802	Hs.47023	ESTs	3.4
	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypothel	3.4
	443242	BE243910	Hs.9082	nucleoporin p54	3.4
50	445469	AW298370	Hs.153714	complement C1q tumor necrosis factor-rel	3.4
	449517	AW500106	Hs.23543	serine/threonine protein kinase MASK	3.4
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.4
	433037	NM_014158	Hs.279938	HSPC067 protein	3.4
	423044	AA320829	Hs.97266	protocadherin 18	3.4
55	434128	W93170	Hs.284164	protein x 0004	3.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.4
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.4
	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.4
	438825	BE327427	Hs.79953	ESTs	3.4
60	446874	AW958304	Hs.56156	ESTs	3.4
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.4
	419131	AA406293	Hs.41167	ESTs	3.4
	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp584C142 (fr	3.4
	433764	AW753676	Hs.39982	ESTs	3.4
65	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	3.4
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.3
	452815	AA418841		gb:zw01e11.s1 Soares_NhHMPu_S1 Homo sapi	3.3
	421234	AA907153	Hs.190060	ESTs	3.3
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.3
70	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	3.3
	420041	AB005142	Hs.94592	klotho	3.3
	426174	AA547959	Hs.115838	ESTs	3.3
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	3.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	3.3
75	436664	AW197887	Hs.253353	ESTs	3.3
	441124	T97717	Hs.119563	ESTs	3.3
	444169	AV648170	Hs.58756	ESTs	3.3
	421476	AW953805	Hs.21887	ESTs	3.3
	422165	AL041199	Hs.1481	histidine decarboxylase	3.3
80	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.3
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	3.3
	401197			ENSP00000229263*: HSPC213.	3.3
	433404	T32982	Hs.102720	ESTs	3.3
	422546	AB007969	Hs.301478	KIAA0500 protein	3.3
	443884	N20617	Hs.194397	leptin receptor	3.3
	414341	D80004	Hs.75909	KIAA0182 protein	3.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.3

	414407	AA147026	Hs.76704	ESTs	3.3
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	3.3
	423453	AW450737	Hs.128791	CGI-09 protein	3.3
5	444170	AW613879	Hs.102408	ESTs	3.3
	445474	AI240014	Hs.259558	ESTs	3.3
	450582	AI339732		G-rich RNA sequence binding factor 1	3.3
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.3
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.3
10	444324	AI301330	Hs.143838	ESTs	3.3
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.3
	429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	3.3
	400880			NM_000611*:Homo sapiens CD59 antigen p18	3.3
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.3
15	451968	H56196	Hs.26409	Homo sapiens mRNA; cDNA DKFZp547K204 (fr	3.3
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.3
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.3
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I7885 serine/th	3.3
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	3.3
20	428523	AW974540	Hs.98626	ESTs	3.3
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	3.3
	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
	438147	AW250553		H-2K binding factor-2	3.3
25	445808	AV555234		ESTs, Moderately similar to PC4259 ferri	3.3
	453058	AW612293	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	3.3
	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	3.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hibr1)	3.3
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.3
30	411373	BE326276	Hs.8861	ESTs	3.3
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.3
	443674	AI081330	Hs.145008	ESTs	3.3
	427528	AI077143	Hs.179565	minichromosome maintenance deficient (S.	3.3
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.3
35	420969	AI636310	Hs.28310	ESTs	3.3
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.3
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.3
	410119	F07841	Hs.13926	ESTs	3.3
	417379	AA196390		gb:zpp99b10.s1 Stratagene muscle 937209 H	3.3
40	423201	NM_000163	Hs.125180	growth hormone receptor	3.3
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.3
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.3
	423427	AL137612	Hs.285848	KIAA1454 protein	3.3
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypothi	3.3
45	426775	AA384564		ESTs	3.3
	432378	AI493046	Hs.146133	ESTs	3.3
	438875	AA827640	Hs.189059	ESTs	3.3
	452959	AI933416	Hs.189674	ESTs	3.3
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.3
50	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	3.2
	433002	AF048730	Hs.279906	cyclin T1	3.2
	430929	AA489166	Hs.156933	ESTs	3.2
	437444	H46008	Hs.31518	ESTs	3.2
	446297	AI346930	Hs.149728	ESTs	3.2
55	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	3.2
	429377	AA813192	Hs.200596	KIAA0547 gene product	3.2
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.2
	420583	H77859	Hs.65450	reticulin 4	3.2
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	3.2
60	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	3.2
	418871	NM_001608	Hs.1209	acyl-Coenzyme A dehydrogenase, long chain	3.2
	421029	AW057782	Hs.293053	ESTs	3.2
	452997	N64777	Hs.44656	ESTs	3.2
	435035	BE568487	Hs.47668	x 006 protein	3.2
65	408412	AW193033	Hs.124436	ESTs	3.2
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	3.2
	421887	AW161450	Hs.109201	CGI-86 protein	3.2
	432409	AA806538	Hs.130732	KIAA1575 protein	3.2
	434378	AA631739	Hs.335440	EST	3.2
70	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	3.2
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	3.2
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	3.2
	410296	AW630675	Hs.271946	ESTs	3.2
	413838	AV661185	Hs.75574	mitochondrial ribosomal protein L19	3.2
75	414342	AA742181	Hs.75912	KIAA0257 protein	3.2
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.2
	425475	W56339	Hs.107057	ESTs	3.2
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	3.2
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypothi	3.2
80	452295	BE379936	Hs.28866	programmed cell death 10	3.2
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	3.2
	432960	AW150945	Hs.144758	ESTs	3.2
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.2
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.2

	421645	AA974127	Hs.129777	ESTs	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	415691	AW963979	Hs.24723	ESTs	3.2
	433852	AI378329	Hs.126629	ESTs	3.2
5	439735	AI635386	Hs.142846	hypothetical protein	3.2
	428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	3.2
	427715	BE245274	Hs.180428	KIAA1181 protein	3.2
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
	415715	F30364	Hs.302204	ESTs	3.2
10	426172	AA371307	Hs.125056	ESTs	3.2
	434825	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.2
	436246	AW450963	Hs.119991	ESTs	3.2
	436401	AI087958	Hs.29088	ESTs	3.2
	408784	AW971350	Hs.63386	ESTs	3.2
15	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.2
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.2
	405558			Target Exon	3.2
	434747	AA837085	Hs.220585	ESTs	3.2
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.2
20	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.2
	426171	AI128606	Hs.6557	zinc finger protein 161	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	412530	AA766268	Hs.266273	hypothetical protein FLJ13348	3.2
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	3.2
25	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	3.2
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	448568	AA149121	Hs.71947	ESTs	3.2
	420131	F08286	Hs.95262	nuclear factor related to kappa B bindin	3.1
30	429299	AI620463	Hs.347408	hypothetical protein MGC13102	3.1
	407913	BE393767	Hs.41569	phosphatidic acid phosphatase type 2A	3.1
	415009	C75253	Hs.220950	ESTs	3.1
	406627	T64904	Hs.163780	ESTs	3.1
	438666	AW014493	Hs.126727	ESTs	3.1
35	419875	AA853410	Hs.93557	proenkephalin	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.1
40	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	3.1
	431416	AA532718	Hs.178604	ESTs	3.1
	422662	BE274778	Hs.119007	RAB4, member RAS oncogene family	3.1
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	3.1
45	437083	AW082597	Hs.244862	ESTs	3.1
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.1
	417380	T06809	Hs.332086	ESTs	3.1
	419965	H16382	Hs.70258	ESTs	3.1
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	3.1
	446146	AI287539	Hs.148078	ESTs	3.1
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.1
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	3.1
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.1
55	423947	AW451954	Hs.135941	KIAA1048 protein	3.1
	451893	AW192083	Hs.290855	ESTs	3.1
	447726	AL137638	Hs.19368	matrilin 2	3.1
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypothi	3.1
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.1
	443331	AI052026	Hs.149995	ESTs	3.1
60	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.1
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	3.1
	427421	AA402414	Hs.3059	coatomer protein complex, subunit beta	3.1
	429399	AA452244	Hs.16727	ESTs	3.1
65	430092	AI821399	Hs.16514	ESTs	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.1
	436894	H80696	Hs.233313	ESTs	3.1
	437756	AA767537	Hs.197096	ESTs	3.1
	438979	AW976218	Hs.32565	ESTs	3.1
70	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.1
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	3.1
	419030	T79957	Hs.188466	ESTs	3.1
75	438308	AI343469	Hs.127685	KIAA1627 protein	3.1
	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	3.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	3.1
	428878	AA436884	Hs.48926	ESTs	3.1
	432205	AI806583	Hs.125291	ESTs	3.1
80	440099	AL080058	Hs.6909	DKFZP584G202 protein	3.1
	428259	AA424793	Hs.24144	ESTs	3.1
	434614	AI249502	Hs.29669	ESTs	3.1
	420380	AA640891	Hs.102406	ESTs	3.1
	433323	AA805132	Hs.159142	ESTs	3.1

5	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
	412088	AI689496	Hs.108932	ESTs	3.1
	434361	AF129755	Hs.88474	ESTs	3.1
	400664			NM_002425:Homo sapiens matrix metallopro	3.1
	436354	AI879252	Hs.5151	RAN binding protein 7	3.1
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	3.1
	410595	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	3.1
	415245	N59650	Hs.27252	ESTs	3.1
10	418647	AA226198		gb:nc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	3.1
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.1
	453716	AA037675	Hs.152675	ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.0
	408705	AA312135	Hs.46967	HSPCO34 protein	3.0
15	430280	AA361258	Hs.237868	interleukin 7 receptor	3.0
	445919	T53519	Hs.334692	hypothetical protein MGC14141	3.0
	441790	AW294909	Hs.132208	ESTs	3.0
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:428026, mRNA,	3.0
20	422788	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.0
	439703	AF086538	Hs.196245	ESTs	3.0
	444489	AI151010	Hs.157774	ESTs	3.0
	453878	AW964440	Hs.19025	DC32	3.0
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.0
25	433680	AI805366	Hs.199945	ESTs	3.0
	426363	M58524	Hs.2025	transforming growth factor, beta 3	3.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	3.0
	426044	AA502490	Hs.170290	ESTs	3.0
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	3.0
30	445084	H38914	Hs.250848	hypothetical protein FLJ14761	3.0
	452737	AK001680	Hs.30488	DKFZP434F091 protein	3.0
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	3.0
	435712	AA694607	Hs.176956	ESTs	3.0
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.0
35	414993	AW819403	Hs.77724	KIAA0586 gene product	3.0
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	3.0
	421988	AW450481	Hs.161333	ESTs	3.0
	432833	N51075	Hs.110028	ESTs	3.0
	445210	H09323	Hs.27133	ESTs	3.0
40	447620	AW290951	Hs.224965	ESTs	3.0
	449375	R07114	Hs.271224	ESTs	3.0
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.0
	443967	AW294013	Hs.200942	ESTs	3.0
	441224	AU076964	Hs.7753	calumenin	3.0
45	448822	BE149845	Hs.289038	hypothetical protein MGC4126	3.0
	435688	H72286	Hs.128387	ESTs	3.0
	441889	AI090455	Hs.268371	hypothetical protein FLJ20274	3.0
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
	415954	AA171850	Hs.42251	ESTs	3.0
50	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	3.0
	420077	AW512260	Hs.87767	ESTs	3.0
	443475	AI066470	Hs.132809	ESTs	3.0
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	3.0
	438436	AA807168	Hs.271552	ESTs	3.0
55	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.0
	443280	AA299688	Hs.24183	ESTs	3.0
	448264	AI478933	Hs.188260	ESTs	3.0
	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	3.0
	453843	D25215	Hs.35804	hect domain and RLD 3	3.0
60	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	3.0
	445943	AW898533	Hs.181574	ESTs	3.0
	432286	AW327432	Hs.255843	ESTs	3.0
	431707	R21326	Hs.267905	hypothetical protein FLJ10422	3.0
	432675	AI791855	Hs.105884	ESTs	3.0
65	443162	T49951	Hs.9029	DKFZP434G032 protein	3.0
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	3.0
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.0
	423583	AL122055	Hs.129836	KIAA1028 protein	3.0
70	418304	AA215702		gb:zr97g10.r1 NCL_CGAP_GC81 Homo sapiens	3.0
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.0
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	3.0
	411850	AK002033	Hs.72782	hypothetical protein FLJ11171	3.0
	438986	AF085888	Hs.269307	ESTs	3.0
75	445921	AW015211	Hs.146181	ESTs	3.0
	447124	AW976438	Hs.17428	RBP1-like protein	3.0
	452953	AI932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	3.0

TABLE 60B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
5	411479	1247077_1
10	411667	1253334_1
10	414372	143909_1
10	414680	147525_1
15	415989	156454_1
15	416288	1585983_1
15	416882	162718_1
20	416913	163001_1
20	417379	167238_1
20	418304	173658_2
20	418647	177521_1
25	418866	179788_1
25	419536	185688_1
25	419544	185760_2
25	423412	228001_1
25	423800	232161_1
25	426226	262918_1
25	426413	266650_1
25	426503	268283_1
25	426775	271683_1
30	426991	27415_1
30	428342	290035_2
35	429163	300543_1
35	429220	301384_1
35	429258	301917_1
35	430935	325772_1
35	430968	326269_1
35	431429	33313_1
40	432093	341283_1
40	432125	341776_1
40	432189	342819_1
40	432340	345248_1
45	432363	345469_1
45	432600	350959_1
45	432810	354375_1
50	434579	38916_1
50	434966	396504_1
50	435023	398093_1
50	437866	44433_2
55	438147	45074_1
55	439092	468554_1
55	439518	47334_1
55	439904	479942_1
55	440840	50357_2
60	441102	509604_1
60	442562	54500_2
65	443161	561305_1
65	445808	65133_1
65	447082	707248_1
65	448212	755099_1
65	449625	8113_1
70	450580	83929_1
75	450582	83933_1
75	452260	9074_1
80	452598	92338_2
80	452815	93255_1
80	453802	981589_1
80	455100	1253334_1

457728 393853_1 AW974811 AA651634 AA650072

5 TABLE 60C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NI_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400695	7249150	Plus	160456-160567,164757-164873
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402031	7656761	Plus	33080-33263,33939-34094,36103-36507
402802	3287156	Minus	53242-53432
402855	9662953	Minus	59763-59909
403046	3540153	Minus	55707-55859,56369-56511
403047	3540153	Minus	59793-59968
403790	8084957	Minus	87826-87947,89835-90002
404571	7249169	Minus	112450-112648
404632	9796668	Plus	45096-45229
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405558	1621110	Plus	4502-4644,5983-6083

Table 61A lists about 440 genes up-regulated in prostate cancer compared to normal prostate and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal prostate tissue was greater than or equal to 2.0 and the ratio to normal adult tissues was greater than or equal to 2.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst prostate tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 61A: ABOUT 440 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE AND NORMAL ADULT TISSUES

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Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of prostate tumor to normal adult body tissue
R2: Ratio of prostate tumor to normal prostate tissue

50

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	
55	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2	42.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	3.2	26.5
	420729	AW964897	Hs.290825	ESTs	3.7	15.8
	401197			ENSP00000229263*.HSPC213.	3.0	12.6
60	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4	12.4
	449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3	12.3
	443271	BE568568	Hs.195704	ESTs	11.6	11.6
	434078	AW680709	Hs.283683	chromosome 8 open reading frame 4	2.1	11.2
65	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4	9.4
	417315	AI080042	Hs.180450	ribosomal protein S24	2.3	9.0
	416182	NM_004354	Hs.79069	cyclin G2	8.4	8.4
	421913	AI934365	Hs.109439	osteoglycin (osteocinductive factor, mime	2.2	8.4
70	434217	AW014795	Hs.23349	ESTs	8.3	8.3
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3	8.3
	442501	AA315267	Hs.23128	ESTs	2.0	8.3
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1	8.1
75	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.1	8.0
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	34.0	7.9
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5	7.5
	419078	M93119	Hs.89584	insulinoma-associated 1	7.4	7.4
80	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	9.4	7.3
	425018	BE245277	Hs.154196	E4F transcription factor 1	7.2	7.2
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0	7.0
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	4.0	6.6
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3	6.3
	411373	BE326276	Hs.8861	ESTs	3.2	6.3
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.7	6.2
	422583	AA410506	Hs.27973	KIAA0874 protein	2.3	6.2
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	6.1	6.1
	437147	AL049964	Hs.8358	hypothetical protein FLJ20366	2.6	6.0

5	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.2	6.0
	449118	R67477	Hs.23103	Bel1 (S. cerevisiae) homolog	5.9	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.3	5.9
	431548	AJ834273	Hs.9711	novel protein	15.7	5.8
10	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.2	5.8
	410889	X91662	Hs.65744	twist (Drosophila) homolog (acrocephalos	3.5	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.9	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7	5.7
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.5	5.6
15	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6	5.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.5	5.5
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.7	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4	5.4
	451684	AF216751	Hs.26813	CDA14	3.9	5.4
20	421470	R27496	Hs.1378	annexin A3	5.3	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.8	5.3
	437571	AA760894	Hs.153023	ESTs	5.2	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2	5.2
25	444917	R68651	Hs.144997	ESTs	5.1	5.1
	417318	AW953937	Hs.240845	ESTs	4.6	5.1
	434170	AA626509	Hs.122329	ESTs	5.1	5.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	3.3	5.0
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.8	5.0
30	421823	N40850	Hs.28625	ESTs	5.0	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	29.8	4.9
	425242	D13635	Hs.155287	KIAA0010 gene product	2.2	4.8
	439024	R96696	Hs.35598	ESTs	5.4	4.8
35	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8	4.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (tr	4.7	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6	4.7
	451952	AL120173	Hs.301663	ESTs	4.7	4.7
	431676	AI685464		gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	9.1	4.7
40	452242	R50956	Hs.159993	glycosyltransferase	4.7	4.7
	401519			C15000476:gi12737279[ref]XP_012163.1]	4.6	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	3.4	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	3.3	4.6
	429467	NM_004477	Hs.203772	FSDH region gene 1	2.1	4.6
45	408380	AF123050	Hs.44532	diubiquitin	4.2	4.6
	425907	AA365752	Hs.155955	ESTs	2.2	4.6
	427078	AI676062	Hs.111902	ESTs	4.8	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.7	4.5
	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5	4.5
50	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	2.5	4.5
	443250	AI041530	Hs.132107	ESTs	8.1	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4	4.4
55	428826	AL048842	Hs.194019	attractin	2.0	4.3
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3	4.3
	418701	AA814948	Hs.95343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2	4.2
	429900	AA460421	Hs.30875	ESTs	4.2	4.2
	439518	W76326		gb:zcd60d04.r1 Soares_fetal_heart_NbHH19W	2.2	4.2
60	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.5	4.2
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	10.0	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.8	4.2
	443622	AI911527	Hs.11805	ESTs	2.2	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1	4.1
65	421129	BE439899	Hs.89271	ESTs	4.1	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.9	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	2.8	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.0	4.1
	433887	AW204232	Hs.279522	ESTs	4.1	4.1
70	436556	AI364997	Hs.7572	ESTs	4.1	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1	4.1
	443646	AI085198	Hs.164226	ESTs	4.1	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	2.2	4.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0	4.0
75	433409	AI278802	Hs.25661	ESTs	4.0	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0	4.0
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9	3.9
	444755	AA431791	Hs.113823	CtpX (caseinolytic protease X, E. coli)	3.9	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	2.2	3.9
80	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.3	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	2.2	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.9	3.9
	423337	NM_004655	Hs.127337	actin 2 (conductin, exil)	3.4	3.8
	452588	AA889120	Hs.110637	homeo box A10	6.5	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	2.3	3.8
	410330	AW023630	Hs.159425	ESTs	6.2	3.8

5	422975	AA347720	Hs.122659	KIAA0264 protein	2.2	3.8
	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.7	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	4.1	3.8
10	418821	AA436002	Hs.183161	ESTs	2.8	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.1	3.8
	453160	AI263307	Hs.239884	H2B histone family, member L	9.2	3.8
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked mol	3.7	3.7
15	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7	3.7
	448807	AI571940	Hs.7549	ESTs	3.6	3.7
	439209	AF087993	Hs.91954	ESTs	2.1	3.6
	420077	AW512260	Hs.87767	ESTs	4.4	3.6
	451009	AA013140	Hs.115707	ESTs	4.1	3.6
20	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.2	3.6
	447033	AI357412	Hs.157601	ESTs	7.7	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6	3.6
25	414680	AA743331		hemoglobin, alpha 2	3.5	3.5
	417380	T06809	Hs.332086	ESTs	3.5	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieli	3.5	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (K0X 4, clone HF.1	2.2	3.5
30	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5	3.5
	432101	AI918950	Hs.123642	EphA3	16.5	3.5
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.3	3.5
	435513	AW404075	Hs.42785	DC11 protein	2.2	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	2.1	3.5
35	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	6.7	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	2.1	3.4
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	2.1	3.4
	440749	W22335	Hs.7392	hypothetical protein MGC3199	2.5	3.3
	408374	AW025430	Hs.155591	forkhead box F1	4.3	3.3
40	400277			Eos Control	2.4	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3	3.3
	443912	R37257	Hs.184780	ESTs	3.3	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	9.9	3.3
45	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.4	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.6	3.3
	451367	AA923729	Hs.26322	cell cycle related kinase	3.3	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	11.5	3.2
50	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	2.0	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2	3.2
	402802			NM_001397:Homo sapiens endothelin conver	4.3	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12541 fis, clone NT	2.7	3.2
55	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.8	3.2
	444489	AI151010	Hs.157774	ESTs	3.2	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2	3.2
60	453078	AF053551	Hs.31584	metaxin 2	2.1	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	10.6	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	2.8	3.1
	434804	AA649530	Hs.348148	gbms44f05.s1 NCL_CGAP_Alv1 Homo sapiens	2.1	3.1
	445840	AI277811	Hs.146291	ESTs	3.1	3.1
65	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	2.2	3.1
	408161	AW962912	Hs.300383	hypothetical protein MGC3032	3.1	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1	3.1
	430519	AF129534	Hs.49210	F-box only protein 4	3.1	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	16.2	3.1
70	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1	3.1
	430226	BE245582	Hs.2551	adrenergic, beta-2-, receptor, surface	9.0	3.1
	400286	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	20.9	3.1
	420154	AI093155	Hs.95420	JM27 protein	27.4	3.1
	453293	AA382267	Hs.10653	ESTs	3.7	3.1
75	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	2.4	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	2.9	3.0
	433285	AW975944	Hs.237396	ESTs	7.7	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0	3.0
80	445921	AW015211	Hs.146181	ESTs	4.3	3.0
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.5	3.0
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	2.5	3.0
	450580	N40087		ESTs	3.0	3.0
	447726	AL137638	Hs.19368	matrilin 2	3.9	2.9
	447816	NM_007233	Hs.274329	TP53 target gene 1	7.2	2.9
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	5.1	2.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	2.6	2.9

	420297	A1628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9	2.9
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.9	2.9
	437812	A1582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debris	2.9	2.9
5	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	2.9	2.9
	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	4.7	2.9
	442320	A1287817	Hs.129636	ESTs	3.7	2.9
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.4	2.9
	433050	A093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	2.9	2.9
10	451796	AL133019	Hs.27038	Homo sapiens mRNA; cDNA DKFZp434G2127 (f	2.9	2.9
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.0	2.9
	459029	AA131376	Hs.343809	fibroblast growth factor 12B	2.9	2.9
	441676	BE564206	Hs.49889	ESTs	4.4	2.9
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.1	2.9
15	453628	AW243307	Hs.83937	hypothetical protein	2.9	2.9
	412324	AW978439	Hs.69504	ESTs	2.0	2.8
	408063	BE086548	Hs.42346	calcineurin-binding protein calcisarcin-1	5.0	2.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4	2.8
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.8	2.8
20	433865	N29862	Hs.44104	ESTs	2.8	2.8
	423201	NM_000163	Hs.125180	growth hormone receptor	6.3	2.8
	450832	AW970602	Hs.105421	ESTs	2.1	2.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8	2.8
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	2.8	2.8
25	427144	X95087	Hs.2126	vasoactive intestinal peptide receptor 2	2.8	2.8
	444668	AA654660	Hs.282906	ESTs	2.2	2.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	3.2	2.8
	432689	AB018320		Arg/Abi-interacting protein ArgBP2	2.1	2.8
	423482	BE280172	Hs.129228	galactokinase 2	2.4	2.8
30	448206	BE622685	Hs.3731	ESTs, Moderately similar to I38022 hypot	2.8	2.8
	450546	AA010200	Hs.175551	ESTs	2.2	2.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.6	2.7
	458332	AI000341	Hs.220491	ESTs	4.9	2.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	2.7	2.7
35	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	2.1	2.7
	412576	AA447718	Hs.107057	ESTs	2.7	2.7
	413336	AI569936	Hs.296178	hypothetical protein FLJ22637	2.7	2.7
	433577	AW007080	Hs.284192	ESTs	2.7	2.7
	439093	AA534163	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	2.7	2.7
40	442633	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.7	2.7
	447401	BE618582	Hs.97661	ESTs	2.7	2.7
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.7	2.7
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	2.2	2.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.2	2.7
45	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	9.0	2.7
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	2.4	2.7
	422805	AA436989	Hs.121017	H2A histone family, member A	13.6	2.7
	446238	T95143	Hs.14511	SCO (cytochrome oxidase deficient, yeast	2.1	2.7
	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG rep	8.1	2.7
50	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.2	2.6
	410592	R94088	Hs.43569	ESTs	2.6	2.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.6	2.6
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.6	2.6
	433419	AI830342	Hs.211272	ESTs	2.9	2.6
55	447509	AF107454	Hs.107537	chromosome 7 open reading frame 2	2.0	2.6
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A45010 X-linked	2.4	2.6
	407252	AA659037	Hs.163780	ESTs	2.6	2.6
	420061	AW024937	Hs.29410	ESTs	2.4	2.6
	424432	AB037821	Hs.146858	protocadherin 10	7.9	2.6
60	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	2.7	2.6
	414312	AA155694	Hs.191060	ESTs	2.6	2.6
	417135	AA422067	Hs.50547	ESTs	2.6	2.6
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.6	2.6
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.0	2.6
65	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.2	2.6
	406627	T64904	Hs.163780	ESTs	8.7	2.6
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.4	2.6
	425815	R94023	Hs.94560	ESTs, Moderately similar to I38022 hypot	2.6	2.6
	433805	AA706910	Hs.112742	ESTs	2.6	2.6
	431474	AL133990	Hs.190642	ESTs	9.3	2.5
70	436204	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	2.2	2.5
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	3.3	2.5
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	2.3	2.5
	437531	AI400752	Hs.112259	T cell receptor gamma locus	2.6	2.5
75	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.4	2.5
	403047			NM_005656: Homo sapiens transmembrane pr	21.1	2.5
	416198	H27332	Hs.99598	hypothetical protein MGC5338	2.5	2.5
	417576	AA339449	Hs.82265	phosphoribosylglycinamide formyltransfer	2.5	2.5
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.5	2.5
80	436401	AI087958	Hs.29088	ESTs	2.5	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5	2.5
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	3.0	2.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	11.9	2.5
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.5	2.5

	446791	AI632278	Hs.195922	ESTs	2.5	2.5
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.5	2.5
	419791	AI579909	Hs.105104	ESTs	2.7	2.5
5	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.0	2.5
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.1	2.5
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	2.5	2.5
	447702	AI420256	Hs.161271	ESTs	2.1	2.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	2.4	2.4
10	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.4	2.4
	429128	AA448869	Hs.119316	ESTs	2.0	2.4
	429258	AA448765		gb:zx10e09.r1 Soares_tclal_fetus_Nb2HF8_	2.4	2.4
	435102	AW899053	Hs.76917	F-box only protein 8	2.4	2.4
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	3.1	2.4
15	407021	U52077		gb:Human mariner1 transposase gene, comp	7.3	2.4
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.1	2.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone e	4.3	2.4
	447713	AI420733	Hs.207083	ESTs	2.4	2.4
	456848	AL121087	Hs.296406	KIAA0685 gene product	2.2	2.4
20	437617	AI026701	Hs.5716	KIAA0310 gene product	2.6	2.4
	432378	AI493046	Hs.146133	ESTs	5.2	2.4
	443180	R15875	Hs.258576	claudin 12	10.1	2.4
	445929	AI089660	Hs.323401	dpy-30-like protein	2.2	2.4
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	2.3	2.4
25	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	2.5	2.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	27.5	2.4
	421709	AA159394	Hs.107056	CED-6 protein	2.3	2.4
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.7	2.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.4	2.4
30	451071	AW138807	Hs.204939	ESTs, Highly similar to A54677 homeotic	2.4	2.4
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.1	2.3
	433037	NM_014158	Hs.279938	HSPC067 protein	2.4	2.3
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	4.1	2.3
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	2.3	2.3
35	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.1	2.3
	450693	AW450461	Hs.203965	ESTs	2.3	2.3
	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	2.3	2.3
	412045	AA099802	Hs.83883	transmembrane, prostate endrogen induced	4.1	2.3
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.0	2.3
40	419438	AA406400	Hs.12482	glyceronephosphate O-acyltransferase	2.7	2.3
	443194	AI954968	Hs.279009	matrix Gla protein	2.1	2.3
	414869	AA157291	Hs.21479	ubiquitin 1	2.5	2.3
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.3	2.3
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.3	2.3
45	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	2.3	2.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hfor1)	4.1	2.3
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.9	2.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	2.2	2.3
	431147	AI767751	Hs.20300	ESTs	5.8	2.3
50	442677	AI557914		peroxisomal acyl-CoA thioesterase	2.5	2.3
	446091	AW022192	Hs.200197	ESTs	4.0	2.3
	431563	AI027643	Hs.120912	ESTs	2.2	2.3
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.1	2.3
	413049	NM_002151	Hs.823	hepslin (transmembrane protease, serine 1	3.5	2.3
55	405885			C2002829:gi4507689[ref][NP_003298.1] tra	2.3	2.3
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	2.3	2.3
	450378	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	2.3	2.3
	429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	2.3	2.3
	417248	AA329449	Hs.247302	twisted gastrulation	2.3	2.2
60	429277	AW452016	Hs.127863	ESTs, Weakly similar to SFR4_HUMAN SPLIC	2.6	2.2
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	4.5	2.2
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.9	2.2
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	3.4	2.2
	431542	H63010	Hs.5740	ESTs	7.0	2.2
65	401558			ENSP00000220478*:SECRETORANIN III.	2.2	2.2
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	2.2	2.2
	422295	AF051151	Hs.114408	tol-like receptor 5	2.2	2.2
	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.2	2.2
	447499	AW262580	Hs.147674	protocadherin beta 16	2.2	2.2
70	452994	AW962597	Hs.31305	KIAA1547 protein	4.0	2.2
	450325	AI935962	Hs.26289	ESTs	11.9	2.2
	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	2.1	2.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6	2.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.8	2.2
75	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.2	2.2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.6	2.2
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	4.2	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	4.8	2.2
	422576	BE548555	Hs.118554	CGI-83 protein	2.1	2.2
80	433293	AF007835	Hs.32417	hypothetical protein MGC4309	11.0	2.2
	410733	D84284	Hs.66052	CD38 antigen (p45)	3.1	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.1	2.2
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.2	2.2
	408833	AW612232	Hs.254835	ESTs	3.0	2.2

	422424	AI186431	Hs.296638	prostate differentiation factor	4.4	2.2
	433444	AW975324	Hs.129816	ESTs	11.7	2.2
	446354	AW449650	Hs.346335	ESTs	2.6	2.2
5	438869	AF075009		gb:Homo sapiens full length insert cDNA	5.9	2.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	12.8	2.2
	424036	AA770688		H2A histone family, member L	3.8	2.2
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.8	2.2
	404641			NM_021965*:Homo sapiens phosphoglucomuta	2.2	2.2
10	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	2.2	2.2
	406068			C2002008:gi 7303957 gb AA59000.1 (AE00	3.1	2.1
	415162	AF035718	Hs.78061	transcription factor 21	2.1	2.1
	423349	AF010258	Hs.127428	homeo box A9	5.9	2.1
	424534	D87682	Hs.150275	KIAA0241 protein	2.3	2.1
15	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5	2.1
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.5	2.1
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.1	2.1
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.1	2.1
	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	2.1	2.1
20	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.1	2.1
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	2.1	2.1
	452959	AI933416	Hs.189674	ESTs	2.1	2.1
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.8	2.1
	408291	AB023191	Hs.44131	KIAA0974 protein	2.1	2.1
25	418727	AA227609	Hs.94834	ESTs	2.1	2.1
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	2.1	2.1
	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3	2.1
	432695	D63480	Hs.278634	KIAA0146 protein	2.3	2.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.2	2.1
30	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 14	2.5	2.1
	434569	AI311295	Hs.344478	KIAA0196 gene product	2.1	2.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	2.1	2.1
	438520	AA706319	Hs.98416	ESTs	2.7	2.1
	414269	AA298489	Hs.303171	olfactory receptor, family 51, subfamily	17.3	2.1
35	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.5	2.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	7.4	2.1
	450861	AI523898	Hs.17617	ESTs	2.4	2.1
	419193	D29643	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1	2.1
	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.2	2.1
40	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.4	2.1
	407182	AA312551	Hs.230157	ESTs	2.1	2.1
	421689	N87820	Hs.106826	KIAA1696 protein	2.1	2.1
	432833	N51075	Hs.110028	ESTs	2.1	2.1
	425170	AU077315	Hs.154970	transcription factor CP2	2.6	2.0
45	436278	BE396290	Hs.5097	synaptogyrin 2	2.8	2.0
	438719	AA357129	Hs.239625	integral membrane protein 2B	2.3	2.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6	2.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.0	2.0
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.6	2.0
50	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.0	2.0
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.0	2.0
	413627	BE182082	Hs.246973	ESTs	3.3	2.0
	414133	AW022188	Hs.41167	ESTs	2.3	2.0
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	14.7	2.0
55	450244	AA007534	Hs.125062	ESTs	3.1	2.0
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.6	2.0
	409219	AA393383	Hs.133331	ESTs	2.1	2.0
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0	2.0
	421969	AF052217	Hs.110099	core-binding factor, runt domain, alpha	2.0	2.0
60	434128	W93170	Hs.284164	protein x 0004	2.7	2.0
	434503	T96231	Hs.17762	ESTs	2.0	2.0
	443292	AK000213	Hs.9196	hypothetical protein	2.0	2.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.0	2.0
	448172	N75276	Hs.135904	ESTs	6.0	2.0
65	452039	AI922988	Hs.172510	ESTs	2.0	2.0
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	6.2	2.0
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	10.1	2.0
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	2.3	2.0
	451369	AA017321	Hs.269691	ESTs	2.1	2.0
70	434011	AW953437	Hs.5486	clone FLB5214	2.1	2.0
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	5.4	2.0
	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	2.7	2.0
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	5.5	2.0
	446783	AW138343	Hs.141867	ESTs	4.4	2.0
75	437323	AA371145	Hs.194397	leptin receptor	2.5	2.0
	410076	T05387	Hs.7991	ESTs	2.9	2.0
	421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	2.1	2.0
80	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	2.5	2.0

TABLE 618

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150955 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
10	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	419544	185760_2	AI909154 AA526337 AA244193 AI909153
	419733	187589_1	AW362955 H59488 AI040666 W60959 W94209 H27231 T84625 H75715 WD4957 W63676 AA659693 AA514302 W63769 BE046412 T91396 AI951970 AW044233 N20018 AW663548 T90114 AI139947 AA809643 AA846232 AA581966 AA789002
	424036	23460_1	AA770688 H15373 AW161070 BE304523 BE378517 AA989300 AA904029 BE254211 AA449148 AI268420 AI300495 AI215637 AI300494 AI268551 AA928971 AA179427 AA947684 BE393792 H98018 AI885781 AI188587 AI290658 C15404
15	426413	266650_1	AA377823 AW954494 AI022688
	429258	301917_1	AA448765 CD4967 CD3045 AA658293
	431676	336411_1	AI685464 AW971336 AA513587 AA525142
	432689	35275_1	AB018320 H56457 AA247916 N83488 N87920 AA095653 T19858 AL134279 AA094167 AI673378 AI000340 R47500 W16595 AW152297 AI625937 AA002027 AI814851 AA902666 AI039729 AW975053 BE302243 AI240793 AA193203 N5581
20	438869	46651_1	AF075009 R63109 R63068
	439518	47334_1	W76326 AF086341 W72300
	442677	548626_1	AI557914 WB1031 AW473764 AI814081 W81068 AW182826 AW173296 AI376594 AI220500 BE257195 BE246486 R55637 C20788 AI014407 AI248353 AW028015
25	445808	65133_1	AV655234 AW956332 AA340239
	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T813
	450580	83929_1	N40087 H12925 AA480779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
30	453802	981589_1	AL134757 AW079131

TABLE 61C

35	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
40	Nt_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
	401187	9719705	Plus	176341-176452
	401519	6649315	Plus	157315-157950
	401558	7139678	Plus	103510-104090
45	402802	3287156	Minus	53242-53432
	403047	3540153	Minus	59793-59968
	404641	9796810	Minus	32247-32362
	405685	4508129	Minus	37956-38097
50	406068	9114084	Plus	382-543

Table 62A lists about 600 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst normal prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 62A: ABOUT 600 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE TISSUES

60

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of prostate tumor to normal prostate tissue

65

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.5
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	16.0
	420729	AW964897	Hs.290825	ESTs	15.8
75	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	14.7
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	13.6
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	13.1
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	12.6
80	401197			ENSP00000229263~HSPC213.	12.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	12.6
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4
	449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3
	443271	BE568568	Hs.195704	ESTs	11.6
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	11.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	11.2

	406038	Y14443		zinc finger protein 200	11.1
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	10.6
	419553	N34145	Hs.10177	ESTs, Moderately similar to ZN91_HUMAN Z	10.4
5	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.3
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	10.1
	421684	BE281591	Hs.105768	hypothetical protein FLJ10511	9.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	9.9
	437866	AA156781		metallothionein 1E (functional)	9.5
10	440274	R24595	Hs.7122	scrapie responsive protein 1	9.4
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4
	405141	Y14443		zinc finger protein 200	9.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	9.2
	417315	AI080042	Hs.180450	ribosomal protein S24	9.0
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCTA00151 mRNA sequ	9.0
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	8.9
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	8.9
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	8.8
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	8.6
20	425174	D87450	Hs.154978	KIAA0261 protein	8.6
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.4
	445230	U97018	Hs.12451	echinoderm microtubule-associated protei	8.4
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	8.4
25	434217	AW014795	Hs.23349	ESTs	8.3
	417353	AW129357	Hs.329700	ESTs	8.3
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3
	442501	AA315267	Hs.23128	ESTs	8.3
	429503	AA394183	Hs.26873	ESTs	8.2
30	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1
	443837	AI984625	Hs.9884	spindle pole body protein	8.0
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	8.0
	444880	AW118683	Hs.154150	ESTs	7.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	7.9
35	436962	AW377314	Hs.5364	DKFZP564I052 protein	7.9
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	7.6
	420120	AL049610	Hs.95243	transcription elongation factor A (StiI)-	7.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	7.4
	419078	M93119	Hs.89584	insulinoma-associated 1	7.4
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	7.3
	451900	AB023199	Hs.27207	KIAA0982 protein	7.3
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	7.3
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-link	7.3
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	7.2
45	425018	BE245277	Hs.154196	E4F transcription factor 1	7.2
	447737	AK000643	Hs.19404	DKFZP564L0862 protein	7.2
	424897	D63216	Hs.153684	frizzled-related protein	7.1
	433867	AK000596	Hs.3618	hippocalcin-like 1	7.1
	427308	D26067	Hs.174905	KIAA0033 protein	7.1
50	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	7.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0
	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	6.9
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	6.9
	448076	AJ133123	Hs.20196	adenylate cyclase 9	6.9
55	426759	AI590401	Hs.21213	ESTs	6.8
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	6.8
	417302	BE245812	Hs.8941	ESTs	6.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.7
	451957	AJ796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	6.7
60	452859	AI300555	Hs.288158	hypothetical protein FLJ23591	6.7
	413431	AW246428	Hs.75365	ubiquitin-conjugating enzyme E2N (homolo	6.7
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	6.7
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.6
	426108	AA622037	Hs.166468	programmed cell death 5	6.6
65	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.6
	454219	X75042	Hs.44313	v-ref avian reticuloendotheliosis viral	6.5
	443020	AI350058	Hs.106129	ESTs	6.5
	415752	BE314524	Hs.78776	putative transmembrane protein	6.4
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	6.4
70	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	6.4
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.4
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	6.3
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3
	424308	AW975531	Hs.154443	minichromosome maintenance deficient [S.	6.3
75	411373	BE326276	Hs.8861	ESTs	6.3
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.2
	422583	AA410506	Hs.27973	KIAA0874 protein	6.2
	418196	AI745649	Hs.26549	KIAA1708 protein	6.1
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1
80	437147	AL049964	Hs.8358	hypothetical protein FLJ20366	6.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.0
	408242	AA251594	Hs.43913	PIBF1 gene product	5.9
	447965	AW292577	Hs.94445	ESTs	5.9

	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	5.9
	431548	AI834273	Hs.9711	novel protein	5.8
5	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.8
	414734	AA151712	Hs.82572	ESTs	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.8
	419047	AW952771	Hs.90043	ESTs	5.8
10	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	5.8
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7
	431055	AL157645	Hs.48793	siatyltransferase 6 (N-acetylglucosaminid	5.7
	434540	NM_016045	Hs.3945	CGI-107 protein	5.7
	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	5.7
15	407938	AA905097	Hs.85050	phospholamban	5.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6
20	406672	M26041	Hs.198253	major histocompatibility complex, class	5.5
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.5
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.5
	416619	AFD13168	Hs.79393	tuberous sclerosis 1	5.5
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	5.5
25	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheli	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	5.4
	416384	AU076903	Hs.79283	selectin P ligand	5.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	5.4
30	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
	451684	AF216751	Hs.26813	CDA14	5.4
	418758	AW959311	Hs.172012	hypothetical protein DKFP434J037	5.4
	445757	AW449065	Hs.13264	KIAA0856 protein	5.4
	449907	AA004825	Hs.103281	ESTs	5.4
35	419159	AW974945	Hs.268049	hypothetical protein	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	5.3
	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFP564D0472 (f	5.3
40	403851			C5002154*gi7299015 gb AA54217.1 (AE0	5.3
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	5.3
	417426	NM_002291	Hs.82124	laminin, beta 1	5.3
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	5.3
45	422746	NM_004484	Hs.119651	glypican 3	5.2
	437571	AA760894	Hs.153023	ESTs	5.2
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFP727C191 (tr	5.2
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2
50	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	5.2
	453204	R10799	Hs.191990	ESTs	5.2
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.1
	438510	AL080220	Hs.6285	DKFP586P0123 protein	5.1
	444917	R68651	Hs.144997	ESTs	5.1
55	414212	AA136569	Hs.10848	KIAA0187 gene product	5.1
	451593	AF151879	Hs.26706	CGI-121 protein	5.1
	417318	AW953937	Hs.240845	ESTs	5.1
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	5.1
	433600	R42833	Hs.22232	ESTs	5.0
60	434170	AA626509	Hs.122329	ESTs	5.0
	424090	X99699	Hs.139262	XIAP associated factor-1	5.0
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.0
	435708	W31254	Hs.7045	GL004 protein	5.0
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	5.0
65	432897	AF155099	Hs.279780	NY-REN-18 antigen	5.0
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	5.0
	410762	AF226053	Hs.66170	HSKM-B protein	5.0
	421823	N40850	Hs.28625	ESTs	5.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.9
70	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.9
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.9
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	4.9
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	4.9
75	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheli	4.9
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	4.9
	411352	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	4.8
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	4.8
	425242	D13635	Hs.155287	KIAA0010 gene product	4.8
80	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	4.8
	439024	R96696	Hs.35598	ESTs	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	4.7
	412953	Z45794	Hs.238809	ESTs	4.7

	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	4.7
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7
	437916	BE566249	Hs.20699	hypothetical protein FLJ23142	4.7
5	451952	AL120173	Hs.301663	ESTs	4.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.7
	451831	NM_001674	Hs.460	activating transcription factor 3	4.7
	414522	AW518944	Hs.76325	slap II splicing factor SLU7	4.7
	427176	AW381569	Hs.40334	ESTs	4.7
10	441390	AI692560	Hs.131175	ESTs	4.7
	447382	AW027790	Hs.182261	ESTs	4.7
	431676	AI685464		gb:tl88f04.x1 NC1_CGAP_Pr28 Homo sapiens	4.7
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7
15	401519			C15000476*:gll12737279[refl]XP_012163.1]	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	4.6
	429467	NM_004477	Hs.203772	F5HD region gene 1	4.6
	414341	D80004	Hs.75909	KIAA0182 protein	4.6
20	408380	AF123050	Hs.44532	diubiquitin	4.6
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.6
	425907	AA365752	Hs.155965	ESTs	4.6
	419111	AA234172	Hs.137418	ESTs	4.6
	425840	AW978731	Hs.301824	hypothetical protein PRO1331	4.6
25	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.5
	427078	AI676062	Hs.111902	ESTs	4.5
	419326	W94915	Hs.42419	ESTs	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.5
	408705	AA312135	Hs.46967	HSPC034 protein	4.5
30	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.5
	449673	AA002064	Hs.18920	ESTs	4.5
	438440	AA807228	Hs.225161	ESTs	4.5
	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	4.5
35	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	4.5
	456974	M12529	Hs.169401	apolipoprotein E	4.4
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.4
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.4
	436420	AA443956	Hs.31595	ESTs	4.4
40	443250	AI041530	Hs.132107	ESTs	4.4
	411962	AA099050		gb:zk85d12.r1 Soares_pregnant_uterus_NbH	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II	4.4
45	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	4.4
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.4
	428328	AA426080	Hs.98489	ESTs, Weakly similar to I38022 hypotheti	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4
	436446	AW016809	Hs.119021	ESTs	4.3
50	450704	H85157	Hs.40696	ESTs	4.3
	438666	AW014493	Hs.126727	ESTs	4.3
	417308	H60720	Hs.81892	KIAA0101 gene product	4.3
	428826	AL048842	Hs.194019	atractin	4.3
	444212	AW503976	Hs.10649	basement membrane-induced gene	4.3
55	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3
	447858	AW080339	Hs.80426	ESTs	4.3
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.3
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	4.3
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
60	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.3
	417986	AA481003	Hs.97128	ESTs	4.3
	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	4.3
	408088	AW157022	Hs.343551	hypothetical protein FLJ22584	4.3
	410853	H04588	Hs.30469	ESTs	4.3
65	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.2
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-in	4.2
	408554	AA836381	Hs.315111	nuclear receptor co-repressorHDAC3 comp	4.2
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	4.2
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2
70	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.2
	429900	AA460421	Hs.30875	ESTs	4.2
	437672	AW748265	Hs.5741	flavohemoprotein b5?	4.2
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbMH19W	4.2
	450661	AW952160	Hs.146550	ESTs	4.2
75	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.2
	456804	AI421645	Hs.139851	caveolin 2	4.2
	414291	AI289619	Hs.13040	G protein-coupled receptor 86	4.2
80	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	4.2
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	4.2
	429570	BE242256	Hs.2441	KIAA0022 gene product	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	4.2
	443622	AI911527	Hs.11805	ESTs	4.1

	436576	AI458213	Hs.77542	ESTs	4.1
	443958	BE241880	Hs.10029	cathepsin C	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1
5	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.1
	421129	BE439899	Hs.89271	ESTs	4.1
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.1
	430383	AI861854	Hs.210778	hypothetical protein FLJ10989	4.1
10	431475	AI567669	Hs.40342	putative nuclear protein	4.1
	446468	AI765890	Hs.16341	MAWD binding protein	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.1
	404390			Target Exon	4.1
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	4.1
15	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	4.1
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.1
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.1
	433887	AW204232	Hs.279522	ESTs	4.1
20	436556	AI364997	Hs.7572	ESTs	4.1
	430157	BE348706	Hs.278543	ESTs	4.1
	451259	NM_006052	Hs.26146	Down syndrome critical region gene 3	4.1
	458776	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1
25	443646	AI085198	Hs.164226	ESTs	4.1
	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	4.1
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothe	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	4.0
	413275	W94748	Hs.48821	ESTs	4.0
30	418432	M14156	Hs.85112	Insulin-like growth factor 1 (somatomedi	4.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	4.0
	433409	AI278802	Hs.25661	ESTs	4.0
	452186	AA120761	Hs.28307	VW domain binding protein 4 (formin bind	4.0
	417187	AB011151	Hs.334659	hypothetical protein MGC14139	4.0
35	421921	H83363	Hs.6820	translocase of inner mitochondrial membr	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0
	415710	J04543	Hs.78637	annexin A7	4.0
	457794	AA689292	Hs.246850	ESTs	4.0
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	4.0
40	424401	H67220	Hs.169681	death effector domain-containing	4.0
	435905	AW997484	Hs.5003	KIAA0456 protein	4.0
	442731	AI868167	Hs.131044	ESTs	4.0
	418650	BE386750	Hs.86978	prolyl endopeptidase	3.9
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9
45	439394	AA149250	Hs.56105	ESTs	3.9
	442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	3.9
	436758	AW977167	Hs.155272	ESTs	3.9
	451030	H40697	Hs.181426	ESTs, Moderately similar to YSHUT threon	3.9
	405934			Target Exon	3.9
50	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.9
55	412978	AI431708	Hs.820	homeo box C6	3.9
	414962	AF273304	Hs.235376	XPMC2 protein	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	3.9
	449590	AA694070	Hs.268835	ESTs	3.9
	450203	AF097994	Hs.301528	L-tyrosine/alpha-aminoadipate aminotra	3.9
60	450899	T77447	Hs.177864	ESTs	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.8
	452588	AA889120	Hs.110637	homeo box A10	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	3.8
65	450506	NM_004460		fibroblast activation protein, alpha	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypothe	3.8
	410330	AW023630	Hs.159425	ESTs	3.8
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.8
	415156	X84908	Hs.78060	phosphorylase kinase, beta	3.8
70	422975	AA347720	Hs.122569	KIAA0264 protein	3.8
	403100			C20010277.g1[7296271]gb AA051562.1 (AE0	3.8
	422449	AF168418	Hs.116784	thyroid hormone receptor interactor 4	3.8
	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	3.8
	424806	AA382523	Hs.105689	MSTP031 protein	3.8
75	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0510	3.8
	432363	AA534489		gb nf76g11.1 NCI_CGAP_Co3 Homo sapiens	3.8
	443441	AW291196	Hs.92195	ESTs	3.8
	432529	AI989507	Hs.162245	ESTs	3.8
	432908	AI861896	Hs.304505	ESTs	3.8
80	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.8
	424855	AW204725	Hs.25560	ESTs	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	3.8

	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	3.8
	418821	AA436002	Hs.183161	ESTs	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.8
5	453160	AI263307	Hs.239884	H2B histone family, member L	3.8
	416072	AL110370	Hs.79000	growth associated protein 43	3.7
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked mol	3.7
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.7
10	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7
	417348	AI940507	Hs.318526	hypothetical protein FLJ12661	3.7
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	3.7
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	3.7
	448807	AI571940	Hs.7549	ESTs	3.7
15	413403	AA129105	Hs.198425	ESTs, Moderately similar to S65657 alpha	3.7
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	3.7
	449125	AI571439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.7
	408089	H59799	Hs.42644	thioredoxin-like	3.7
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.7
20	439209	AF087993	Hs.91954	ESTs	3.6
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	3.6
	431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	3.6
	456619	AV647917	Hs.107153	inhibitor of growth family, member 1-lik	3.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
25	411213	AA676939	Hs.69285	neuropilin 1	3.6
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
	415339	NM_015156	Hs.78398	KIAA0071 protein	3.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.6
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.6
30	452260	AA453208		RAB9, member RAS oncogene family	3.6
	439506	AI361238	Hs.41136	ESTs	3.6
	420077	AW512260	Hs.87767	ESTs	3.6
	451009	AA013140	Hs.115707	ESTs	3.6
	436473	AI193122	Hs.132275	ESTs	3.6
35	413198	AW157712	Hs.47534	ESTs, Weakly similar to I38022 hypotheti	3.6
	443067	AI077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.6
	433269	AI343543	Hs.126890	ESTs	3.6
40	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.6
	447033	AI357412	Hs.157601	ESTs	3.6
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6
45	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	3.5
	443399	AI452659	Hs.61153	proteasome (prosome, macropain) 26S subu	3.5
	401807			C7001350:gil6578126lgblAAAF17706.1jAF0496	3.5
	413979	BE218090	Hs.279453	ESTs	3.5
	414680	AA743331		hemoglobin, alpha 2	3.5
50	417380	T06809	Hs.332086	ESTs	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopolei	3.5
	445183	AB007877	Hs.12385	KIAA0417 gene product	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.5
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	446416	AV658299	Hs.163959	ESTs	3.5
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	3.5
	456719	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.5
60	432101	AI918950	Hs.123642	EphA3	3.5
	453565	BE298808	Hs.33363	DKFZP434N093 protein	3.5
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	3.5
	412922	M60721	Hs.74870	H2O (Drosophila)-like homeo box 1	3.5
	450066	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.5
65	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.5
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.5
	415528	R17236		gb:yg12c04.r1 Soares infant brain 1N1B H	3.5
	435613	AW404075	Hs.42785	DC11 protein	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	3.5
70	409068	AW236991	Hs.102495	ESTs, Moderately similar to I38022 hypot	3.5
	439132	H72803	Hs.38363	ESTs	3.5
	451173	AI765082	Hs.48317	ESTs	3.5
	422673	N59027		gb:yy59d111.r1 Soares fetal liver spleen	3.4
	401597	AA172106		Rag C protein	3.4
75	401744			Target Exon	3.4
	432723	D29677	Hs.3085	KIAA0054 gene product; Helicase	3.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	3.4
	450628	AW382884	Hs.204715	ESTs	3.4
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.4
80	435411	AW444619	Hs.138211	ESTs	3.4
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.4
	437158	AW090198		KIAA1150 protein	3.4
	416375	H95567	Hs.124700	ESTs	3.4
	419441	AW023731	Hs.274368	MSTP032 protein	3.4

5	432741	AI72358	Hs.185118	ESTs, Moderately similar to A37413 calbl	3.4
	439192	AW970536	Hs.105413	ESTs	3.4
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	3.4
	428466	AF151063	Hs.184456	hypothetical protein	3.4
	447397	BE247676	Hs.18442	E-1 enzyme	3.4
10	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	3.4
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.4
	424779	AL046851	Hs.153053	CD37 antigen	3.4
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	3.4
15	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.4
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.4
	414671	AA832479	Hs.72080	ESTs	3.4
	431689	AA305688	Hs.267695	UDP-GalbetaGlcNAc beta 1,3-galactosyltr	3.4
	444480	AI150730	Hs.265640	ESTs, Moderately similar to A47582 B-cel	3.4
20	403389			C3001393*gi 3327090 dbj BAA31613.1 (AB	3.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	3.3
	408374	AW025430	Hs.155591	forkhead box F1	3.3
	410494	M36564	Hs.64016	protein S (alpha)	3.3
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.3
25	433505	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	3.3
	400277			Eos Control	3.3
	411031	W37943	Hs.34892	KIAA1323 protein	3.3
	417285	AW993524	Hs.43148	ESTs	3.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.3
30	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3
	443912	R37257	Hs.184780	ESTs	3.3
	445270	AI762154	Hs.54982	Homo sapiens cDNA FLJ14014 fis, clone HE	3.3
	425836	AW955696	Hs.90960	ESTs	3.3
35	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	3.3
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALL5_HUMAN A	3.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.3
	436499	AJ276678	Hs.283102	HEF like Protein	3.3
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3
40	426848	H72531	Hs.36190	ESTs	3.3
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	3.3
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.3
45	430280	AA361258	Hs.237868	interleukin 7 receptor	3.3
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	3.3
	453548	AL079983	Hs.116774	Integrin, alpha 1	3.3
	451367	AA923729	Hs.26322	cell cycle related kinase	3.2
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	3.2
50	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	3.2
	400658			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
	410366	AI267589	Hs.302689	hypothetical protein	3.2
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.2
55	421246	AW582962	Hs.102897	CGI-47 protein	3.2
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2
	439047	AW979177		gb:EST391287 MAGE resequences, MAGP Homo	3.2
	444451	AV650179	Hs.282431	ESTs	3.2
60	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	406973	M34996	Hs.198253	major histocompatibility complex, class	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	3.2
	406247			Target Exon	3.2
65	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	3.2
	412639	AW961284	Hs.296235	ESTs	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.2
	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2
70	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	455473	AW984788		gb:RC1-HN0015-120400-021-c07 HN0015 Homo	3.2
	441683	BE564214	Hs.102946	ESTs	3.2
	417386	AL037228	Hs.82043	D123 gene product	3.2
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	3.2
75	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	3.2
	422473	U94780	Hs.117242	meningioma expressed antigen 6 (coiled-c	3.2
	407816	AW500857	Hs.40137	anaphase-promoting complex 1; meiotic ch	3.2
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2
80	448944	AB014605	Hs.22599	atrophin-1 Interacting protein 1; activi	3.2
	435129	AI381659	Hs.267086	ESTs	3.2
	424894	H83520	Hs.153678	reproduction 8	3.2
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.2
	410185	BE294068	Hs.737	immediate early protein	3.2
	451149	AL047586	Hs.10283	RNA binding motif protein 8B	3.2
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	3.2
	411954	AA652523	Hs.269496	ESTs, Weakly similar to I38022 hypotheti	3.2

	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	3.2
	444489	AI151010	Hs.157774	ESTs	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2
	452413	AW082633	Hs.212715	ESTs	3.1
5	409390	AI927212	Hs.3734	ESTs	3.1
	453078	AF053551	Hs.31584	melaxin 2	3.1
	453024	AW846787		gb:QV3-CT0194-181099-004-e01 CT0194 Homo	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	3.1
	441124	T97717	Hs.119563	ESTs	3.1
10	416128	AA173632		CDC14 (cell division cycle 14, S. cerevi	3.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.1
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	3.1
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.1
15	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	3.1
	427399	NM_014883	Hs.177654	KIAA0914 gene product	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	3.1
	442906	AW296888	Hs.170939	ESTs	3.1
	445840	AI277811	Hs.146291	ESTs	3.1
20	446084	AL137658	Hs.13768	Homo sapiens mRNA; cDNA DKFZp434i1216 (f	3.1
	435293	AI040777	Hs.117170	ESTs	3.1
	400750			Target Exon	3.1
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	3.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.1
25	409558	BE253407	Hs.72363	Homo sapiens mRNA for FLJ00116 protein,	3.1
	400194			NM_003763:Homo sapiens syntaxin 16 (STX1	3.1
	400479			Target Exon	3.1
	402895			ENSP00000252117:Myelin transcription fac	3.1
	403423			Target Exon	3.1
30	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1
	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1
	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	430519	AF129534	Hs.49210	F-box only protein 4	3.1
35	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypothe	3.1
	422481	AL050163	Hs.117339	DNAX-activation protein 10	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	3.1
	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	3.1
40	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1
	431286	AW263476	Hs.44268	myelin gene expression factor 2	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	3.1
	408051	AI623351	Hs.172148	ESTs	3.1
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.1
45	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
	414279	AW021691		GCN5 (general control of amino-acid synt	3.1
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	420154	AI093155	Hs.95420	JM27 protein	3.1
50	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	3.1
	453293	AA382267	Hs.10653	ESTs	3.1
	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.0
	441527	W19504	Hs.7884	solute carrier family 21 (organic anion	3.0
55	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	3.0
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	3.0
	411315	AW836547		gb:PM3-LT0032-030100-006-e08 LT0032 Homo	3.0
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypothe	3.0
	441401	AI824338	Hs.126891	ESTs	3.0
60	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	3.0
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypothe	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	3.0
65	421786	AI188653	Hs.21351	ESTs	3.0
	433285	AW975944	Hs.237396	ESTs	3.0
	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA10	3.0
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	3.0
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	3.0
70	445345	AW003850	Hs.12532	chromosome 1 open reading frame 21	3.0
	450671	AI356987	Hs.43086	ESTs, Weakly similar to A45010 X-linked	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	434953	BE049102	Hs.179982	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.0
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.0
75	428130	AW444985	Hs.77603	ESTs	3.0
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	3.0
	445784	AI253155	Hs.146065	ESTs	3.0
	446677	AI800311	Hs.156291	ESTs	3.0
	426448	RO6054		gb:ye89g07.r1 Soares fetal liver spleen	3.0
80	445921	AW015211	Hs.146181	ESTs	3.0
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.0
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	3.0
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.0
	435907	AW304025	Hs.258397	ESTs	3.0

451102	AA015583	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (I	3.0
416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochondrion)	3.0
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	3.0
450580	N40087		ESTs	3.0

TABLE 62B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410531	1207200_1	AW752953 H88044 BE156092
410886	1225822_1	AW809324 BE144977 BE144956
411315	1238570_1	AW836547 AW836513 AW836587
411962	126744_1	AA099050 AA099526 T47733
414279	143227_1	AW021691 AI537404 R45431 AI333439 AI741845 AI674468 R44190 R52535 R52617 AI220925 AI979148 AI744688 AW242437 AA618148
414680	147525_1	AI983837 AA399623 AI676204 AI420077 N24944 D51042 AA282786 AA137264 AW236107 AW769
415528	1539409_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288
416128	157163_1	AA708749 AA644620 AA652769 AA242975 AA151074 T19890
416882	162718_1	R17236 R52580 F11642
422673	219674_1	AA173632 AI174858 AA581361 AI700024 AA173988 BE165417 AI366964
426448	267323_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
430935	325772_1	AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
430968	326269_1	N59027 AA314694 N53937 R08100
431304	331286_1	R06054 AA378789 AW956453
431676	336411_1	AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
432125	341776_1	AW972830 AA527647 AA489820 AA570362
432363	345469_1	BE157283 BE157287 AA502438
437158	43392_5	AI685464 AW971336 AA513587 AA525142
437866	44433_2	AW972667 AA526539 AI057032 AW167842
439047	468139_1	AA534489 AW970240 AW970323
439518	47334_1	AW090198 AW173544 AW439860 AW007307 AI762577 W86516 AA160485 AA974203 AI589521 AW451857 AW450602 AI702529 AA630766
450506	836_1	AI801808 AW611634 AI393606 AW235356 AW000736 AW468599 AI582546 AA962057 AA523012 AW51
450580	83929_1	AA156781 AW293839 U52054 AA024953 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
452260	9074_1	AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA04
453024	944876_28	AW979177 AA846994 AA829672
454573	1292917_1	W76326 AF086341 W72300
456719	222707_1	NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772
		AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296
		N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
		AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
		AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228
		BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI
		AW846787 AW903370 AW903378 AW752032 AW839052 AW839051 AW839054 AW839058 AW903374 AW839045 AW903373 AW903352
		AW839043 AW839049 AW903372 AW846755 AW846767 AW903368 AW846766 BE146826 AW839056 AW846802 AW
		AW984788 AW984816 AW984811 AW984807 AW984819 AW984790 AW984782 AW984784 AW984780 AW984814 AW984795 AW984793
		AW984789 AW984823 AW984801 AW984802 AW984800 AW984799 AW984825 AW984792 AW984821 AW984820 AW
		Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE602530 Z25032 AA805324 AA449241 AI651825 AI264863
		AW196918 AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW2

TABLE 62C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400479	8439786	Minus	115386-116348
400658	8118459	Minus	73525-73644
400750	8118067	Plus	198991-199168,199316-199548
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401597	3293210	Plus	65838-66031
401744	2576349	Plus	14595-14751
401807	7331536	Plus	152325-152912
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402802	3287166	Minus	53242-53432
402895	9967547	Plus	85537-85671,86379-86469
403100	8954402	Minus	13683-13874
403389	9438331	Minus	163415-163634
403423	7105492	Plus	69340-69615
403851	7708872	Plus	22733-23007
404390	8887030	Minus	39824-40072
405141	8980911	Plus	99861-100054
405934	6758795	Plus	159913-160605
406038	8389537	Plus	37764-37877
406247	7417725	Minus	46234-46461

5

Table 63A lists about 366 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2.5. The "average" normal prostate level was set to the 75th percentile of normal prostate tissues. The "average" prostate cancer level was set to the 75th percentile amongst tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

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TABLE 63A: ABOUT 366 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

15

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of normal prostate tissue to prostate tumor tissue

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Pkey	ExAccn	Unigene ID	Unigene Title	R1
425932	M81650	Hs.1968	semenogelin I	89.4
407245	X90568	Hs.172004	titin	35.4
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	32.2
426752	X69490	Hs.172004	titin	29.5
400440	X83957	Hs.83870	nebulin	20.7
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	13.9
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	12.0
420813	X51501	Hs.99949	prolactin-induced protein	11.8
415337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	10.2
407013	U35637		gb:Human nebulin mRNA, partial cds	9.1
433331	A1738815	Hs.117323	ESTs	8.9
432117	AL036195	Hs.2909	protamine 1	8.3
453863	X02544	Hs.572	orosomucoid 1	8.2
431847	A1791314		gb:aa46g12y5 Stratagene lung carcinoma	7.4
408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	7.1
448059	A459021	Hs.170425	ESTs	6.8
403612			Target Exon	6.4
405001	U58196		interleukin enhancer binding factor 1	6.2
441490	N46901	Hs.266720	ESTs	6.2
435805	AW470260	Hs.48496	ESTs	6.0
401917	AL050149		RAN binding protein 3	5.9
455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	5.7
450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	5.6
404606			Target Exon	5.6
432326	A1280308	Hs.274361	amiloride-sensitive cation channel 2, na	5.5
459708	AA776881	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	5.5
440808	AK001339	Hs.7432	hypothetical protein FLJ10477	5.5
458339	AW976853	Hs.172843	ESTs	5.2
454278	AF217525	Hs.49002	Down syndrome cell adhesion molecule	5.2
417032	AA192469	Hs.271838	ESTs	5.2
434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
439175	AF086021	Hs.271113	ESTs	5.0
439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	4.9
417364	N73749	Hs.222475	ESTs	4.9
400831			C11000936[gil3746443]gb AAC63969.1 (AF0	4.8
416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	4.8
442082	R41823	Hs.7413	ESTs	4.8
452625	AA724771	Hs.61425	ESTs	4.7
440965	A1523846	Hs.169859	ESTs	4.7
456815	NM_013348	Hs.144011	potassium inwardly-rectifying channel, su	4.7
430611	AA837120	Hs.156481	ESTs	4.6
415981	R35694		gb:yg67b04.r1 Soares infant brain 1NIB H	4.6
441040	AW449782	Hs.178903	ESTs	4.6
442764	A1762254	Hs.131122	ESTs	4.6
411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	4.6
433081	Z85986	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	4.6
401896			Target Exon	4.5
445323	AW207282	Hs.213049	ESTs	4.5
458895	A1535663	Hs.39379	ESTs	4.5
417729	Z43798	Hs.6777	ESTs	4.5
431627	AW609720	Hs.265540	HSPC042 protein	4.5
420721	AA927802	Hs.159471	ZAP3 protein	4.4
449519	W04244	Hs.49829	ESTs	4.4
442089	A1801500	Hs.128457	ESTs	4.4
436781	A1914535	Hs.221377	ESTs	4.4
402797			Target Exon	4.4
404267			NM_004348*:Homo sapiens runt-related tra	4.3
442931	A1024376	Hs.150473	ESTs	4.3
418626	AW299508	Hs.135230	ESTs	4.3
423772	AA306637		EAP30 subunit of ELL complex	4.3
457138	AA428240	Hs.126083	ESTs	4.3
436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, seq	4.3
458840	A1580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	4.3
403649			Target Exon	4.2
435866	AA704538	Hs.119740	ESTs	4.2
423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	4.2

	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.2
	400164			Eos Control	4.1
	435519	AI218950	Hs.125461	hypothetical protein FLJ11539	4.1
5	425094	AJ955956	Hs.21417	ESTs	4.1
	415928	R46799	Hs.23966	ESTs	4.1
	415746	AA167670	Hs.21413	solute carrier family 12, (potassium-chl	4.1
	426663	AK028767	Hs.262603	ESTs	4.1
	453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmel2)	4.1
10	404260			Target Exon	4.0
	453412	AJ003290		gb:AJ003290 Selected chromosome 21 cDNA	4.0
	401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	4.0
	415925	H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	4.0
	402817	H24185		hypothetical protein	4.0
15	449233	BE048401	Hs.196511	ESTs	3.9
	435457	AA682421	Hs.59125	ESTs	3.9
	444105	AW189097	Hs.166597	ESTs	3.9
	430610	AJ821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.9
	411320	AW836646		gb:PM3-LT0032-090100-008-e05 LT0032 Homo	3.8
20	409679	BE250521		ras homolog gene family, member A	3.8
	415386	Z43087		gb:HSC13A121 normalized infant brain cDN	3.8
	446175	AL036568	Hs.291	glutaryl aminopeptidase (aminopeptidase	3.8
	459707	AA631362	Hs.120866	gb:mp86b01.s1 NCI_CGAP_Thy1 Homo sapiens	3.8
	406917	X65964		gb:H.sapiens nestin gene.	3.8
25	455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo	3.8
	443313	AI796730	Hs.55513	ESTs	3.8
	452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W	3.8
	400499			C10001858:gil6679124[ref]NP_032759.1] ne	3.7
	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	3.7
30	408229	AW176091		gb:QV0-BT0107-250899-007-b08 BT0107 Homo	3.7
	427318	AF186081	Hs.175783	zinc transporter	3.7
	417620	R02530	Hs.191198	ESTs	3.7
	404660			C9000841*:gil12654691[gb]AAH01185.1[AAH0	3.7
	409144	AW341187	Hs.279714	ESTs	3.7
35	436524	AA922236	Hs.221037	ESTs	3.7
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.7
	418833	AW974899	Hs.292776	ESTs	3.7
	424887	AA348112	Hs.259461	ESTs	3.7
	404984			Target Exon	3.7
40	454549	AW806910		gb:QV4-ST0023-160400-172-f04 ST0023 Homo	3.7
	426736	AA431615	Hs.130722	ESTs	3.7
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962, mRNA, comp	3.6
	438040	AI222422	Hs.121846	ESTs	3.6
	443618	T82009	Hs.300700	hypothetical protein FLJ20727	3.6
45	442097	AW015799	Hs.128474	ESTs	3.6
	435186	AL119470	Hs.145631	ESTs	3.6
	429853	AB020625	Hs.225949	butyrophilin-like 3	3.6
	456521	AW373450	Hs.286212	hypothetical protein FLJ11729	3.6
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	3.6
50	400749			NM_003105*:Homo sapiens sorilin-related	3.6
	450295	AI766732	Hs.210628	ESTs	3.5
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	3.5
	434378	AA631739	Hs.335440	EST	3.5
	421342	AA504749		gb:aa63108.r1 NCI_CGAP_GCB1 Homo sapiens	3.5
55	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.5
	429043	AI824977	Hs.145319	ESTs	3.5
	438211	T08401	Hs.290856	ESTs, Moderately similar to ALU4_HUMAN A	3.5
	405258			Target Exon	3.4
	440207	AI371978	Hs.128326	ESTs	3.4
60	445045	AI652676	Hs.147256	ESTs	3.4
	406177			Target Exon	3.4
	438535	L09078		gb:Homo sapiens mRNA fragment	3.4
	405735			ENSP00000252164*:KIAA1578 protein (Fragm	3.4
	445797	AI253414		gb:aaq14f04.x1 Stanley Frontal NS pool 2	3.4
65	444286	AI625304	Hs.190312	ESTs	3.4
	442027	AI652926	Hs.128395	ESTs	3.4
	447889	AW469180	Hs.346398	ESTs	3.4
	405152			Target Exon	3.4
	402460			C1001261*:gil2695979[emb]CAA70854.1] (Y0	3.4
70	448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	3.4
	450588	AA010319	Hs.60389	ESTs	3.4
	447600	AI420990		ESTs	3.4
	406085			Target Exon	3.3
	417959	AW977642	Hs.291742	ESTs	3.3
	418672	L44284	Hs.12915	ESTs	3.3
75	446593	W79572	Hs.13277	hypothetical protein FLJ22054	3.3
	446516	AW996692	Hs.257557	ESTs, Weakly similar to I38022 hypotheti	3.3
	415896	H08311	Hs.14822	ESTs, Weakly similar to I78885 serine/th	3.3
	410140	AL134435	Hs.247837	neurexin 3	3.3
80	458539	AI733837	Hs.145661	ESTs	3.3
	422399	AW410380	Hs.116056	mesenchymal stem cell protein DSC43	3.3
	413381	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo	3.3
	429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	3.3
	428561	AW973652	Hs.283105	ESTs	3.2

5	445608	AI830851	Hs.200014	ESTs, Weakly similar to ACIDIC PROLINE-R	3.2
	449017	AW002425	Hs.224142	ESTs	3.2
	415908	H08623	Hs.22833	ESTs	3.2
	457733	AW974812	Hs.291971	ESTs	3.2
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	3.2
10	428134	AA421773	Hs.161008	ESTs	3.2
	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo	3.2
	429973	AI423317	Hs.164680	ESTs	3.2
	418092	R45154	Hs.338439	ESTs	3.2
	411356	H45377		gb:yn99h03.r1 Soares adult brain N2b5HB5	3.1
15	443366	AI053501	Hs.278869	ESTs, Moderately similar to 2109260A B c	3.1
	422069	AJ010063	Hs.343603	filin-cap (telethonin)	3.1
	420778	AW970512		gb:EST382593 MAGE resequences, MAGK Homo	3.1
	403451			Target Exon	3.1
	451686	AA059246	Hs.110293	ESTs	3.1
20	423637	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	3.1
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	3.1
	450049	AI681234	Hs.258509	EST	3.1
	428656	AB037798	Hs.188790	KIAA1377 protein	3.1
	401278			Target Exon	3.1
25	418087	AA961613	Hs.127838	ESTs	3.1
	421813	BE048255		gb:tz49b05.y1 NCL_CGAP_Bm52 Homo sapien	3.1
	402490			Target Exon	3.1
	448001	AW293237	Hs.202037	ESTs	3.1
	445316	AI219833	Hs.166767	ESTs	3.1
30	405150			Target Exon	3.1
	413784	BE165819	Hs.207684	ESTs	3.1
	425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
	433224	AB040919	Hs.210958	KIAA1486 protein	3.1
	421894	AI418464	Hs.190836	ESTs	3.1
35	419386	AA236867		ESTs, Weakly similar to I38022 hypothei	3.1
	402422			Target Exon	3.1
	435849	BE305242	Hs.16098	claudin 2	3.1
	405422			ENSP00000216658*:HYPOTHETICAL 133.5 kDa	3.0
	420543	AA278221	Hs.173344	ESTs	3.0
40	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.0
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.0
	406600			Target Exon	3.0
	408025	AI692784	Hs.41767	PTD002 protein	3.0
	426349	AI308855	Hs.301497	arginyltransferase 1	3.0
45	444576	AI400974	Hs.182045	ESTs	3.0
	430661	AC005551	Hs.130714	Homo sapiens HSPC323 mRNA, partial cds	3.0
	441335	BE222470	Hs.150825	ESTs, Weakly similar to antigen NY-CO-33	3.0
	459647	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 1	3.0
	435713	AA699313	Hs.114071	ESTs	3.0
50	407275	AI364186		gb:qw34h07.x1 NCL_CGAP_UI4 Homo sapiens	3.0
	456103	Z39430	Hs.72350	ESTs	3.0
	435200	AA670310	Hs.145903	ESTs	3.0
	449245	AI635539	Hs.224296	ESTs	3.0
	428132	AA421765		gb:zu24g02.s1 Soares_NhHMPu_S1 Homo sapi	3.0
55	443454	AI057494	Hs.133421	ESTs	2.9
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	2.9
	411944	AW877139		gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.9
	432718	AA563943	Hs.244371	ESTs	2.9
	435534	AA830927	Hs.117306	ESTs	2.9
60	430348	AA476915	Hs.189225	ESTs, Weakly similar to I38022 hypothei	2.9
	410289	AW901618	Hs.61835	Homo sapiens mRNA; cDNA DKFZp7611071 (fr	2.9
	453126	AA032155	Hs.61622	ESTs	2.9
	459421	AA233154	Hs.12532	chromosome 1 open reading frame 21	2.9
	441543	AI733014	Hs.269715	ESTs	2.9
65	442252	AI733395	Hs.129124	ESTs	2.9
	419254	AI469453	Hs.222760	ESTs	2.9
	443727	Z25389	Hs.18459	ESTs	2.9
	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	2.9
	453898	AW003512	Hs.232770	arachidonate lipooxygenase 3	2.9
70	415098	D59687		gb:HUM056E10B Clontech human fetal brain	2.9
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.9
	406398			Target Exon	2.9
	433942	AW272166	Hs.123465	ESTs	2.9
	400461			Target Exon	2.9
75	442640	AI205646	Hs.147220	ESTs	2.9
	438814	AA826278	Hs.249596	ESTs	2.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.9
	422482	AI439905	Hs.344476	gb:ti57g08.x1 NCL_CGAP_Lym12 Homo sapien	2.8
	407142	AA412535		gb:zi199b10.s1 Soares_testis_NHT Homo sap	2.8
80	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527 hypothei	2.8
	442907	AI023763	Hs.79707	ESTs	2.8
	456075	N73442		gb:yz31h09.r1 Soares_multiple_sclerosis_	2.8
	438690	AA815031	Hs.123598	ESTs	2.8
	452570	AW861293	Hs.336940	Homo sapiens cDNA: FLJ20861 fis, clone A	2.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.8
	447556	AI885187	Hs.210710	ESTs, Moderately similar to ALU6_HUMAN A	2.8
	451632	BE005934	Hs.310625	EST	2.8

	426481	AW963941		gb:EST376014 MAGE resequences, MAGH Homo	2.8
	401656			Target Exon	2.8
	407269	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.8
5	435754	AA700752	Hs.117341	ESTs	2.8
	433565	AA599763	Hs.112520	ESTs	2.8
	451004	AA044967		gb:z53409.r1 Soares retina N2b4HR Homo	2.8
	425223	AA352825	Hs.146065	gb:EST60880 Activated T-cells XX Homo sa	2.8
	405770			NM_002362:Homo sapiens melanoma antigen,	2.8
10	456227	T84239	Hs.189788	ESTs	2.8
	454445	AW749432		gb:RC3-BT0386-301299-011-a09 BT0386 Homo	2.8
	419494	W01060	Hs.34382	ESTs	2.8
	427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	2.8
	428079	AA421020	Hs.208919	ESTs	2.7
15	406337			C14000021:gl 7242973 dbj BAA92547.1 (AB	2.7
	401884			Target Exon	2.7
	406881	D16154		gb:Human gene for cytochrome P-450c11, e	2.7
	428986	AA442884	Hs.201201	ESTs	2.7
	450044	R66444	Hs.51891	ESTs	2.7
20	403630			C3001708*gl 4758028 ref NP_004360.1 co	2.7
	445514	AI241280	Hs.148906	ESTs	2.7
	446362	AW612481	Hs.104105	ESTs	2.7
	432492	AW275110	Hs.271106	ESTs	2.7
	430889	U22491	Hs.248117	G protein-coupled receptor 7	2.7
25	434316	AW411330	Hs.118796	annexin A6	2.7
	413155	BE067952		gb:CM0-BT0365-061299-122-g09 BT0365 Homo	2.7
	433329	AF015041	Hs.199291	numb (Drosophila) homolog-like	2.7
	446523	NM_003063	Hs.334629	sarcoplasmic	2.7
	449923	BE258051		gb:601111034F1 NIH_MGC_16 Homo sapiens c	2.7
30	453826	AL138129		gb:DKFZp547F152_r1 547 (synonym: hbrf1)	2.7
	405678			CX001454:gl 8393794 ref NP_058681.1 myo	2.7
	432789	D26361	Hs.3104	KIAA0042 gene product	2.7
	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	449109	AW270992	Hs.120949	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
35	436255	F01143	Hs.284284	zinc finger 1111	2.7
	415984	R19046	Hs.5010	gb:yg21f11.r1 Soares infant brain 1N1B H	2.7
	402844			C1000118*gl 9951913 ref NP_052832.1 pr	2.7
	456666	AA452512	Hs.76719	U6 snRNA-associated Sm-like protein	2.7
	414620	AA150120	Hs.244621	ribosomal protein S14	2.7
40	404979			Target Exon	2.7
	412318	AW936911	Hs.325729	hypothetical protein MGC11082	2.7
	424361	AK001551	Hs.145944	Homo sapiens cDNA FLJ110689 fis, clone NT	2.7
	412542	AW961516	Hs.95097	ESTs	2.7
	441975	AW173248	Hs.344285	EST	2.7
45	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
	457861	AW450205	Hs.305890	BCL2-like 1	2.7
	439204	AF087987	Hs.42695	EST	2.7
	415642	U19878	Hs.336224	transmembrane protein with EGF-like and	2.7
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.7
50	443359	AI792583	Hs.135354	ESTs	2.7
	447336	AW139383	Hs.245437	ESTs	2.7
	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.7
	422185	AL117530	Hs.112822	DKFZP434B172 protein	2.7
	436030	R02287	Hs.121052	ESTs	2.7
55	449589	AW752437	Hs.135258	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6
	436092	AI345995	Hs.127383	ESTs	2.6
	415054	AI733907		gb:zo86h09.y5 Stratagene ovarian cancer	2.6
	412908	AA121913	Hs.293896	pregnancy-associated plasma protein-E	2.6
	409583	AW440117	Hs.256879	ESTs	2.6
60	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.6
	435383	R61083		wee1 (S. pombe) homolog	2.6
	426629	AI203933	Hs.97142	ESTs	2.6
	415831	H15145	Hs.30509	ESTs	2.6
	412281	AI810054	Hs.14119	ESTs	2.6
65	434898	AW500458	Hs.29956	KIAA0460 protein	2.6
	422229	AF134414	Hs.113271	ABO blood group (transferase A, alpha 1-	2.6
	447518	T80061		gb:yd22f08.s1 Soares fetal liver spleen	2.6
	458546	AI215667	Hs.175044	ESTs	2.6
	438548	AA813125	Hs.146335	ESTs	2.6
70	450399	AW511049	Hs.202007	ESTs	2.6
	420833	R47948	Hs.188732	ESTs	2.6
	453903	AW299606	Hs.232777	ESTs	2.6
	443650	AI698330	Hs.151444	ESTs	2.6
	427419	NM_000200	Hs.177888	histatin 3	2.6
75	423741	AA330362		gb:EST34074 Embryo, 12 week II Homo sapi	2.6
	451577	N69101	Hs.40730	ESTs	2.6
	441358	AW173212	Hs.129041	ESTs	2.6
	402706			Target Exon	2.6
	436054	AI076262	Hs.119813	ESTs	2.6
80	402749			Target Exon	2.6
	442472	AW806859		gb:MR0-ST0020-081199-004-c03 ST0020 Homo	2.6
	445762	AI734002	Hs.264590	ESTs, Moderately similar to ALU5_HUMAN A	2.6
	441420	AA932872		gb:zo57d07.s1 NCL_CGAP_Lu5 Homo sapiens	2.6
	405564			Target Exon	2.6

	405003		Target Exon	2.6	
	459584	AI910884	Hs.346429	ESTs	2.6
	441597	AW135032	Hs.203625	ESTs	2.6
5	411280	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	2.6
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfam	2.6
	445060	AA830811	Hs.282908	ESTs	2.6
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.6
	428717	T78001	Hs.133546	hypothetical protein FLJ21120	2.6
10	401716			C16000902:gi403440[gb]AAA73168.1] (M817	2.6
	416628	W03955		gb:za62d04.r1 Soares fetal liver spleen	2.6
	443864	N37059	Hs.36250	ESTs, Weakly similar to I38022 hypothe	2.6
	440702	AA904178	Hs.148233	ESTs	2.6
	456310	AA225522		gb:nc25c06.r1 NCI_CGAP_Pr1 Homo sapiens	2.6
15	451255	AA020857	Hs.90744	ESTs	2.6
	455737	BE072246		gb:QV4-BT0536-271299-059-b12 BT0536 Homo	2.6
	445326	AI220072	Hs.344672	ESTs	2.6
	408432	AW195262		gb:cm67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.6
	445874	BE326671	Hs.170058	ESTs	2.6
20	441063	AA913819	Hs.188025	ESTs	2.6
	455505	AW970640	Hs.309071	ESTs	2.6
	453491	AL040177		gb:DKFZp434F0213_r1 434 (synonym: htes3)	2.6
	455048	AW852749		gb:PM1-CT0247-080100-008-h09 CT0247 Homo	2.6
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	2.6
25	444130	AI125263	Hs.170410	ESTs	2.5
	422210	BE269319	Hs.171937	steroid dehydrogenase-like	2.5
	424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase kina	2.5
	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.5
	400427	AB044934	Hs.287388	histamine H4 receptor	2.5
30	410443	BE062906	Hs.28338	KIAA1546 protein	2.5
	455210	AW866599		gb:QV4-SN0024-210400-181-b10 SN0024 Homo	2.5
	429909	AW977090	Hs.184860	CGI-203 protein	2.5
	441191	AI693930	Hs.148816	ESTs	2.5
	413489	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo	2.5
35	448215	N34740	Hs.6658	ESTs	2.5
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	2.5
	447610	AW296286	Hs.255534	ESTs	2.5
	450724	R55428		gb:yf79b05.r1 Soares breast 2NbHBst Homo	2.5
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	2.5
40	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	2.5
	447730	AI421251	Hs.114085	Homo sapiens mRNA for KIAA1755 protein,	2.5
	434152	AI792665	Hs.291190	ESTs	2.5
	412671	AW977734	Hs.37931	gb:EST389963 MAGE resequences, MAGO Homo	2.5
	456401	W28146		gb:43f11 Human retina cDNA randomly prim	2.5
45	404678			Target Exon	2.5
	408520	AA225063	Hs.161614	ESTs	2.5
	411332	AW837212		gb:QV2-LT0038-140300-081-c01 LT0038 Homo	2.5
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	2.5
	429906	AL080137	Hs.193743	ESTs	2.5
50	433712	AF090887	Hs.306562	Homo sapiens clone HQ0085	2.5
	438353	BE539951	Hs.306996	Homo sapiens, clone IMAGE:3447073, mRNA,	2.5
	446224	AW450551	Hs.13308	ESTs	2.5

TABLE 63B

55	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
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	409579	114787_1
65	410483	1204995_1
	411320	1238624_1
	411332	1239102_1
	411356	1240273_1
	411426	1245515_1
70	411829	1260309_1
	411944	1266482_1
	413155	1351148_1
	413381	1365950_1
	413489	1373392_1
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	415098	1522174_1
	415131	1523680_1
	415386	1535560_1
	415881	1564242_1
80	416628	1604848_1
	416935	163179_1
	419386	184356_1
	419896	1888662_1
	420778	196389_1
		AW176091 H24234
		AW195262 R27868 AW811262
		BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AI221491 AA194239 D63046 AA193426 AA773243 AA193293
		BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
		AW836646 AW836580 AW836610 AW836636 AW836603 AW836632
		AW837212 AW837408 AW837265 AW837380 AW837213 AW837411 AW837418
		H45377 H21137 AW838640
		BE141714 AW845993 AW845989
		AW865749 BE179419 BE179492
		AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
		BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067946
		BE090690 BE090688 BE090681 BE090693 BE090675
		BE144228 BE144291
		AI733907 AA159708 AI732614
		D59687 D59694 D59656 D59589
		D61119 D81508 D81734
		Z43087 F07410 H15506 H54108 R95033 H98000
		R35694 H12035 R53312
		W03955 H82332 H69247 H72486
		AA190712 AA190665 AA252564
		AA236867 AA237068 AA354236 AW957759 H08961
		Z99362 Z99363
		AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481

5	421342	201427_1	AA504749 AA287498
	421813	207654_1	BE048255 AA313083 AA298419
	422731	220507_1	AL138411 AL138412 AA315860
	423741	231582_1	AA330362 AW962525 H87796
	423772	23188_1	AA306637 NM_007241 AF156102 BE388339 BE614027 AW935016 AA315261 AW376418 AW304951 AI859820 AA367436 AW516957 BE614519
			AI453152 AI453149 AI453139 AW168378 AI139491 AI538368 AW458227 AI680027 AW090513 AA662830 F30995 AI351985 AI424349 AW009599
			C02215 AI6525
	423871	232749_1	AA331906 AA332484
10	426481	267878_1	AW963941 AW963944 AA379825 AA379564
	428132	287430_1	AA421765 AA456076 AI290275 AA455579
	431847	338402_1	AI791314 AI791434 AA516511
	434407	385744_1	AW815333 AW815409 AA632563
	435383	405360_1	R61083 R13743 AA679174 AA679193 Z42903
	436190	41555_1	AK001059 AA633055
15	438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
	441420	516748_1	AA932872 W28068 W28643 T96110
	442472	543371_1	AW806859 AW806852 AF049582
	445797	650943_1	AI253414 AI366014 R34822
	447518	724787_1	T80061 AI382804
20	447600	728288_1	AI420990 AI399725 AI401757
	448516	766241_1	AW898595 AW898588 AW898590 AW898663 AW898592 AI525093
	449923	81926_1	BE258051 R45758 AA004732 BE255126
	450724	844585_1	R55428 AI820704 AI732283 R54983
25	451004	85453_1	AA044967 H86327 AA013079 AA058776 BE242713 AA019987
	452351	91233_1	AA025647 R45716 AW753786
	453412	966264_1	AJ003290 AJ003288 AW276947
	453491	969172_1	AL040177
	453752	979899_1	AL120800 BE378580
30	453826	982669_1	AL138129 AL138179 BE064231
	454445	1204468_1	AW749432 AW749434 R47332
	454549	1223789_1	AW806910 AW866461 AW866396 AW866373 AW866611 AW866616
	455048	1250599_1	AW852749 AW852755 AW852620
	455210	1260650_1	AW866599 AW866294 AW866468 AW866467
35	455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636
	455737	1353892_1	BE072248 BE072229 BE072225 BE072210 BE072211 BE072256 BE072211 BE072242
	455791	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
	455887	1380836_1	BE154173 BE154098 BE154096
	456075	1476756_1	N73442 R98100 BE410380
40	456310	177089_1	AA225522 AA225465 AI820979 AW973985 AI791935 AA558735
	456401	1844649_2	W28146 W28187

TABLE 63C

45	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
50	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	400461	9929654	Plus	32727-32846,32929-33051
	400499	9796071	Minus	148495-148806
55	400749	7331445	Minus	9162-9293
	400831	8576271	Minus	56502-57407
	401278	9799936	Plus	98428-98573
	401411	7799787	Minus	144144-144329
	401656	9100664	Minus	1-382
60	401716	6715703	Plus	174722-174911
	401884	8140731	Minus	89182-90053
	401896	8569194	Plus	115129-115294
	401917	9502466	Plus	25054-25229
	402422	9796344	Minus	32843-33008
65	402460	9796884	Minus	108901-109254,110246-110581,113613-113960
	402490	9797648	Plus	149982-150929
	402706	8894426	Minus	148640-148805
	402749	9212740	Minus	68787-68882,76602-76768
	402797	3421043	Minus	15758-15930
70	402817	6822166	Minus	48611-49012
	402844	9369286	Plus	54958-55313
	403451	9838240	Plus	77382-78300
	403612	8469060	Minus	94723-94859
	403630	8569999	Minus	13909-14466,15251-15760,16898-17431,41742-42440
75	403649	8705159	Minus	27141-27247
	404260	9366879	Plus	51396-51513
	404267	9581792	Minus	12209-12313,18241-18397
	404608	9212936	Minus	22310-23269
	404660	9797068	Plus	168215-168916
	404678	9797204	Plus	115196-115448
80	404979	4160139	Minus	87762-88217
	404984	6939882	Plus	87221-87505
	405001	6015406	Minus	104646-104819
	405150	9929758	Plus	126475-126773

5	405152	9965561	Minus	137662-137969
	405258	7329310	Plus	129930-130076
	405422	7243869	Minus	101938-102079, 102261-102443, 102896-103202
	405564	2114222	Minus	16766-17344
	405678	4079670	Plus	151821-152027
	405735	9931101	Minus	29854-29976
	405770	2735037	Plus	61057-62075
	406003	8247800	Plus	42079-42516
10	406085	9123888	Plus	18665-18843
	406177	7279760	Minus	18930-19148
	406337	9213455	Plus	90117-90337
	406398	9256276	Minus	118691-118959
	406600	8248616	Minus	36296-36610

15

Table 64A lists about 703 genes up-regulated in BPH compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

20

TABLE 64A: ABOUT 703 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO NORMAL ADULT TISSUES

25
 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of BPH tissue to normal adult body tissue

30	Pkey	ExAccn	Unigene ID	Unigene Title	R1
	420154	AI093155	Hs.95420	JM27 protein	49.6
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	47.2
	419526	AI821895	Hs.193481	ESTs	43.6
	432441	AW292425	Hs.163484	ESTs	42.7
35	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	30.2
	407202	N58172	Hs.109370	ESTs	26.1
	432101	AI918950	Hs.123642	EphA3	25.8
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	25.5
	425075	AA508324	Hs.1852	acid phosphatase, prostate	24.6
40	414569	AF109298	Hs.118258	prostate cancer associated protein 1	24.4
	410929	H47233	Hs.30643	ESTs	21.1
	400287	S39329	Hs.181350	kallikrein 2, prostatic	20.3
	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	19.8
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	18.6
45	415989	AI267700		ESTs	17.8
	426336	AA503115	Hs.183752	microseminoprotein, beta-	17.3
	450693	AW450461	Hs.203965	ESTs	16.7
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	16.7
	407168	R45175	Hs.117183	ESTs	15.5
50	408369	R38438	Hs.182575	solute carrier family 15 (H?? transport	15.5
	454119	BE549773	Hs.40510	uncoupling protein 4	14.5
	428819	AL135623	Hs.193914	KIAA0575 gene product	14.5
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	14.4
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	14.3
55	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	14.2
	433444	AW975324	Hs.128816	ESTs	13.8
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	13.5
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	12.9
60	401424			NM_001172:Homo sapiens arginase, type II	12.7
	432435	BE218886	Hs.282070	ESTs	12.5
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	12.3
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	12.0
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.9
65	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U04 Homo sapiens	11.8
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.7
	432473	AI202703	Hs.152414	ESTs	11.3
	410330	AW023630	Hs.159425	ESTs	11.2
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	11.2
70	452792	AB037765	Hs.30652	KIAA1344 protein	11.2
	418848	AI820961	Hs.193465	ESTs	10.9
	400292	AA250737	Hs.72472	BMP-R18	10.9
	433647	AA603367	Hs.222294	ESTs	10.8
	453160	AI263307	Hs.239884	H2B histone family, member L	10.8
75	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	10.6
	431474	AL133990	Hs.190642	CEGP1 protein	10.3
	429220	AW207206		ESTs	10.3
	428134	AA421773	Hs.161008	ESTs	10.2
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	10.1
80	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	9.8
	434792	AA649253	Hs.132458	ESTs	9.7
	433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	9.5
	428398	AI249368	Hs.98558	ESTs	9.4

	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	9.3
	407709	AA456135	Hs.23023	ESTs	9.3
	415293	R49462	Hs.106541	ESTs	9.1
5	429918	AW873986	Hs.119383	ESTs	9.1
	440260	AI972867	Hs.71130	copine IV	9.1
	453096	AW294631	Hs.11325	ESTs	9.1
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.8
10	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.8
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	453006	AI362575	Hs.303171	ESTs	8.7
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	8.7
	420424	AB033036	Hs.97594	KIAA1210 protein	8.7
15	450642	R39773	Hs.71130	copine IV	8.7
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	8.7
	428927	AA441837	Hs.90250	ESTs	8.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	8.5
	420345	AW295230	Hs.25231	ESTs	8.5
20	446336	AW815036	Hs.151251	ESTs	8.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.4
	428728	NM_016625	Hs.191381	hypothetical protein	8.3
	417169	R13550	Hs.246773	ESTs	8.2
	453387	AI990741	Hs.252809	ESTs	8.2
25	434666	AF151103	Hs.112259	T cell receptor gamma locus	8.1
	417958	AA767382	Hs.193417	ESTs	8.0
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	7.9
	444609	AW571659	Hs.278081	ESTs	7.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.8
30	433923	AI823453	Hs.146625	ESTs	7.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	7.7
	441690	R81733	Hs.33106	ESTs	7.6
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.6
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	7.5
35	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	7.5
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
	413597	AW302885	Hs.117183	ESTs	7.4
	404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
40	409557	BE182896	Hs.211193	ESTs	7.3
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.155689	ESTs	7.3
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	7.1
	449300	AI656959	Hs.346514	ESTs	7.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	7.1
45	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	430187	AI799909	Hs.156989	ESTs	7.0
	434217	AW014795	Hs.23349	ESTs	7.0
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	6.9
50	430188	AL049242	Hs.234794	Homo sapiens mRNA: cDNA DKFZp564B083 (fr	6.9
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	6.9
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	6.8
	426384	AI472078	Hs.303662	ESTs	6.8
	458509	AA654650	Hs.282906	ESTs	6.8
55	449821	AI671141	Hs.211122	ESTs	6.8
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.8
	443250	AI041530	Hs.132107	ESTs	6.7
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	6.7
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
60	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	6.6
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	6.5
	431467	N71831	Hs.256398	Homo sapiens mRNA: cDNA DKFZp434E0528 (f	6.5
	424433	H04607	Hs.9218	ESTs	6.5
65	450164	AI239923	Hs.63931	ESTs	6.5
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	6.5
	450497	H64159	Hs.15328	ESTs	6.5
	425312	AA354940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
70	440911	AA909536	Hs.143562	ESTs	6.4
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.3
	432600	AI821085		gb:ns95a12.y5 NCL_CGAP_Pr3 Homo sapiens	6.3
	435375	AI733610	Hs.187832	ESTs	6.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	6.3
75	431359	AW993522	Hs.292934	ESTs	6.2
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	6.1
	403667			Target Exon	6.1
	424846	AU077324	Hs.1832	neuropeptide Y	6.1
	439569	AW602166	Hs.222399	CEGP1 protein	6.1
80	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
	448004	AW451477	Hs.257456	ESTs	6.1
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.0
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	6.0
	415621	AI648602	Hs.55468	ESTs	6.0

	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	6.0
	442481	N99828		gbza32c04.r1 Soares fetal liver spleen	6.0
	432527	AW975028	Hs.102754	ESTs	5.9
	447156	AW274731	Hs.157920	ESTs	5.9
5	404003			Target Exon	5.9
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.9
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.9
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	5.9
10	438138	R98299	Hs.177502	ESTs	5.9
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.8
	434973	AW449285	Hs.313636	EST	5.8
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	5.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	5.8
	434485	AI623511	Hs.118567	ESTs	5.8
15	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	5.7
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	5.7
	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gbzv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
20	432966	AA650114	Hs.325198	ESTs	5.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	5.7
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	5.7
	425810	AI923627	Hs.31903	ESTs	5.6
	414312	AA155694	Hs.191060	ESTs	5.6
25	404571			NM_015902*:Homo sapiens progesterin induce	5.6
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
	439092	AA830149		gboc44f08.s1 NCI_CGAP_GC81 Homo sapiens	5.6
	427078	AI676062	Hs.111902	ESTs	5.6
	422805	AA436989	Hs.121017	H2A histone family, member A	5.6
30	417511	AL049176	Hs.82223	chordin-like	5.6
	449625	NM_014253		odt (odd Oz/ten-m, Drosophila) homolog 1	5.6
	433927	AI557019	Hs.116467	small nuclear protein PRAC	5.5
	441676	BE564206	Hs.49889	ESTs	5.5
	421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
35	432682	AI376400	Hs.159588	ESTs	5.5
	435021	AA922192	Hs.54709	ESTs	5.5
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	5.5
	426581	AB040956	Hs.135890	KIAA1523 protein	5.5
	439079	AF085937	Hs.38348	ESTs	5.5
40	443635	AI080230	Hs.134214	ESTs	5.5
	400080			Eos Control	5.5
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.5
	436578	AI091435	Hs.134859	ESTs	5.5
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
45	450325	AI935962	Hs.26289	ESTs	5.4
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	5.4
	435072	AW592176	Hs.116932	ESTs	5.4
	428647	AA830050	Hs.124344	ESTs	5.4
50	441111	AI806867	Hs.126594	ESTs	5.4
	433087	AI720686	Hs.162520	ESTs	5.3
	450244	AA007534	Hs.125062	ESTs	5.3
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.3
	415539	AI733881	Hs.72472	BMP-R1B	5.3
55	437267	AW511443	Hs.258110	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
	446715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	5.3
	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
60	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.3
	423101	MB3941	Hs.123642	EphA3	5.3
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	5.3
	450813	AI739625	Hs.203376	ESTs	5.3
	409079	W87707	Hs.82065	Interleukin 6 signal transducer (gp130,	5.2
65	415890	H08225	Hs.268712	ESTs	5.2
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	441054	AA913591	Hs.126480	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
70	448072	AI459306	Hs.24908	ESTs	5.2
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	5.2
	421040	AA715026	Hs.135280	ESTs	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	415263	AA948033	Hs.130853	ESTs	5.2
75	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	445238	AA883971	Hs.187506	ESTs	5.1
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.1
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
80	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	440995	T57773	Hs.10263	ESTs	5.0
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	5.0

	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.0
	418334	AA319233	Hs.5521	ESTs	5.0
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	5.0
5	418564	AA631143	Hs.278695	Homo sapiens prostain mRNA, complete cds	5.0
	407198	H91679		gb:yr04a07.s1 Soares fetal liver spleen	5.0
	403696			C4001100:gil5852342[gb]AAD54015.1 (AF0	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CLUA	5.0
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
10	430261	AA305127	Hs.237225	hypothetical protein HT023	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	443180	R15875	Hs.258576	claudin 12	4.9
15	414422	AA147224	Hs.249195	Homeo box A13	4.9
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.9
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.9
	428715	AW293716	Hs.53126	ESTs	4.9
	435937	AA830893	Hs.119769	ESTs	4.8
20	435136	R27299	Hs.10172	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
	447058	AI939456	Hs.160870	ESTs	4.8
	419187	AA234852	Hs.44693	ESTs	4.8
	433523	H29882		ESTs	4.8
25	420871	AA702972	Hs.65300	ESTs	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	453843	D25215	Hs.35804	hect domain and RLD 3	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypothi	4.7
30	452843	AI796769	Hs.208320	ESTs	4.7
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	4.7
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	440354	AA889386	Hs.125468	ESTs	4.7
35	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
	443361	AI792628	Hs.133273	ESTs	4.6
	409731	AA125885	Hs.56145	thymosin, beta, identified in neuroblast	4.6
	420026	AI831190	Hs.166676	ESTs	4.6
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.6
40	415788	AW628686	Hs.78851	KIAA0217 protein	4.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	434408	AI031771	Hs.132586	ESTs	4.6
	454024	AA993627	Hs.293907	hypothetical protein FLJ23403	4.6
45	447805	AW627932	Hs.302421	gemin4	4.6
	438875	AA827640	Hs.189059	ESTs	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
50	452277	AL049013	Hs.28783	KIAA1223 protein	4.6
	418836	AI655499	Hs.161712	ESTs	4.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	430701	AI760833	Hs.293971	ESTs	4.5
55	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	420133	AA426117	Hs.155543	ESTs	4.5
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	4.5
	439752	T78968	Hs.14411	ESTs	4.5
60	447816	NM_007233	Hs.274329	TP53 target gene 1	4.5
	431060	AF039307	Hs.249171	homeo box A11	4.5
	445372	N36417	Hs.144928	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.4
65	418019	R68911	Hs.176275	ESTs	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	412643	AW971239	Hs.136433	ESTs	4.4
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.4
	445210	H09323	Hs.27133	ESTs	4.4
	416705	AA314676	Hs.288945	hypothetical protein FLJ13448	4.4
	420608	BE548277	Hs.103104	ESTs	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
75	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	444030	AW021254	Hs.135055	ESTs	4.4
	435655	AW105663	Hs.6947	HSPC069 protein	4.4
	400533			ENSP00000209376::PRED65 protein (Fragmen	4.4
	435285	AW272603	Hs.266134	ESTs	4.4
80	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	4.3
	432960	AW150945	Hs.144758	ESTs	4.3
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	4.3
	430535	AW968485		gb:EST380561 IMAGE resequences, MAGJ Homo	4.3

	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	454159	AW968065	Hs.44143	polybromo 1	4.3
	435176	AA744875	Hs.189413	ESTs	4.3
5	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	4.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.3
	420111	AA255652		gb:zs21h11.1 NCI_CGAP_GC81 Homo sapiens	4.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	405348			C7001664:gil12698061[dbj]BAB21849.1 (AB	4.3
10	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.3
	449603	AI655662	Hs.197698	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	423782	AI472209	Hs.323117	ESTs	4.3
	432887	AI926047	Hs.162859	ESTs	4.3
15	420905	AA521307	Hs.186651	ESTs	4.2
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	4.2
20	450597	AI701635	Hs.207077	ESTs	4.2
	434022	R18374	Hs.117956	ESTs	4.2
	427761	AA412205	Hs.140996	ESTs	4.2
	433209	AB040907	Hs.278436	KIAA1474 protein	4.2
25	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.2
	449655	AI021987	Hs.59970	ESTs	4.2
	440774	AI420611	Hs.153934	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	440594	AW445167	Hs.126036	ESTs	4.2
30	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	435743	T66861	Hs.12962	ESTs	4.1
35	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
	436714	AA728964	Hs.293399	ESTs	4.1
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.1
	408177	AI241733	Hs.43871	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
40	430523	AW451385	Hs.161954	ESTs	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	452335	AW188944	Hs.61272	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	449907	AA004825	Hs.103281	ESTs	4.1
45	430487	D87742	Hs.241552	KIAA0268 protein	4.1
	448152	AJ741053	Hs.170770	ESTs	4.1
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	4.1
	423242	AL039402	Hs.125783	DEME-6 protein	4.1
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	4.1
50	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	446416	AV658299	Hs.163959	ESTs	4.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	4.1
	427203	AW629517	Hs.244855	ESTs	4.0
55	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	4.0
	442338	AI761976	Hs.156080	ESTs	4.0
	446307	T50083	Hs.22247	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	415861	Z43123	Hs.144513	ESTs	4.0
60	418259	AA215404		ESTs	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	432229	AW290976	Hs.143587	ESTs	4.0
	418310	AA814100	Hs.86693	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
65	419083	AJ479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	448131	AI675064	Hs.200481	ESTs	4.0
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	4.0
	418243	W51873	Hs.171857	Homo sapiens testis protein mRNA, partial	4.0
70	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	4.0
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	4.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	4.0
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
75	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	4.0
	441568	AJ733322	Hs.127176	ESTs	4.0
	441736	AW282779	Hs.8182	ESTs	4.0
	457498	AJ732230	Hs.191737	ESTs	3.9
80	433234	AB040928	Hs.65366	KIAA1495 protein	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	448568	AA149121	Hs.71947	ESTs	3.9
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.9
	424940	AA985308	Hs.283902	ESTs	3.9

	416288	HS1299	gb:yp07c06.s1 Soares breast 3NbHst Homo	3.9
	420301	AA767526	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	ESTs	3.9
5	435878	R08330	ESTs	3.9
	446862	AV660697	ESTs	3.9
	447530	AW192063	ESTs, Moderately similar to JC5238 galac	3.9
	452619	AW298597	Homo sapiens, clone IMAGE:4298026, mRNA,	3.9
	401403		Target Exon	3.9
10	448779	BE042877	ESTs	3.9
	420533	AI809510	ESTs	3.9
	411084	T18987	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	KIAA0888 protein	3.9
	423453	AW450737	CGI-09 protein	3.9
15	434833	AF156548	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.9
	455646	BE064420	gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	411479	AW848047	gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	419038	AW134924	ESTs	3.9
	421129	BE439899	ESTs	3.9
20	424332	AA338919	ESTs	3.9
	441766	R53790	hypothetical protein FLJ14393	3.9
	447033	AI357412	ESTs	3.9
	439306	BE220199	WD40 protein C1a01	3.8
	410352	AW969725	KIAA0373 gene product	3.8
25	407961	AW672939	origin recognition complex, subunit 2 (y	3.8
	410252	AW821182	microfibrillar-associated protein 1	3.8
	439560	BE565647	hypothetical protein FLJ12820	3.8
	440450	AI333129	ESTs	3.8
	458611	AI268407	DC-specific transmembrane protein	3.8
30	419589	AW973708	Homo sapiens cDNA FLJ13446 fis, clone PL	3.8
	431576	M76665	hydroxysteroid (11-beta) dehydrogenase 1	3.8
	447280	BE617907	ESTs	3.8
	438379	N23018	C-terminal binding protein 2	3.8
	416009	Z43062	gb:HSC12E041 normalized infant brain cDN	3.8
35	416534	H69043	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	423044	AA320829	protocadherin 18	3.8
	424701	NM_005923	mitogen-activated protein kinase kinase	3.8
	433507	AI817336	ESTs	3.8
	437718	AI927288	ESTs	3.8
40	419831	AW448930	ESTs	3.8
	424830	AW270580	ESTs, Weakly similar to putative p150 IH	3.8
	426981	AL044675	KIAA0530 protein	3.8
	431447	AA505138	ESTs	3.8
	435932	W03928	ESTs	3.8
45	442447	AA999723	ESTs	3.8
	403242		Target Exon	3.8
	433908	AW298141	ESTs	3.8
	452323	W44356	ESTs, Weakly similar to T33468 hypothei	3.7
50	412095	AI624707	Homo sapiens cDNA: FLJ21592 fis, clone C	3.7
	418759	AA227879	ESTs	3.7
	422299	AK000181	hypothetical protein FLJ20174	3.7
	452462	BE173515	gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
	423096	AA732684	progesterin induced protein	3.7
	454037	AW998716	gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
55	428055	AA420564	ESTs	3.7
	447785	AL041765	ESTs	3.7
	451746	M86178	ESTs	3.7
	453293	AA382267	ESTs	3.7
	436671	AW137159	ESTs	3.7
60	407437	AF220264	gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	408418	AW963897	KIAA1435 protein	3.7
	420092	AA814043	ESTs	3.7
	446947	AF146747	polycythemia rubra vera 1; cell surface	3.7
	441865	AA384726	hypothetical protein FLJ23316	3.7
65	419875	AA853410	proenkephalin	3.7
	431231	AA653552	ESTs	3.7
	418348	AI537167	hypothetical protein FLJ23560	3.7
	419261	X07876	wingless-type MMTV integration site faml	3.7
	422899	D16471	Human mRNA, Xq terminal portion	3.7
70	429163	AA884766	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.7
	439075	AF085933	ESTs	3.7
	440947	AA910403	ESTs	3.7
	404561		trichorhinophalangeal syndrome 1 gene (T	3.6
	430096	U91935	Retina-derived POU-domain factor-1	3.6
75	430320	BE245290	uncharacterized hypothalamus protein HCD	3.6
	444794	AI419991	ESTs	3.6
	426991	AK001536	Homo sapiens cDNA FLJ10674 fis, clone NT	3.6
	431316	AA502663	ESTs	3.6
	414178	AW957372	ESTs, Weakly similar to I38022 hypothei	3.6
80	450630	AA010429	ESTs	3.6
	411057	AI681006	ESTs	3.6
	436326	BE085236	aldo-keto reductase family 1, member B1	3.6
	410268	AA316181	six transmembrane epithelial antigen of	3.6
	423590	AW952412	ESTs, Weakly similar to A40348 Elav/Sex-	3.6

	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	416239	AL038450	Hs.48948	ESTs	3.6
5	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.6
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.6
	423349	AF010258	Hs.127428	homeo box A9	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
10	433563	AI732637	Hs.277901	ESTs	3.6
	425465	L18964	Hs.1904	protein kinase C, iota	3.5
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.5
	401132			C12000517*gi4758712[ref]NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
15	435177	AI018174	Hs.42936	ESTs	3.5
	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	3.5
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	3.5
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	3.5
	419994	AA282881	Hs.190057	ESTs	3.5
20	427304	AA761526	Hs.163853	ESTs	3.5
	434763	AA648618		gb:ns07a11.1 r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	447497	AW167254	Hs.205722	ESTs	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.5
25	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.5
	438680	AA906121	Hs.173421	ESTs	3.5
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheti	3.5
	443273	AI042063	Hs.132156	ESTs	3.5
	403510			Target Exon	3.5
30	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435981	H74319	Hs.188620	ESTs	3.5
	449845	AW971183	Hs.9583	DnaJ (Hsp40) homolog, subfamily C, membe	3.5
	436024	AI800041	Hs.190555	ESTs	3.5
35	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	458332	AI000341	Hs.220491	ESTs	3.5
	435688	H72286	Hs.128387	ESTs	3.4
40	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.4
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.4
	409047	AW961434	Hs.31539	ESTs	3.4
	404848			ENSP00000240769*BG153Q3.1 (similar to C	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
45	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
50	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	444324	AI301330	Hs.143838	ESTs	3.4
55	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	419964	AA811657	Hs.220913	ESTs	3.4
	424026	AI798295	Hs.137576	ribosomal protein L34 pseudogene 1	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	453942	AW190920	Hs.19928	hypothetical protein SP329	3.4
60	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.4
	408784	AW971350	Hs.63386	ESTs	3.4
	420184	AA188408	Hs.95665	hypothetical protein	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN81_HUMAN ZINC	3.4
65	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.4
	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.4
	412505	AA974491	Hs.21734	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
70	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.3
	436345	AA873008	Hs.121572	ESTs	3.3
	423023	N50128	Hs.173400	ESTs	3.3
75	427615	BE410107	Hs.179817	CGI-82 protein	3.3
	429588	AI080271	Hs.134533	ESTs	3.3
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	3.3
80	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	3.3
	414818	BE541217	Hs.23606	ESTs	3.3

5	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	436854	AA749167	Hs.173911	ESTs	3.3
	430865	AI073424	Hs.5232	HSPC125 protein	3.3
	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	423645	AI215632	Hs.147487	ESTs	3.3
10	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	3.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	3.3
	418051	AW192535	Hs.19479	ESTs	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	437714	AA766346	Hs.293242	ESTs	3.3
15	455710	BE072049		gb:PM4-BT0532-170100-004-f05 BT0532 Homo	3.3
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.3
20	423412	AF109300		prostate cancer associated protein 5	3.3
	436962	AW377314	Hs.5364	OKFZP564I052 protein	3.3
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	3.3
	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	433213	AW665130	Hs.137190	ESTs	3.3
25	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.2
	428043	T92248	Hs.2240	uteroglobin	3.2
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypothe	3.2
	423595	R82826	Hs.220702	ESTs	3.2
30	407021	U52077		gb:Human mariner1 transposase gene, comp	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
35	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.2
	425657	T89839	Hs.119471	ESTs	3.2
	459546	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.2
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.2
	451025	AW028689	Hs.301985	ESTs	3.2
40	401416			C14000338*gl 7459502 pir J574665 outer	3.2
	421928	AF013758	Hs.109843	polyadenylate binding protein-interactin	3.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.2
	436995	AI160015	Hs.118112	ESTs	3.2
	428736	AK001331	Hs.192662	hypothetical protein FLJ10469	3.2
45	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
	429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	3.2
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
50	447597	AI886036	Hs.213675	ESTs	3.2
	437866	AA156781		metallothionein 1E (functional)	3.2
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.2
	410870	U81599	Hs.66731	homeo box B13	3.2
	438899	AF085833	Hs.135624	ESTs	3.2
55	415862	R51034	Hs.144513	ESTs	3.2
	420969	AI636310	Hs.28310	ESTs	3.2
	415467	R60891	Hs.260274	ESTs	3.2
	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	417380	T06809	Hs.332086	ESTs	3.2
60	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
	419088	AI538323	Hs.52620	integrin, beta 8	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AI458682		gb:lk13e01.x1 NCL_CGAP_Lu24 Homo sapiens	3.2
	452862	AW378065	Hs.8687	ESTs	3.2
65	405548			Target Exon	3.1
	439584	AA838114	Hs.221612	ESTs	3.1
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.1
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
70	434512	AW139932	Hs.188941	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.1
	416836	D54745	Hs.80247	cholecystokinin	3.1
	432589	AL135725	Hs.131708	ESTs	3.1
75	420512	AA262886	Hs.143817	ESTs	3.1
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypothe	3.1
	423855	AA331761	Hs.254859	ESTs	3.1
	425805	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	3.1
80	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	421823	N40850	Hs.28625	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	445784	AI253155	Hs.146065	ESTs	3.1
	434384	AA631910	Hs.162849	ESTs	3.1
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	3.1

5	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL)	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21168	ESTs	3.1
	433610	AA806822	Hs.112547	ESTs	3.1
	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	444800	AW119071	Hs.153287	ESTs	3.1
10	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.1
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	3.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	3.1
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.1
	407349	AA825449	Hs.83332	Homo sapiens cDNA: FLJ22437 fis, clone H	3.1
15	410859	AW808361		gb:MR1-ST0111-111099-003-404 ST0111 Homo	3.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
	425480	AB023198	Hs.158135	KIAA0981 protein	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
20	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	3.1
	433852	AI378329	Hs.126629	ESTs	3.0
	448558	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.0
	452242	R50955	Hs.159993	glycosyltransferase	3.0
	424690	BE538355	Hs.151777	eukaryotic translation initiation factor	3.0
25	405264			NM_030813*:Homo sapiens suppressor of po	3.0
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.0
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothei	3.0
	434497	AI821803	Hs.136580	ESTs	3.0
	420355	AW968263	Hs.123126	ESTs	3.0
30	403481			Target Exon	3.0
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.0
	416642	T96118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
35	426174	AA547859	Hs.115838	ESTs	3.0
	430459	BE178539	Hs.278634	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	446258	AI283476	Hs.263478	ESTs	3.0
	448686	AA158659	Hs.334712	hypothetical protein FLJ14744	3.0
40	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	3.0
	414441	AA234759	Hs.132950	ESTs	3.0
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	3.0
	437048	AA743240	Hs.91582	ESTs	3.0
	450963	AI864668	Hs.48832	ESTs	3.0
45	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.0
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.0
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	3.0
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
50	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-l	3.0
	426743	AA383833	Hs.245022	ESTs	3.0
	442326	H92952	Hs.124813	hypothetical protein MGC14817	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
55	437323	AA371145	Hs.194397	tepln receptor	3.0
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.0
	450580	N40087		ESTs	3.0
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.0
	418365	AW014345	Hs.161690	ESTs	3.0
60	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.0
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	418819	AA228776	Hs.191721	ESTs	3.0
	428634	AA811845	Hs.106290	Kelch motif containing protein	3.0
65	431869	AA521136	Hs.190176	ESTs	3.0
	435008	AF150262	Hs.162898	ESTs	3.0
	448880	AW205507	Hs.32360	ESTs, Highly similar to I38587 retroviri	3.0
	451391	AA017410	Hs.40668	ESTs	3.0
	452959	AI933416	Hs.189674	ESTs	3.0

TABLE 64B

Pkey: Unique Eos probe set identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

80	Pkey	CAT Number	Accession
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8 AW846433 AW846159 AW846377 AW846528
	411436	1245660_1	

411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214 BE046680 BE046738 BE044958 BE064415 BE064430 BE064448 BE145899 BE145848 BE145849 BE145853 BE145927 BE145925 AI267700 AI720344 AA191424 AI023543 AI468633 AA172056 AW958465 AA172236 AW953397 AA355086 Z43062 R13213 H14422 H51299 H44619 H46391 R86024 H51892 T72744 AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24577 R40635 H05100 R40597 AA215404 AI990909 BE464132 AW271459 N74332 AI262061 T65754 AA228857 AA229658 AI217097 AW886090 W38035 W38792 AA232835 AW936043 AA603305 AA244095 AA244183 AA255652 AA280911 AW957920 AA262684 BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280 AF109300 AI299378 AI202654 AA337221 AA336756 AW966196 AA377823 AW954494 AI022688 AA380153 AA380233 AW963529 AK001536 AA191092 AW510354 AI554256 AL353968 AA134266 AA418703 AA418711 BE071915 BE071920 BE071912 AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340 AA884766 AW974271 AA592975 AA447312 AW207206 AW341473 AA448195 AI951341 AW968485 AW968670 AA480922 BE350425 AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339 AI003429 AI003367 AA564825 H29682 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320 AA648618 AW974389 H51771 N73895 AJ001872 BE085236 BE085317 X04236 AA577934 AA578392 AA502836 AA595852 AA578258 AW270791 AA507151 AA559152 T57040 BE503281 AW593405 AI825755 AI350499 AI655710 AI972281 AI654949 BE073961 BE073962 BE041399 AW750214 AA228488 BE074016 AI908706 AW270601 AW873282 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188 AA830149 AW978407 M85983 AW503637 BE220199 W01813 AF086118 N70760 BE221405 AW629656 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207 AA921877 AA910403 AI815593 W58361 AW162520 AI816550 N98828 BE079873 AI110738 AF074645 AV653771 BE089370 AI458682 H24240 R14537 R18426 AW867082 AI151418 W60401 AW531238 AI346936 AA862855 W60310 N72501 H90060 BE150445 AW380821 AI540906 C04881 W03542 AA641764 H97053 AW889353 AA521308 AA001203 W92828 AI207798 AA746655 R78710 W24617 AA024605 C01747 AW173095 W61229 W92685 AA742467 H00789 R76925 AW1828 AA001793 AA001871 NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48874 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 AI692689 R14223 T18395 N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303 AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878 AA495800 AA495737 AA010736 AA654716 AA640726 BE173515 BE173560 AI902860 T79703 T96307 AL079725 AW998716 AW022148 N68020 AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892 AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 AW753456 AW753036 AW854868 AW854862 AW835767 AW835537 BE160187 AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033 BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362 BE064420 BE064435 BE064429 BE064414 BE064400 BE064517 BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464 AA493662 AW897396 BE154814 AI911066 AI933734 AI690888 AJ003599
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TABLE 64C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
------	-----	--------	-------------

5	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401403	7710966	Plus	146180-146294
	401416	7452889	Minus	121456-121626
	401424	8176894	Plus	24223-24428
	403242	7637817	Minus	11297-12511
	403481	9865004	Plus	93496-93633
10	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403696	3135242	Minus	143467-143634
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
15	404571	7249169	Minus	112450-112648
	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23955-24034,25143-25264
	405264	7329374	Plus	28556-28684
	405348	2914717	Minus	43310-43462
20	405510	7630909	Minus	101028-101174
	405548	1532158	Plus	11552-11686

25 Table 65A lists about 347 genes up-regulated in BPH compared to prostate cancer tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer tissue level was set to the 85th percentile amongst malignant prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

30 TABLE 65A: ABOUT 347 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER TISSUES

35	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
40	R1:	Ratio of BPH tissue to prostate tumor tissue		
	Pkey	ExAccn	Unigene ID	Unigene Title
	428134	AA421773	Hs.161008	ESTs
	446336	AW815036	Hs.151251	ESTs
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K
	400533			ENSP00000209376*:PRED65 protein (Fragmen
	418310	AA814100	Hs.86693	ESTs
	404592			NM_022739*:Homo sapiens E3 ubiquitin lig
45	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo
	400080			Eos Control
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c
	438231	AW594539	Hs.155689	ESTs
50	418387	R18085		gb:yg16b12.r1 Soares infant brain 1N1B H
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe
	404967			Target Exon
55	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens
	400440	X83957	Hs.83870	nebulin
60	454171	AW854832		gb:QV2-CT0261-201099-011-405 CT0261 Homo
	400086			Eos Control
	440911	AA909536	Hs.143562	ESTs
	425312	AA354940	Hs.145958	ESTs
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence
65	419015	T79262	Hs.14463	ESTs
	453789	AA628517	Hs.118502	ESTs
	424940	AA985308	Hs.283902	ESTs
	403667			Target Exon
	429014	AI800518	Hs.118158	ESTs
70	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitte
	419999	AI760942	Hs.191754	ESTs
	405348			C7001664:gi12698051 dbj BAB21849.1 (AB
	404003			Target Exon
	453200	AA033832	Hs.212433	ESTs
75	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi
	432319	AW510770	Hs.128388	ESTs
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi
	443361	AI792628	Hs.133273	ESTs
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo
80	439079	AF085937	Hs.38348	ESTs
	422081	AW136820	Hs.196011	ESTs
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked
	423529	T87318	Hs.120411	ESTs

	436578	AI091435	Hs.134859	ESTs	5.5
	450920	AA011626	Hs.133324	ESTs	5.5
	435072	AW592176	Hs.116932	ESTs	5.4
5	414403	AW963551	Hs.76064	ribosomal protein L27a	5.4
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	5.4
	433087	AI720586	Hs.152520	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	414818	BE541217	Hs.23606	ESTs	5.3
10	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
15	435375	AI733610	Hs.187832	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	5.2
	405321			Target Exon	5.1
20	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	438206	AA780385	Hs.187885	ESTs	5.1
	445238	AA883971	Hs.187506	ESTs	5.1
	455747	BE074910		gb:RCS-BT0580-170300-021-F12 BT0580 Homo	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
25	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	440354	AA889386	Hs.125468	ESTs	5.0
	440388	AI693520	Hs.223000	ESTs	4.9
	421188	AA284658	Hs.261493	ESTs	4.9
	403481			Target Exon	4.8
30	438132	AA907076	Hs.122060	ESTs	4.8
	403333			NM_002518*:Homo sapiens neuronal PAS dom	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	433597	AA708205	Hs.100343	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
35	452843	AI796769	Hs.208320	ESTs	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	442123	AI697790	Hs.159961	EST	4.7
	438727	AW978756	Hs.205679	ESTs	4.7
40	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	442160	AI337127	Hs.156325	ESTs	4.6
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.6
	434589	AF147363		gb:Homo sapiens full length insert cDNA	4.6
	404995			ENSP00000251890*:Monocytic leukemia zinc	4.6
45	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.5
	405549			C7001976*:gl 4758712[ref]NP_004659.1 al	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	443998	AI620661	Hs.296276	ESTs	4.5
	455801	BE140643		gb:RC0-HT0015-310599-016 HT0015 Homo sap	4.5
50	444800	AW119071	Hs.153287	ESTs	4.5
	403371			Target Exon	4.5
	438431	AW207860	Hs.293116	ESTs	4.5
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	4.5
	439752	T78968	Hs.14411	ESTs	4.5
55	414441	AA234759	Hs.132950	ESTs	4.5
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	4.5
	454585	BE059128		gb:QV3-BT0379-310100-071-g06 BT0379 Homo	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
60	418059	AA211586		gb:zn56d05.s1 Stralagene muscle 937209 H	4.4
	451469	NM_014809	Hs.26441	KIAA0319 gene product	4.4
	433072	AI928037	Hs.158832	ESTs	4.4
	443318	AI051603	Hs.133141	ESTs	4.4
	424686	AA345504		gb:EST51529 Gall bladder II Homo sapiens	4.3
65	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	415467	R60891	Hs.260274	ESTs	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	415417	F12038	Hs.140970	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.3
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	4.3
70	441620	R59595	Hs.26675	ESTs	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	448108	AW300021	Hs.170685	ESTs	4.2
	436345	AA873008	Hs.121572	ESTs	4.2
75	409500	U08098	Hs.54576	sulfotransferase, estrogen-prefering	4.2
	413525	BE145899		gb:MRO-HT0208-221299-204-b10 HT0208 Homo	4.2
	403305	NM_006825		transmembrane protein (63kD), endoplasmic	4.2
	436338	W92147	Hs.118394	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
80	430124	AW204994	Hs.253450	ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	416385	H54253	Hs.205241	ESTs, Weakly similar to S65657 alpha-1C-	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1

	445206	AI350199	Hs.269990	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	448152	AJ741053	Hs.170770	ESTs	4.1
	453713	R20640	Hs.79133	cadherin 8, type 2	4.1
5	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	442338	AI761976	Hs.156080	ESTs	4.0
	455388	AW936234		gb:QVO-DT0020-090200-106-g05 DT0020 Homo	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
10	421312	AA824627	Hs.291670	ESTs	4.0
	431421	AW959118	Hs.108144	ESTs, Weakly similar to unnamed protein	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, moto	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
15	424765	AA282211	Hs.284256	hypothetical protein FLJ14033 similar to	3.9
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.9
	453387	AI990741	Hs.252809	ESTs	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	454806	AW872430	Hs.273743	ESTs	3.9
20	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JCS238 galac	3.9
	407834	AW084991	Hs.26100	ESTs	3.9
25	400398	AF137396	Hs.283879	ubiquitin 3	3.9
	421353	AW292857	Hs.255130	ESTs	3.9
	401459			C14000482*gi 9790241 ref NP_062628.1 S	3.9
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.9
30	444911	U06117	Hs.250	xanthene dehydrogenase	3.9
	436350	AA713661	Hs.121091	ESTs	3.9
	447930	R44574	Hs.107510	ESTs	3.9
	410559	AW754192		gb:RC2-CT0321-131299-012-a04 CT0321 Homo	3.8
	452320	AA042873	Hs.160412	ESTs	3.8
35	402145			Target Exon	3.8
	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN IIII	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.8
	416009	Z43052		gb:HSC12E041 normalized infant brain cDN	3.8
40	434381	AA631834		gb:np77h05.s1 NC1_CGAP_Pr2 Homo sapiens	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	433523	H29882		ESTs	3.8
	411436	AW846433		gb:QVO-CT0179-070300-143-b02 CT0179 Homo	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
45	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	403242			Target Exon	3.8
50	455490	AW953477		gb:EST365547 MAGE resequences, MAGB Homo	3.8
	448264	AI637649	Hs.196105	ESTs	3.8
	443535	AI080230	Hs.134214	ESTs	3.7
	428200	AI039624	Hs.98388	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-03 HT0560 Homo	3.7
55	418759	AA227879	Hs.187621	ESTs	3.7
	450497	H64159	Hs.15328	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	416321	H94331	Hs.34024	ESTs	3.7
60	448135	AI470874	Hs.343799	ESTs	3.7
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	3.7
65	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	3.7
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.7
	434306	AW081757	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	3.7
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.7
70	419261	X07876	Hs.89791	wingless-type MMTV integration site fam1	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	411421	BE272110	Hs.21177	ESTs	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
75	440947	AA910403		ESTs	3.7
	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	446658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
80	429073	AA446167	Hs.47385	ESTs	3.6
	419002	T78625	Hs.268594	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-43882	3.6

5	439481	AF086294	Hs.125844	ESTs	3.6
	419622	AA452054	Hs.119338	ESTs	3.6
	449821	AI671141	Hs.211122	ESTs	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	412701	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.6
	419611	AB031479	Hs.91600	SEEK1 protein	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	427235	AI126288	Hs.192232	ESTs	3.6
10	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.5
	401132			C12000517*:g 4758712 ref NP_004659.1 a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	405264			NM_030813*:Homo sapiens suppressor of po	3.5
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.5
15	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	416379	N38857	Hs.203933	ESTs	3.5
	407557	Z83803		gb:H.sapiens mRNA for axonemal dynein he	3.5
	437956	AA773283	Hs.203559	hypothetical protein FLJ12701	3.5
20	403510			Target Exon	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	427125	AA683362	Hs.97612	ESTs	3.5
	424287	AL133105	Hs.144633	hypothetical protein DKFZp434F2322	3.4
25	434497	AI821803	Hs.136580	ESTs	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	442231	W02434	Hs.222413	ESTs	3.4
30	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.4
35	427033	AI457449	Hs.192817	ESTs	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	410551	R36730	Hs.21816	ESTs	3.4
	423357	AI285124	Hs.157505	ESTs	3.4
	450582	AI339732		G-rich RNA sequence binding factor 1	3.4
40	437662	AA765387	Hs.145096	ESTs	3.4
	442388	AW663442	Hs.129485	ESTs	3.4
	445004	AI204616	Hs.148701	ESTs	3.4
	450597	AI701635	Hs.207077	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
45	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
	407344	AI038025	Hs.271418	gb:ox29f07.x1 Soares_tetal_fetus_Nb2HF8_	3.3
50	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	437115	AA744703	Hs.129030	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989953	Hs.197505	ESTs	3.3
55	453328	AW292635	Hs.346145	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	449256	AA059050	Hs.59847	ESTs	3.3
	432550	AW297206	Hs.164018	ESTs	3.3
	423101	M83941	Hs.123642	EphA3	3.3
60	424853	BE549737	Hs.132957	Human EST clone 122887 mariner transpos	3.3
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	402703			Target Exon	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
65	452011	AW628911	Hs.211429	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	420355	AW968263	Hs.123126	ESTs	3.2
	418898	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypothe	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
70	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.2
	402454			C1002501*:g 129092 sp P23270 OLF7_RAT O	3.2
	411552	AW851255		gb:IL3-CT0220-160200-066-H02 CT0220 Homo	3.2
75	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	3.2
	435786	H09175	Hs.26085	ESTs	3.2
	447697	AI886036	Hs.213675	ESTs	3.2
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
80	447183	AI554733	Hs.173182	ESTs	3.2
	426629	AI203933	Hs.97142	ESTs	3.2
	447892	AI435848	Hs.172978	ESTs	3.2
	457136	AA428240	Hs.126083	ESTs	3.2
	443585	AW466983	Hs.263949	enamelin	3.1

5	451399	AL042110	Hs.326728	ESTs	3.1
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	458251	AL040927	Hs.210422	ESTs	3.1
	439950	AW937417	Hs.293561	ESTs	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
10	403805			Target Exon	3.1
	422666	AA677981	Hs.119023	SMC2 (structural maintenance of chromoso	3.1
	408799	AA059412	Hs.47986	hypothetical protein MGC10940	3.1
	429350	AI754634	Hs.131987	ESTs	3.1
	430454	AW469011	Hs.105635	ESTs	3.1
15	441817	AW969706	Hs.293332	ESTs	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.1
	445758	R60715	Hs.25804	ESTs	3.1
	403291			Target Exon	3.1
20	436295	N73895		gb:za62d05.s1 Soares fetal liver spleen	3.1
	455772	W28799		gb:52g11 Human retina cDNA randomly prim	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	438142	T90309	Hs.269651	ESTs	3.1
	416423	H54375	Hs.268921	ESTs	3.1
25	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	3.1
	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	3.1
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.1
	420721	AA927802	Hs.159471	ZAP3 protein	3.1
	436013	AA703419	Hs.287749	Homo sapiens cDNA: FLJ23593 fis, clone L	3.1
30	441492	AI149998	Hs.146346	ESTs	3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	435628	W88732	Hs.36107	ESTs	3.0
	444326	AI939357	Hs.270710	ESTs	3.0
35	413774	AA131782	Hs.182314	ESTs	3.0
	434352	AF129505	Hs.86492	small muscle protein, X-linked	3.0
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.0
	416422	H60457		ESTs, Moderately similar to ZN91_HUMAN Z	3.0
	416642	T96118	Hs.226313	ESTs	3.0
40	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	418948	AI217097		gb:q043h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	427813	D29833	Hs.2207	salivary proline-rich protein	3.0
	405733			NM_021140*:Homo sapiens ubiquitously tra	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Sts20-fik	3.0
	410929	H47233	Hs.30643	ESTs	3.0
50	458187	D56919	Hs.265848	myomegalin	3.0
	429430	AI381837	Hs.155335	ESTs	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0

55 TABLE 65B

Pkey:		Unique Eos probeset identifier number	
CAT number:		Gene cluster number	
Accession:		Genbank accession numbers	
60	Pkey	CAT Number	Accession
	408304	1050848_1	AW810279 BE146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515 AW810330 AW810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810635 AW810288 AW810263 AW810325 AW810443 AW8
65	409189	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 AA085208 AA085045
	410559	1208283_1	AW754192 W00554 AW857797 AW754203 AW754197 AW754193
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
70	410669	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808613 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1	AW846433 AW846159 AW846377 AW846528
	411518	1248692_1	AW850246 AW850251 AW850302
75	411552	1249255_1	AW851255 AW851432 AW850955
	412701	1322288_1	AW984757 AW984797 AW984734 AW984745
	412988	1342150_1	BE046680 BE046738 BE044958
	413081	1348563_1	BE064415 BE064430 BE064448
	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
80	416009	1566379_1	Z43062 R13213 H14422
	416422	1593811_1	H60457 H68709 H73528 H54335 R87154
	418059	171879_1	AA211586 F35799 AA211641 F29720 AW937387 AW937408
	418387	174731_1	R18085 AA219028 R17712 Z44345
	418948	180808_1	AI217097 AW986090 W38035 W38792 AA232835 AW936043

5	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	421926	209246_1	AA300591 AW963893 AA300493
	424200	236595_1	AA337221 AA336756 AW966196
	424686	242486_1	AA345504 AA345251 AW963243
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
10	432765	353907_1	AJ003429 AJ003367 AA564825
	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	434381	385155_1	AA631834 AA633425 AA632455 AI792312 AI792311
	434589	38929_1	AF147363 T47219 T47218
	434763	392847_1	AA648618 AW974389 H51771
	436295	41733_1	N73895 AJ001872
15	440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
	442481	543588_1	N99828 BE079873 AI110738 AF074645
	445432	63943_1	AV653771 BE089370
	449570	81018_1	AA001793 AA001871
20	450317	831956_1	AI692689 R14223 R18395
	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW9336878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 AI902860
	453682	977454_1	T79703 T96307 AL079725
25	454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454585	1225852_1	BE069128 BE069023 AW809375
	454665	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
30	454860	1237732_1	AW835767 AW835537 BE160187
	454958	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854538 AW854418 AW854412
	455135	1254729_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
	455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
35	455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
	455490	1297826_1	AW953477 Z141970 F12435 T73989 T09387
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
40	455772	1363114_1	W28799 BE086078
	455801	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
	456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101
	457374	328758_1	AA493662 AW897396 BE154814

TABLE 65C

50	Pkey:	Unique number corresponding to an Eos probe set		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	NI_position:	Indicates nucleotide positions of predicted exons.		
55	Pkey	Ref	Strand	NI_position
	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401459	9212270	Minus	182001-183323
60	402145	8018280	Plus	113086-114800
	402454	7534025	Minus	14826-15803
	402703	8705069	Minus	15335-15500
	403242	7637817	Minus	11297-12511
	403291	7230870	Plus	95177-95435
	403305	8099945	Plus	114632-114805
65	403333	8568833	Minus	124794-124941
	403371	9087278	Plus	106655-106050
	403433	9719611	Minus	72225-72437
	403481	9965004	Plus	93496-93633
	403510	7652047	Plus	61866-62027
70	403667	6850483	Minus	1344-1442,1545-1697
	403805	8140491	Minus	51483-51742,53429-53511
	404003	8655948	Plus	198349-199096
	404561	9796980	Minus	69039-70100
	404592	9943965	Minus	39067-39225
75	404848	8248647	Minus	23955-24034,25143-25264
	404967	7523744	Minus	89944-90729
	404995	6006247	Minus	154015-154123
	405264	7329374	Plus	28556-28684
	405321	3419846	Minus	44654-45210
80	405348	2914717	Minus	43310-43462
	405510	7630909	Minus	101028-101174
	405549	1552494	Plus	10878-11048
	405733	9884689	Plus	124832-125051

5 Table 66A lists about 370 genes up-regulated in BPH compared to prostate cancer and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer and normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer and normal adult tissue level was set to the 85th percentile amongst malignant prostate tissues and normal adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

10 TABLE 66A: ABOUT 370 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER AND NORMAL ADULT TISSUES

15				
Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of BPH tissue to prostate tumor and normal body tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
410929	H47233	Hs.30643	ESTs	21.1
450693	AW450461	Hs.203965	ESTs	16.7
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
432473	AI202703	Hs.152414	ESTs	11.3
446336	AW815036	Hs.151251	ESTs	10.9
407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	10.7
428134	AA421773	Hs.161008	ESTs	10.2
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	9.8
433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
415293	R49462	Hs.106541	ESTs	9.1
458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
428927	AA441837	Hs.90250	ESTs	8.6
420345	AW295230	Hs.25231	ESTs	8.5
453387	AI990741	Hs.252809	ESTs	8.2
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoleti	7.5
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	7.4
400080			Eos Control	7.4
431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
438231	AW594539	Hs.155689	ESTs	7.3
410330	AW023630	Hs.159425	ESTs	7.2
449300	AI656959	Hs.346514	ESTs	7.1
449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
426384	AI472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	6.8
454171	AW854832		gb:QV2-CT0261-201099-011-005 CT0261 Homo	6.6
408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.6
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
424433	H04607	Hs.9218	ESTs	6.5
442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.4
425312	AA354940	Hs.145958	ESTs	6.4
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
440911	AA909536	Hs.143562	ESTs	6.4
400533			ENSP00000209376*:PRE065 protein (Fragmen	6.2
418310	AA814100	Hs.86693	ESTs	6.2
403667			Target Exon	6.1
435396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
404003			Target Exon	5.9
424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	5.9
438138	R98299	Hs.177502	ESTs	5.9
424940	AA985308	Hs.283902	ESTs	5.8
434485	AI623511	Hs.118567	ESTs	5.8
453200	AA033832	Hs.212433	ESTs	5.7
428002	AA418703		gb:zv98c03.s1 Soares_NhiMPu_S1 Homo sapi	5.7
424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
443361	AI792628	Hs.133273	ESTs	5.6
421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
439079	AF085937	Hs.38348	ESTs	5.5
430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	5.5
436578	AI091435	Hs.134859	ESTs	5.5
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (f	5.4
435072	AW592176	Hs.116932	ESTs	5.4
435375	AI733610	Hs.187832	ESTs	5.4
444609	AW571659	Hs.278081	ESTs	5.4
416602	NM_006159	Hs.79389	nel (chicken)-like 2	5.4
433087	AI720686	Hs.152520	ESTs	5.3
439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.3
437267	AW511443	Hs.258110	ESTs	5.3
441916	AA933571	Hs.129075	ESTs	5.3
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypothe	5.3

	423101	M83941	Hs.123642	EphA3	5.3
	437587	AJ591222	Hs.72325	Human DNA sequence from clone RP1-187J11	5.2
	415890	H08225	Hs.268712	ESTs	5.2
5	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	5.2
10	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	416705	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.1
15	445238	AA883971	Hs.187506	ESTs	5.1
	450582	AJ339732		G-rich RNA sequence binding factor 1	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	440354	AA889386	Hs.125468	ESTs	5.0
20	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
	457374	AA493662		gb:rh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	4.9
25	450497	H64159	Hs.15328	ESTs	4.8
	438132	AA907076	Hs.122050	ESTs	4.8
	414818	BE541217	Hs.23606	ESTs	4.8
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
	433523	H29882		ESTs	4.8
30	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	443635	AI080230	Hs.134214	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	452843	AI796769	Hs.208320	ESTs	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
35	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.7
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420831	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	454024	AA933527	Hs.293907	hypothetical protein FLJ23403	4.6
40	405348			C7001664:gil12698061[kbj]BAB21849.1 (AB	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	447058	AI939456	Hs.160870	ESTs	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
	430697	AA484207	Hs.211867	ESTs	4.5
45	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	4.5
	449821	AI671141	Hs.211122	ESTs	4.5
	420805	AA521307	Hs.186651	ESTs	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFp564B083 (fr	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	420154	AI093155	Hs.95420	JM27 protein	4.4
55	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	4.4
	458527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	433597	AA708205	Hs.100343	ESTs	4.3
60	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	420111	AA255652		gb:cs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	433433	AI692623	Hs.121513	Homo sapiens clone Z3-1 placenta expres	4.2
65	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	420355	AW968263	Hs.123126	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
70	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	442786	H50733	Hs.256251	ESTs, Moderately similar to ALU8_HUMAN A	4.1
75	450597	AI701635	Hs.207077	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
80	438875	AA827640	Hs.189059	ESTs	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	404967			Target Exon	4.0
	427203	AW629517	Hs.244855	ESTs	4.0

	442338	AI761976	Hs.156080	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypothe	4.0
5	435136	R27299	Hs.10172	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
10	448882	AJ001531	Hs.22404	protease, serine, 12 (neurolypsin, moto	4.0
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
15	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.9
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
20	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	414441	AA234759	Hs.132950	ESTs	3.9
	425810	AI923627	Hs.31903	ESTs	3.9
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	3.9
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
25	440450	AI333129	Hs.156147	ESTs	3.8
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	3.8
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
30	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
35	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
	433908	AW298141	Hs.157975	ESTs	3.8
	454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
40	432101	AI918950	Hs.123642	EphA3	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-403 HT0560 Homo	3.7
	448568	AA149121	Hs.71947	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
45	436345	AA873008	Hs.121572	ESTs	3.7
	446862	AV660697	Hs.282700	ESTs	3.7
	419875	AA853410	Hs.93557	proenkephalin	3.7
	421040	AA715026	Hs.135280	ESTs	3.7
50	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.7
	450687	AA495800		gb:czw05b07.s1 Soares_NhiHMPu_S1 Homo sapi	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	431474	AL133990	Hs.190642	CEGP1 protein	3.7
	448004	AW451477	Hs.257456	ESTs	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site faml	3.7
55	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	403481			Target Exon	3.6
60	404561			trichorhinophalangeal syndrome I gene (T	3.6
	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	449655	AI021987	Hs.59970	ESTs	3.6
65	450630	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	420026	AI831190	Hs.166576	ESTs	3.6
70	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	3.5
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.5
75	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.5
	401132			C120005177:g 4758712[ref NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	434763	AA648618		gb:ns07a11.1 NCI_CGAP_Ew1 Homo sapiens	3.5
80	449588	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5

5	430865	AI073424	Hs.5232	HSPC125 protein	3.5
	444800	AW119071	Hs.153287	ESTs	3.5
	428647	AA830060	Hs.124344	ESTs	3.5
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.5
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	430124	AW204994	Hs.253450	ESTs	3.4
	430701	AI760833	Hs.293971	ESTs	3.4
10	436714	AA728964	Hs.293399	ESTs	3.4
	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
15	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
20	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
25	419964	AA811657	Hs.220913	ESTs	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.4
	430829	AW451999	Hs.194024	ESTs	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
30	433628	AI821784	Hs.188578	ESTs	3.4
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.4
	427235	AI126288	Hs.192232	ESTs	3.4
	459646	AW883958	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.4
35	428923	BE047698	Hs.188785	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
40	448108	AW300021	Hs.170885	ESTs	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
45	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	432229	AW290976	Hs.143587	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f08 BT0532 Homo	3.3
50	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.3
	416662	T25853	Hs.7538	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	3.3
	428715	AW293716	Hs.53126	ESTs	3.3
55	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	434497	AI821803	Hs.136580	ESTs	3.2
	439306	BE220199		WD40 protein C1a01	3.2
60	420608	BE548277	Hs.103104	ESTs	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
65	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	3.2
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	402145			Target Exon	3.2
	448131	AI675054	Hs.200481	ESTs	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
70	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	447183	AI554733	Hs.173182	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
	415467	R60891	Hs.260274	ESTs	3.2
75	434408	AI031771	Hs.132586	ESTs	3.2
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pl p	3.2
	453789	AA628517	Hs.118502	ESTs	3.2
	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
80	419088	AI538323	Hs.52620	Integrin, beta 8	3.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AI458682		gb:k13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	3.1

	405321		Target Exon	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th
	434512	AW139932	Hs.188941	ESTs
5	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-
	433444	AW975324	Hs.129816	ESTs
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypothe
	415861	Z43123	Hs.144513	ESTs
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174
10	432527	AW975028	Hs.102754	ESTs
	427773	AA412290	Hs.98124	ESTs
	441817	AW969706	Hs.293332	ESTs
	416812	H91010	Hs.44940	ESTs
	417958	AA767382	Hs.193417	ESTs
15	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL
	416423	H54375	Hs.268921	ESTs
	418037	AI990212	Hs.86447	ESTs
	419197	N48921	Hs.27441	KJAA1615 protein
	420179	N74530	Hs.21168	ESTs
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen
	405548		Target Exon	3.1
	423595	R82826	Hs.220702	ESTs
	412533	AA679863	Hs.69606	ESTs
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds
25	405264			NM_030813*:Homo sapiens suppressor of po
	410869	AW808361		gb:MR1-ST0111-111099-003-r04 ST0111 Homo
	425354	U62027	Hs.155935	complement component 3a receptor 1
	441492	AI149998	Hs.146346	ESTs
	447078	AW885727	Hs.9914	ESTs
30	435021	AA922192	Hs.54709	ESTs
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC
	450580	N40087		ESTs
	432319	AW510770	Hs.128386	ESTs
	453713	R20640	Hs.79133	cadherin 8, type 2
35	445784	AI253155	Hs.146065	ESTs
	416642	T96118	Hs.226313	ESTs
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W
	433796	AA810867	Hs.186997	ESTs
	439182	AF086030	Hs.21621	hypothetical protein DKFZp7620076
40	404995			ENSP00000251890*:Monocytic leukemia zinc
	444794	AI419991	Hs.145225	ESTs
	443634	H73972	Hs.134460	ESTs
	420133	AA426117	Hs.155543	ESTs
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197
45	426743	AA383833	Hs.245022	ESTs
	442326	H92962	Hs.124813	hypothetical protein MGC14817
	449913	AA004696	Hs.333016	ESTs
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo
	419622	AA452054	Hs.119338	ESTs
50	449745	AI668593		gb:yl38a05.x5 Soares breast 3NbHBst Homo
	428412	AA428240	Hs.126083	ESTs
	428200	AI038624	Hs.98388	ESTs
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600
	431869	AA521136	Hs.190176	ESTs
55	451391	AA017410	Hs.40568	ESTs
	452959	AI933416	Hs.189674	ESTs

TABLE 66B

60	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
<hr/>		
65	Pkey _i	CAT Number Accession
	410790	1221131_1 AW803357 AW803423 AW812233 R06814
	410869	1225123_1 AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
70	411436	1245660_1 AW846433 AW846159 AW846377 AW846528
	411479	1247077_1 AW846047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214 BE046680 BE046738 BE044958 BE064415 BE064430 BE064448 BE145899 BE145848 BE145849 BE145853 BE145927 BE145925 Z43062 R13213 H14422 AI217097 AW886090 W38035 W38792 AA232835 AW936043 AA255652 AA280911 AW967920 AA262684 BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
75	412988	1342150_1
	413081	1348563_1
	413525	1374635_1
	416009	1566379_1
	418948	180808_1
	420111	190755_1
	420352	192979_1
80	424200	236595_1
	424994	245786_1
	428002	285602_1

428342	290035_2	A1739168 AA426249 A1199636 AW505198 AW977291 AA824583 AA883419 AA724079 A1015524 A1377728 AW293682 A1928140 AA731438 A1092404 A1085630 AA731340
430535	319643_1	AW968485 AW968670 AA480922 BE350425
432765	353907_1	AJ003429 AJ003367 AA564825
433523	368873_1	H29882 AW665533 AW149901 A1572917 AA598500 A1686466 A1336390 AW864390 AW864320
434763	392847_1	AA648618 AW974389 H51771
436295	41733_1	N73895 AJ001872
439092	468554_1	AA830149 AW978407 M85983 AW503637
439306	47088_1	BE220199 W01813 AF086118 N70760 BE221405
440947	505904_1	AA910403 A1815593 W58361 AW162520 A1816550
442481	543588_1	N99828 BE079873 A1110738 AF074645
445432	63943_1	AV653771 BE089370
448044	747195_1	A1458682 H24240 R14537 R18426 AW867082
449570	81018_1	AA001793 AA001871
449745	814534_1	A1668593 A1820774 R86205 H39971 H22177 H26241
450317	831956_1	A1692689 R14223 R18395
450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
450582	83933_1	AA164518 AA730973 W00417 W65303
450687	84327_1	A1339732 AA010300 AW515041 AA768334 N28860 AA425874 AA425118 AA865829 AW936878
452462	918580_1	AA495800 AA495737 AA010736 AA654716 AA640726
453682	977454_1	BE173515 BE173560 A1902860
454037	996287_1	T79703 T96307 AL079725
454096	1007449_1	AW998716 AW022148 N68020
454171	1049240_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
454457	1207274_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
454655	1228599_1	AW753456 AW753036 AW854868 AW854862
454860	1237732_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
454968	1247029_1	AW835767 AW835537 BE160187
455067	1252050_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
455276	1272541_1	AW854538 AW854418 AW854412
455646	1348557_1	BE176479 BE176678 BE176357 BE176550 AW888079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
455710	1352368_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
457374	328758_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
458912	823104_1	AA493662 AW897396 BE154814
		A1911066 A1933734 A1680888 AJ003599

TABLE 66C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400533	6981826	Minus	277132-277595
400746	7329328	Minus	147703-147896
401132	8705350	Minus	85679-85795
402145	8018280	Plus	113086-114800
403242	7637817	Minus	11297-12511
403481	9965004	Plus	93496-93633
403510	7652047	Plus	61866-62027
403667	6850483	Minus	1344-1442,1545-1697
404003	8655948	Plus	198349-199096
404581	9795980	Minus	69039-70100
404592	9943965	Minus	39067-39225
404848	8248647	Minus	23955-24034,25143-25264
404967	7523744	Minus	89944-90729
404995	6006247	Minus	154015-154123
405264	7329374	Plus	28556-28684
405321	3419846	Minus	44654-45210
405348	2914717	Minus	43310-43452
405510	7630909	Minus	101028-101174
405548	1532158	Plus	11552-11686

TABLE 67A: 689 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 67A lists about 689 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 689 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
5	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	73.2
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	65.0
	432441	AW292425	Hs.163484	ESTs	56.0
	446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cati	55.0
	400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	48.1
10	414569	AF109298	Hs.118258	prostate cancer associated protein 1	41.4
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	40.3
	419526	AI821895	Hs.193481	ESTs	35.9
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	35.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
15	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	33.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	32.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	32.6
	400292	AA250737	Hs.72472	BMP-R1B	28.8
	400287	S39329	Hs.181350	kallikrein 2, prostatic	28.8
20	425075	AA506324	Hs.1852	acid phosphatase, prostate	28.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.8
	415539	AI733881	Hs.72472	BMP-R1B	27.0
	428819	AL135623	Hs.193914	KIAA0575 gene product	25.7
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	25.5
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	24.8
	407168	R45175	Hs.117183	ESTs	24.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	23.6
	428336	AA503115	Hs.183752	microseminoprotein, beta-	23.5
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	23.4
30	403047			NM_005656*:Homo sapiens transmembrane pr	23.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	22.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	21.6
	407709	AA456135	Hs.23023	ESTs	21.5
	401424			NM_001172:Homo sapiens arginase, type II	20.6
35	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	19.7
	434666	AF151103	Hs.112259	T cell receptor gamma locus	18.5
	415989	AI267700		ESTs	17.9
	437052	AA861697	Hs.120591	ESTs	17.8
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	16.8
40	431548	AI834273	Hs.9711	novel protein	16.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	16.5
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	16.5
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	16.5
	413597	AW302885	Hs.117183	ESTs	16.1
45	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	15.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	15.3
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	15.3
	407122	H20276	Hs.31742	ESTs	15.1
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	14.1
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	13.9
	426501	AW043782	Hs.293616	ESTs	13.9
	428898	AB033070	Hs.194408	KIAA1244 protein	13.7
	418961	AW967646	Hs.23023	ESTs	13.3
	448519	AW175665	Hs.278695	Homo sapiens protein mRNA, complete cds	13.2
55	418848	AI820961	Hs.193465	ESTs	13.1
	428398	AI249368	Hs.98558	ESTs	13.0
	429220	AW207206		ESTs	12.7
	401451			NM_004496*:Homo sapiens hepatocyte nucle	12.4
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	12.4
60	419078	M93119	Hs.89584	insulinoma-associated 1	12.3
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.9
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.4
	429918	AW873986	Hs.119383	ESTs	11.3
65	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	412446	AI768015		ESTs	11.1
	433404	T32982		ESTs	10.9
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	10.6
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	10.4
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.3
	418278	AI088489	Hs.83937	hypothetical protein	10.3
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	10.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	10.2
75	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	10.1
	449625	NM_014253		odc (odd Oz/ten-m, Drosophila) homolog 1	10.1
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	10.0
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheu	9.8
	437718	AI927288	Hs.196779	ESTs	9.8
80	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	9.7
	453160	AI263307		H2B histone family, member L	9.7
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	9.7
	450325	AI935962	Hs.91973	ESTs	9.6
	434170	AA626509	Hs.122329	ESTs	9.6
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	9.6

	447033	AI357412	Hs.157601	ESTs	9.5
	401747			Homo sapiens keratin 17 (KRT17)	9.3
	434423	NM_006769	Hs.3844	LIM domain only 4	9.3
5	411887	AW182924	Hs.128790	ESTs	9.2
	457211	AW972565	Hs.32399	ESTs, Weakly similar to SS1797 vasodilat	9.2
	415263	AA948033	Hs.130853	ESTs	9.2
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	9.2
	421895	N62293	Hs.45107	ESTs	9.1
10	432101	AI918950	Hs.123642	EphA3	9.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.0
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	8.9
	420218	AW958037		ribosomal protein L4	8.8
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	8.6
15	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	8.6
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	8.5
	445100	AW967109	Hs.13804	hypothetical protein dJ462023.2	8.5
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	8.5
20	416182	NM_004354	Hs.79069	cyclin G2	8.5
	431542	H63010	Hs.5740	ESTs	8.4
	447397	BE247676	Hs.18442	E-1 enzyme	8.3
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothe	8.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	8.1
25	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	8.1
	451684	AF216751	Hs.26813	CDA14	8.1
	437124	AA554458		KIAA0666 protein	8.0
	416239	AL038450	Hs.48948	ESTs	8.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.9
30	424800	AL035588	Hs.153203	MyoD family inhibitor	7.9
	428728	NM_016625	Hs.191381	hypothetical protein	7.9
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	7.8
	442049	AA310393	Hs.190044	ESTs	7.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.8
35	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	7.7
	443180	R15875	Hs.258576	claudin 12	7.5
	433285	AW975944	Hs.237396	ESTs	7.5
	410870	U81599	Hs.66731	homeo box B13	7.4
	418836	AI655499	Hs.161712	ESTs	7.4
40	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	7.3
	431992	NM_002742	Hs.2891	protein kinase C, mu	7.3
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	7.3
	432586	AA568548		ESTs	7.3
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	7.3
45	435047	AA454985	Hs.54973	cadherin-like protein VR20	7.3
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypothe	7.3
	422728	AW937828	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.2
	426108	AA622037	Hs.166468	programmed cell death 5	7.1
	433323	AA805132	Hs.159142	ESTs	7.1
50	423349	AF010258	Hs.127428	homeo box A9	7.0
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	6.9
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	6.9
	438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	6.8
55	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.8
	418601	AA279490	Hs.86368	catmegin	6.8
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	6.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	6.8
	425465	L18964	Hs.1904	protein kinase C, iota	6.6
60	450377	AB033091		KIAA1265 protein	6.6
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	6.6
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	6.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	6.5
65	440774	AI420611	Hs.153934	ESTs	6.5
	413992	W26276	Hs.136075	RNA, U2 small nuclear	6.4
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	6.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.4
70	451027	AW519204	Hs.40808	ESTs	6.4
	436063	AK000028		ribosomal protein S24	6.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	6.3
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.2
75	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	6.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.2
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.1
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	6.1
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	6.1
80	448045	AI297436	Hs.20166	prostate stem cell antigen	6.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.0
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.0
	433517	AW022133	Hs.189838	ESTs	6.0
	424036	AA770688		H2A histone family, member L	5.9

	420092	AA814043	Hs.88045	ESTs	5.9
	410268	AA316181	Hs.61635	sbx transmembrane epithelial antigen of	5.8
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	5.8
5	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	5.8
	450244	AA007534	Hs.125062	ESTs	5.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.7
	451952	AL120173	Hs.301663	ESTs	5.7
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	5.7
10	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1	5.7
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.7
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheli	5.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	5.7
	415621	AI648602	Hs.55468	ESTs	5.7
15	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.6
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.5
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	5.5
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	5.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.4
20	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	5.4
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	5.4
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.4
	410762	AF226053	Hs.66170	HSKM-B protein	5.4
	440594	AW445167	Hs.126036	ESTs	5.4
25	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.3
	447805	AW627932	Hs.302421	gemin4	5.3
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	5.3
	453308	AW959731	Hs.323099	ESTs	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
30	418555	AJ417215	Hs.87159	hypothetical protein FLJ12577	5.2
	404632			NM_022490:Homo sapiens hypothetical prot	5.1
	450861	AI523898	Hs.17617	ESTs	5.1
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.1
35	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.1
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.1
	410037	AB020725	Hs.58009	KIAA0918 protein	5.1
	410240	AL157424	Hs.61289	synaptotagmin 2	5.0
	403046			NM_005656*:Homo sapiens transmembrane pr	5.0
	419647	AA348947	Hs.91816	hypothetical protein	5.0
40	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	5.0
	450164	AJ239923	Hs.63931	ESTs	5.0
	417318	AW953937	Hs.240845	ESTs	4.9
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	4.9
45	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	4.9
	433852	AI378329	Hs.126629	ESTs	4.9
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.9
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.8
50	441021	AW578716	Hs.7644	H1 histone family, member 2	4.8
	453171	R76472	Hs.65646	ESTs	4.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	4.8
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	4.8
	419440	AB020689	Hs.90419	KIAA0882 protein	4.8
55	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.8
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	4.8
	421685	AF189723	Hs.105778	ATPase, Ca transporting, type 2C, member	4.7
60	431724	AA514535	Hs.283704	ESTs	4.7
	423242	AL039402	Hs.125783	DEME-6 protein	4.7
	434485	AI623511	Hs.118567	ESTs	4.7
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	4.6
65	414085	AA114016	Hs.75748	aldehyde dehydrogenase 1 family, member	4.6
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.6
	439735	AI635386	Hs.142846	hypothetical protein	4.6
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	4.6
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	4.5
70	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	4.5
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	4.5
	426006	R49031	Hs.22627	ESTs	4.5
	451982	F13038	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	4.5
75	415082	AA160000	Hs.137396	ESTs, Weakly similar to JCS238 galactosy	4.5
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.5
	423583	AL122055	Hs.129836	KIAA1028 protein	4.4
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	4.4
80	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.4
	429467	NM_004477	Hs.203772	FSHD region gene 1	4.4
	451752	AB032997		KIAA1171 protein	4.3
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.3
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.3
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.3

	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.3
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.3
	427308	D26087	Hs.174905	KIAA0033 protein	4.3
5	435706	W31254	Hs.7045	GL004 protein	4.3
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.2
	451406	AJ694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	4.2
	410076	T05387	Hs.7991	ESTs	4.2
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.2
10	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.2
	442501	AA315267	Hs.23128	ESTs	4.2
	436761	AJ817776	Hs.236557	ESTs	4.2
	420380	AA640891	Hs.102406	ESTs	4.2
	436556	AI364997	Hs.7572	ESTs	4.2
15	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	4.2
	446416	AV658299	Hs.163959	ESTs	4.2
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	4.2
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.1
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	4.1
20	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.1
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.1
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	4.1
	408418	AW963897	Hs.44743	KIAA1435 protein	4.1
	430945	U80669	Hs.55599	NK homeobox (Drosophila), family 3, A	4.1
25	432363	AA534489		gb:nf76g11.s1 NCL_CGAP_Co3 Homo sapiens	4.1
	447574	AF162666	Hs.18895	lousled-like kinase 1	4.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.0
	453857	AL080235	Hs.35861	DKFZP586E1521 protein	4.0
	444108	R55784	Hs.140942	ESTs	4.0
30	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.0
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
35	438825	BE327427	Hs.79953	ESTs	4.0
	433233	AB040927	Hs.301804	KIAA1494 protein	4.0
	415276	U88666	Hs.78353	SFRS protein kinase 2	4.0
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.0
	407819	R42185		ESTs	4.0
40	450402	BE218027	Hs.89969	ESTs	4.0
	432527	AW975028	Hs.102754	ESTs	4.0
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	3.9
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	3.9
	432435	BE218886	Hs.282070	ESTs	3.9
45	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	3.9
	411031	W37943	Hs.34892	KIAA1323 protein	3.9
	429259	AA420450	Hs.292911	Plakophilin	3.9
50	407813	AL120247	Hs.40109	KIAA0872 protein	3.9
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.9
	417958	AA767382	Hs.193417	ESTs	3.9
	427176	AW381569	Hs.40334	ESTs	3.9
55	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	3.8
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.8
	432675	AF791855		ESTs	3.8
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.8
	427479	BE410092	Hs.178471	KIAA0798 gene product	3.8
60	443162	T49951	Hs.9029	DKFZP434G032 protein	3.8
	413950	AA249096	Hs.32793	ESTs	3.8
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.8
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	3.8
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	3.8
65	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	3.8
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.8
	447620	AW290951		ESTs	3.8
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.8
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.8
70	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8
	459284	AF155660	Hs.300496	mitochondrial solute carrier	3.8
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	3.7
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	3.7
75	417081	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	3.7
	423337	NM_004655	Hs.127337	exin 2 (conductin, end)	3.7
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	3.7
	453469	AB014533	Hs.33010	KIAA0633 protein	3.7
	408063	BE086548	Hs.42346	calcineurin-binding protein calcarein-1	3.7
80	422072	AB018255	Hs.111138	KIAA0712 gene product	3.7
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	420522	AW957137	Hs.98541	hypothetical protein	3.6
	408833	AW612232	Hs.254835	ESTs	3.6
	426647	AA243464	Hs.294101	pro-B-cell leukemia transcription factor	3.6

	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.6
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	3.6
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.6
5	422424	AI186431	Hs.296638	prostate differentiation factor	3.6
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22552 fis, clone H	3.6
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.6
	421887	AW161450	Hs.109201	CGI-86 protein	3.6
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.6
10	412520	AA442324	Hs.795	H2A histone family, member O	3.6
	436476	AA326108	Hs.33829	bHLH protein DEC2	3.6
	414224	AU076964	Hs.7753	calumenin	3.5
	404922			NM_003071:Homo sapiens SWI/SNF related,	3.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.5
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.5
15	429686	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.5
	408001	AA046458	Hs.95296	ESTs	3.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.5
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.5
20	428055	AA420564	Hs.101760	ESTs	3.5
	418827	BE327311	Hs.47166	HT021	3.5
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.5
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	3.5
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.5
25	409151	AA306105		SEC22, vesicle trafficking protein (S. c	3.5
	439671	AW162840	Hs.6641	kinesin family member 6C	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to t54374 gene NF2	3.4
30	443884	N20617	Hs.194397	leptin receptor	3.4
	403752			NM_002753*:Homo sapiens mitogen-activate	3.4
	427723	AI355260	Hs.279789	histone deacetylase 3	3.4
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.4
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.4
35	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.4
	433647	AA603367	Hs.222294	ESTs	3.4
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	427715	BE245274	Hs.180428	KIAA1181 protein	3.3
40	437617	AI026701	Hs.5716	KIAA0310 gene product	3.3
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.3
	414407	AA147026	Hs.76704	ESTs	3.3
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.3
	435655	AW105663	Hs.6947	HSPC069 protein	3.3
45	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.3
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.3
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.3
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.3
50	420568	F09247	Hs.247735	protocadherin alpha 10	3.3
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	3.3
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	3.3
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.3
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	3.3
55	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.3
	409960	BE261944		hexokinase 1	3.3
	433891	AA613792		gb:nc97h03.s1 NCL CGAP_Pr2 Homo sapiens	3.3
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.3
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3
60	419972	AL041465	Hs.182982	golgin-67	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.3
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.3
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.3
65	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.3
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.3
	414922	D00723		glycine cleavage system protein H (amino	3.3
	437898	W81260	Hs.43410	ESTs	3.2
	426126	AL118747	Hs.26691	ESTs	3.2
70	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.2
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.2
	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.2
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.2
	401519			C15000476*:gil12737279[ret]XP_012163.1]	3.2
75	419517	AF052107	Hs.90797	Homo sapiens clone Z3620 mRNA sequence	3.2
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.2
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.2
	453288	AW583292	Hs.274412	similar to yeast Upi3, variant A	3.2
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.2
80	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.2
	439593	BE073597	Hs.124863	ESTs	3.2
	451945	BE504055	Hs.211420	ESTs	3.2
	434614	AI249502	Hs.29669	ESTs	3.2
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.2

	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
	425810	AI923627	Hs.31903	ESTs	3.2
5	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.2
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.1
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.1
	436087	BE300296	Hs.5054	CGI-133 protein	3.1
10	414222	AL135173		sorbinol dehydrogenase	3.1
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.1
	418559	AA225048	Hs.104207	ESTs	3.1
	408784	AW971350	Hs.63386	ESTs	3.1
	424285	BE207168	Hs.146630	nuclear receptor subfamily 2, group F, m	3.1
15	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.1
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.1
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.1
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	3.1
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.1
20	445943	AW898533	Hs.181574	ESTs	3.1
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.1
	432426	AW973152	Hs.31050	ESTs	3.1
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.1
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.1
25	423453	AW450737	Hs.128791	CGI-09 protein	3.1
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.1
	436278	BE396290	Hs.5097	synaptogyrin 2	3.1
	432908	AI861896		ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.1
30	438705	AI049624	Hs.283390	ESTs, Weakly similar to T109260A B cell	3.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.1
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.1
	409757	NM_001898	Hs.123114	cystatin SN	3.1
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.1
35	434293	NM_004445	Hs.3796	EphB6	3.1
	410001	AB041036	Hs.57771	kallikrein 11	3.1
	434970	AW272262	Hs.225767	ESTs	3.1
	432800	BE391046	Hs.278962	AIM-1 protein	3.1
	423392	AA195037	Hs.169341	HTPAP protein	3.1
40	432205	AI806583	Hs.125291	ESTs	3.1
	448807	AI571940	Hs.7549	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1
	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.0
45	427315	AA179949	Hs.175563	Homo sapiens mRNA: cDNA DKFZp564N0763 (f	3.0
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.0
	432621	AI298501	Hs.211192	ESTs, Weakly similar to T46428 hypotheti	3.0
	429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	3.0
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.0
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.0
50	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.0
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.0
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.0
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.0
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	3.0
55	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.0
	449459	BE546846	Hs.195048	ESTs	3.0
	438523	H56220	Hs.278177	ESTs	3.0
	434263	N34895	Hs.44648	ESTs	3.0
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.0
60	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypotheti	3.0
	429966	BE081342	Hs.283037	HSPC039 protein	3.0
	412652	AI801777		ESTs	3.0
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	3.0
	450832	AW970602	Hs.105421	ESTs	3.0
65	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	3.0
	436032	AA150797	Hs.109276	latexin protein	3.0
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.0
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	2.9
	432302	AA345857	Hs.274307	KIAA1442 protein	2.9
70	415172	AF079529	Hs.78106	phosphodiesterase 6B	2.9
	412925	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.9
	413142	M81740	Hs.75212	omithine decarboxylase 1	2.9
	437179	AA393508		serologically defined colon cancer antig	2.9
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	2.9
75	439609	AW971945	Hs.293236	ESTs	2.9
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	2.9
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	2.9
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	2.9
	420061	AW024937	Hs.29410	ESTs	2.9
80	431663	NM_016569	Hs.267182	TBX3-iso protein	2.9
	417622	AW298163	Hs.82318	WAS protein family, member 3	2.9
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.9
	446791	AI632278	Hs.195922	ESTs	2.9
	433313	W20128	Hs.296039	ESTs	2.9

	428465	AW970976	Hs.293653	ESTs	2.9
	457489	AI693815	Hs.127179	cryptic gene	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
5	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	2.9
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	2.9
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.9
	413125	BE244589	Hs.75207	glyoxalase I	2.9
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.9
10	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	2.9
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.9
	437296	AA350994	Hs.20281	KIAA1700	2.9
	421254	AK001724	Hs.102950	coat protein gamma-cop	2.9
	445109	AF039916	Hs.12330	ecolynucleoside triphosphate diphosphohyd	2.9
15	423551	AA327598	Hs.89633	ESTs	2.9
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	2.9
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.9
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	2.9
	423396	AI382555	Hs.127950	bromodomain-containing 1	2.8
20	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	2.8
	441345	AW068579	Hs.7780	Homo sapiens mRNA: cDNA DKFZp564A072 (fr	2.8
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	2.8
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.8
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	2.8
25	418166	AI754416		Cdc42 effector protein 3	2.8
	448734	BE614070	Hs.326416	Homo sapiens mRNA: cDNA DKFZp564H1916 (f	2.8
	413550	W03011	Hs.306881	MSTP043 protein	2.8
	426170	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	2.8
	444101	R19175	Hs.169793	ribosomal protein L32	2.8
30	425320	U29344	Hs.83180	fatty acid synthase	2.8
	431631	AA548906	Hs.122244	ESTs	2.8
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.8
	431416	AA532718		ESTs	2.8
35	447881	BE620886		GCN1 (general control of amino-acid synt	2.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	2.8
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	2.8
	439778	AL109729	Hs.99364	putative transmembrane protein	2.8
	425010	T16837	Hs.4241	ESTs	2.8
40	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.8
	450546	AA010200	Hs.175551	ESTs	2.7
	431674	AA098901	Hs.301642	G-protein coupled receptor	2.7
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.7
	443181	AI039201	Hs.283316	ESTs	2.7
	448913	AA194422	Hs.22564	myosin VI	2.7
45	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	2.7
	452941	AL110347	Hs.31074	N-sulfolglucosamine sulfolhydrolase (sulfa	2.7
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	2.7
	411190	AA306342	Hs.69171	protein kinase C-like 2	2.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	2.7
50	407192	AA609200		gb:af12a02.s1 Soares_testis_NHT Homo sap	2.7
	434747	AA837085		ESTs	2.7
	428171	AA489323	Hs.182825	ribosomal protein L35	2.7
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	2.7
55	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	2.7
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.7
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.7
	445596	R89543	Hs.12942	vesicle trafficking protein	2.7
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.7
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	2.7
60	438157	AW137011	Hs.49576	ESTs	2.7
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	2.7
	409648	AW451449	Hs.57749	ESTs	2.7
	401866			Target Exon	2.7
	400301	X03635	Hs.1657	estrogen receptor 1	2.7
65	453390	AA862496	Hs.28482	ESTs	2.7
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.7
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	2.7
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.7
70	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	2.7
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	2.7
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	2.7
	445098	AL050272	Hs.12305	DKFZP566B183 protein	2.7
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.7
75	409650	T08490	Hs.288969	HSCARG protein	2.7
	452707	AI093823	Hs.45070	ESTs	2.7
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.7
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.7
80	420818	AW963635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	2.7
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.7
	406627	T64904	Hs.163780	ESTs	2.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.7
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.6
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.6

	440695	AW088363	Hs.246240	ESTs	2.6
	416941	BE000150	Hs.48778	ribon protein	2.6
	422717	AI557623	Hs.119475	cold Inducible RNA-binding protein	2.6
5	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	2.6
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.6
	401197			ENSP00000229263*-HSPC213.	2.6
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.6
	410297	AA148710		lumican	2.6
10	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.6
	437546	AW074836	Hs.173984	T-box 1	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.6
15	408157	AA047685	Hs.62946	ESTs	2.6
	420805	L10333	Hs.99947	reticulin 1	2.6
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.6
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f	2.6
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	2.6
20	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	2.6
	425174	D87450	Hs.154978	KIAA0261 protein	2.6
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.6
	413435	X51405	Hs.75360	carboxypeptidase E	2.6
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	2.6
25	426180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.6
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	2.6
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.6
	406670	W79632	Hs.256301	hypothetical protein MGC13170	2.6
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.6
30	429922	Z97630	Hs.226117	H1 histone family, member 0	2.6
	449518	BE395253	Hs.30861	ESTs	2.6
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.6
	428343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.6
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.6
35	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.6
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.6
	434672	AW294020	Hs.117721	ESTs	2.6
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.6
40	452576	AB023177	Hs.29900	KIAA0960 protein	2.6
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor I	2.6
	430375	AW371048	Hs.93758	H4 histone family, member H	2.6
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.6
	424339	BE257148		endoglycan	2.6
45	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	2.6
	451040	AA324743	Hs.40808	ESTs	2.6
	445636	AW105401		ribosomal protein L29	2.6
	419175	AW270037		KIAA0779 protein	2.6
	422000	M30599	Hs.110637	homeo box A10	2.6
50	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.6
	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	2.6
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	2.5
	406789	AI041403		ribosomal protein L29	2.5
55	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.5
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.5
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.5
	436165	AI373544	Hs.331328	intermediate filament protein syncollin	2.5
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.5
	452827	AI571835	Hs.55468	ESTs	2.5
60	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.5
	431108	AA991508	Hs.105317	ESTs	2.5
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.5
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.5
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	2.5
	438821	AA826425	Hs.192375	ESTs	2.5
65	421091	W22821		ribosomal protein L26	2.5
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.5
	400263			Eos Control	2.5
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.5
70	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (o-erb-b2,	2.5
	431615	AW295859	Hs.235860	ESTs	2.5
	433037	NM_014158	Hs.279938	HSPC067 protein	2.5
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.5
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.5
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	2.5
75	450628	AW382884	Hs.204715	ESTs	2.5
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.5
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.5
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.5
	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.5
80	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.5
	416737	AF154335	Hs.79691	LIM domain protein	2.5
	414869	AA157291	Hs.21479	ubiquitin 1	2.5
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.5
	403532			NM_024638:Homo sapiens hypothetical prot	2.5

5	418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.5
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothet	2.5
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.5
	414556	AW975063	Hs.343443	ribosomal protein L36	2.5
	446911	N27605	Hs.16492	DkFZP564G2022 protein	2.5
	435126	AI393666	Hs.42315	p10-binding protein	2.5
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.5
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.5
10	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	2.5
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.5
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fls, clone NT	2.5
	443837	AI984625	Hs.9884	spindle pole body protein	2.5
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	2.5
15	435021	AA922192	Hs.73962	ESTs	2.5
	435750	AB029012	Hs.4990	KIAA1089 protein	2.5
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.5
	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.5
	425976	C75094	Hs.334514	NG22 protein	2.5
20	449458	AI805078	Hs.208261	ESTs	2.5
	428013	AF151020	Hs.181444	hypothetical protein	2.5
	424369	R87622	Hs.26714	KIAA1831 protein	2.5
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.5
	452779	AA418775	Hs.47234	ESTs	2.5
25	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.5
	438682	AA354489	Hs.222103	EBP50-PDZ Interactor of 64 kD	2.5
	427515	T79526	Hs.179516	Integral type I protein	2.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	2.5
30	TABLE 67B				
	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
35	Pkey	CAT Number	Accession		
	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153		
			BG285837 AI720344 BF541715 AA355086 AA172236		
40	429220	15103_7	AW341473 AA448195 AW207208 AI951341 AA969259		
	412446	63467_1	BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514		
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			AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815		
45	433404	7392_1	BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261		
			AV725377 AI423298 AI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421		
			N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433		
	449625	249224_1	BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526		
			BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360		
50	453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307		
			AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H07705 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991		
			AA084581 AA033610 AV742510 AV735788 R08336		
	420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756		
			AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727		
55	437124	59408_1	AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA829715 AI453010		
			N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 AI47364 N34880 AI147024 T86860		
			AI219716 AA960926 H25544 BI85123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742		
			AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA869970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080		
			AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744		
			T98800 N56980 BG108636 N49381 R49886 D61278 BI756612 AA508234 R49885 BF850422		
60	432586	6633_1	BC022881 AI150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548		
	438869	52134_1	AF075009 R63109 R63068		
	450377	12109_1	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695		
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65			AW072470 AI041596 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699		
			AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398		
			BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866		
			AI699181 N73808 H08164		
	436063	5483_1	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970		
			N40094 N28596 AA884747 AA512890 BG436553		
70	428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469529 AW968804 AA425658		
			AA769094 BF446026 AW118719 AI332765 AW500888 AW576558 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361		
			AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040		
			AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967		
			AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166		
75	424036	6226_1	NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377		
			AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096		
			BM045465 AL531028 BG437151 BE868021 AA179427		
	450203	19009_1	AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846		
			AI024796 AW020098 BI491127 AI336444 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192		
80	451752	10408_5	AB032997 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW259901		
			BF057835 BE465977 AI621269 BE465983 BF756369 N74056 AI817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333		
	432363	1234917_1	AW970240 AA534489 AW970323		

422890	61426_1	AK057805 AW162343 AJ190479 AI093318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 AI632565 BE502530 BI792383 BF056928 AA449241 AI651825 AA805324 AI264883 AW196918 AA948267 AI953735 AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI356013 AI867923 BG911906 D81142 C15616 AL153897 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW204071 BI819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
5	417379 407819	AA196390 AA507837 AA196468 AK056626 AI800896 BF939022 BE644718 AI954754 BE218177 BE348567 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185
10	419733	AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA805643 AW188870 BE705664 BE706539 BE153177 BF084925 AI133779 AW951788 AA659693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF687723 H28581 AA249370 BF726698 BE841554 BI045099 T84625 AW129678 BG770826
15	432675 447620 409151	AW973834 AI791932 AI791855 AI732640 AA558833 AA559897 AI821610 AI973051 AI400921 AI796154 AW241817 AW290951 NM_004892 AF047442 BE275338 BF724863 BI917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 AI902726 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435520 AI356111 H00525 AV749060 BG944497 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE050972 BF693195 AV738979 R65855 R80136 AA484677
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25	433891 414922	AW182329 AA613792 T05304 AW858385 BG107484 AA632009 AI432670 AI656660 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI091245 AI651454 BF434889 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI460102 BM023318 BE328188 AI952820 AI581363 AA557165 AI695577 AI562079 AI700926 AI470561 BF063058 AW196387 AU132984 BI064046 AI970157 R02122 H55924 AI521721 AA808262 AA725223 BI756003 AW339821 AA805951 AI287969 AW664827
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40	434194 432908 412652	AF119847 AA437261 AA436987 AI132965 AF150424 AI861896 AA570057 AV738855 AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981
45	437179	AK055109 BC019085 AA187684 BGG65226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N09081 AA771919 AI092259 AI028416 AI074114 BGG65638 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422
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70		
75		
80		

445636	8561_5	BF339388 AJ345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 AA090672
419175	35068_1	AB018322 BC012480 BI524873 AW655554 AJ934469 AJ479916 BF096179 BF096162 BF096132 AA744972 AJ951988 AI858339 BE076331 AA886998 AJ570585 AJ916688 AJ678811 AJ693109 AJ308135 AA669046 AA961064 AJ018062 H80618 BE221942 R52609 AJ915164 AA365626 Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AJ275392 AJ273455 R52553 AA829920 H80652 AA360728 F10618 AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AJ341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AJ364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AJ187299 AJ609644 Z40516 AW952314
441128	20932_1	BC014072 BE328850 AJ356567 AI148171 AJ022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AJ359627 BG674574 BE903322
406789	0_0	AI041403 Z49148
421091	24941_2	AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645896 AJ922406 AA778161 BF345973 AW195853 AI687121 AJ336147 AJ091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI536396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AL568301 AL567278 BI522445 BI754384 BG819375 BF835950 AA323718 AA860955 AO89847 AL520776 AL526045 AL538507 AL567798 AL536876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896 Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AJ560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033488 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE833685 BE166758 BM452445 AJ937808 AW026128 N23684 AW006041 AJ337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084

TABLE 67C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NI_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816, 119119-119244, 119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859, 56369-56511
404922	7341893	Plus	13248-13428
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401519	6649315	Plus	157315-157950
401785	7249190	Minus	165776-165996, 166189-166314, 166408-16656
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833, 5708-5895
401197	9719705	Plus	176341-176452
403532	8076842	Minus	81750-81901

TABLE 68A: 995 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 68A lists about 995 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 995 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 85th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	85.5
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	68.6
446057	AA202227	Hs.149358	Trp-p8 transient receptor potential catl	65.6
400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	61.9
432441	AW292425	Hs.163484	ESTs	60.4
419526	AJ821895	Hs.193481	ESTs	45.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	45.7
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	45.2
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	44.9
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	40.9
453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	39.6

	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	37.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.7
	400292	AA250737	Hs.72472	BMP-R1B	31.4
5	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.4
	409262	AK000531	Hs.52256	hypothetical protein FLJ20524	31.4
	428819	AL135623	Hs.193914	KIAA0575 gene product	31.2
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	30.3
	407168	R45175	Hs.117183	ESTs	29.6
10	400287	S39329	Hs.181350	kallikrein 2, prostatic	29.6
	415539	AI733881	Hs.72472	BMP-R1B	28.8
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	28.8
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	28.1
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	27.5
15	403047			NM_005656*:Homo sapiens transmembrane pr	27.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	25.7
	428336	AA503115	Hs.183752	microseminoprotein, beta-	25.0
	401424			NM_001172:Homo sapiens arginase, type II	24.9
20	407709	AA456135	Hs.23023	ESTs	24.7
	407122	H20276	Hs.31742	ESTs	24.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	23.2
	415989	AI267700		ESTs	23.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	22.7
	437052	AA861697	Hs.120591	ESTs	22.6
25	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	22.5
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	21.2
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	20.8
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	20.5
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	20.5
30	431548	AI834273	Hs.9711	novel protein	19.8
	434666	AF151103	Hs.112259	T cell receptor gamma locus	19.4
	426501	AW043782	Hs.293616	ESTs	19.3
	413597	AW302885	Hs.117183	ESTs	18.9
35	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	18.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	18.0
	429220	AW207206		ESTs	17.9
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	17.6
	418961	AW967646	Hs.23023	ESTs	17.3
40	428898	AB033070	Hs.194408	KIAA1244 protein	17.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	16.8
	428398	AI249368	Hs.98558	ESTs	16.3
	419078	M93119	Hs.89584	insulinoma-associated 1	15.8
	450382	AA397658	Hs.50257	Homo sapiens cDNA FLJ13598 fis, clone PL	15.4
45	449625	NM_014253		odt (odd Oz/tan-m, Drosophila) homolog 1	15.2
	401451			NM_004496*:Homo sapiens hepatocyte nucle	14.9
	447033	AI357412	Hs.157601	ESTs	14.9
	452594	AI076405	Hs.29981	solute carrier family 26 (sulfate transp	14.7
	448519	AW175665	Hs.278695	Homo sapiens protein mRNA, complete cds	14.6
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	14.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	14.4
	418848	AI820961	Hs.193465	ESTs	14.3
	429918	AW873986	Hs.119383	ESTs	14.2
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	14.1
55	418278	AI088489	Hs.83937	hypothetical protein	14.1
	408000	L11690	Hs.198689	bulbous pemphigoid antigen 1 (230/240kD)	13.9
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	13.3
	432101	AI918950	Hs.123642	EphA3	13.3
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	13.1
60	412446	AI768015		ESTs	12.7
	437718	AI927288	Hs.196779	ESTs	12.6
	433404	T32982		ESTs	12.6
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	12.6
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.5
65	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	12.5
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	12.4
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	12.4
	453160	AI263307		H2B histone family, member L	12.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	12.1
70	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	12.1
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	11.9
	424692	AA429834	Hs.151791	KIAA0092 gene product	11.7
	415263	AA948033	Hs.130853	ESTs	11.3
75	416182	NM_004354	Hs.79069	cyclin G2	11.3
	420218	AW958037		ribosomal protein L4	11.3
	411887	AW182924	Hs.128790	ESTs	11.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.2
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	11.2
80	450325	AI935962	Hs.91973	ESTs	11.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	11.1
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.0
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	11.0
	428600	AW863261	Hs.138860	hypothetical protein DKFp434K1421	11.0

5	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	11.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	10.7
	434423	NM_006769	Hs.3844	LIM domain only 4	10.6
	434170	AA626509	Hs.122329	ESTs	10.6
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.5
10	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	10.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	10.4
	421896	N62293	Hs.45107	ESTs	10.3
	401747			Homo sapiens keratin 17 (KRT17)	10.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	10.1
15	431542	H63010	Hs.5740	ESTs	10.0
	447397	BE247676	Hs.18442	E-1 enzyme	10.0
	433285	AW975944	Hs.237396	ESTs	10.0
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	9.9
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	9.8
20	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	9.6
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	9.6
	442049	AA310393	Hs.190044	ESTs	9.6
	443180	R15875	Hs.258576	claudin 12	9.5
	406964	M21305		GENES predicted novel secreted protein	9.5
25	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	9.5
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	9.5
	448045	AJ297436	Hs.20166	prostate stem cell antigen	9.5
	451684	AF216751	Hs.26813	CDA14	9.5
	440594	AW445167	Hs.126036	ESTs	9.4
30	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	9.3
	418601	AA279490	Hs.86368	calmegin	9.3
	433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.2
	437124	AA554458		KIAA0666 protein	9.2
	428728	NM_016625	Hs.191381	hypothetical protein	9.2
35	438869	AF075009		gb:Homo sapiens full length insert cDNA	9.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	8.9
	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.9
	428342	AJ739168		Homo sapiens cDNA FLJ13458 fis, clone PL	8.9
	418836	AJ655499	Hs.161712	ESTs	8.8
40	409799	D11928	Hs.76845	phosphoserine phosphatase-like	8.8
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	8.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	8.7
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofor	8.7
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger)	8.7
45	418329	AW247430	Hs.84152	cystathionine-beta-synthase	8.7
	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	8.7
	425465	L18964	Hs.1904	protein kinase C, iota	8.5
	416239	AL038450	Hs.48948	ESTs	8.5
	436962	AW377314	Hs.5364	DKFZP5641052 protein	8.4
50	450164	AJ239923	Hs.63931	ESTs	8.4
	452744	AJ267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	8.4
	440774	AJ420611	Hs.153934	ESTs	8.3
	444922	AJ921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.3
	410870	U81599	Hs.66731	homeo box B13	8.3
55	435047	AA454985	Hs.54973	cadherin-like protein VR20	8.2
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	8.2
	451027	AW519204	Hs.40808	ESTs	8.2
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-4	8.2
	423349	AF010258	Hs.127428	homeo box A9	8.1
60	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.1
	432586	AA568548		ESTs	8.0
	426108	AA622037	Hs.166468	programmed cell death 5	8.0
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary osteo	8.0
	416653	AA768553	Hs.183145	metallothionein 1E (functional)	7.9
65	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.9
	450377	AB033091		KIAA1265 protein	7.8
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	7.7
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.7
	433323	AA805132	Hs.159142	ESTs	7.7
70	451952	AL120173	Hs.301663	ESTs	7.7
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	7.7
	421470	R27496	Hs.1378	annexin A3	7.7
	420092	AA814043	Hs.88045	ESTs	7.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (7.6
75	440749	W22335	Hs.7392	hypothetical protein MGC3199	7.6
	441866	BE464341	Hs.21201	necdin 3; DKFZP566B0846 protein	7.6
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	7.5
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.4
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	7.4
80	433517	AW022133	Hs.189838	ESTs	7.4
	415621	AJ648602	Hs.55468	ESTs	7.4
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	7.3
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	7.3
	450244	AA007534	Hs.125062	ESTs	7.2
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	7.2
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	7.2
	434485	AJ623511	Hs.118567	ESTs	7.2

5	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.1
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	7.1
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta)	7.0
	408418	AW963897	Hs.44743	KIAA1435 protein	7.0
	436063	AK000028		ribosomal protein S24	7.0
10	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.9
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	6.9
	428465	AW970976	Hs.293653	ESTs	6.9
	436476	AA326108	Hs.33829	bHLH protein DEC2	6.8
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	6.8
15	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.7
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.7
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	6.6
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	6.6
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	6.6
20	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.5
	410037	AB020725	Hs.58009	KIAA0918 protein	6.5
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.4
	409648	AW451449	Hs.57749	ESTs	6.4
25	448148	NM_016578	Hs.20509	HBV pX associated protein-8	6.4
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	6.4
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.3
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.3
	404632			NM_022490-Homo sapiens hypothetical prot	6.3
30	412935	BE267045	Hs.75064	tubulin-specific chaperone c	6.3
	453308	AW959731	Hs.323099	ESTs	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.3
	410762	AF226053	Hs.66170	HSKM-B protein	6.3
	436032	AA150797	Hs.109276	latexin protein	6.3
35	455508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	6.3
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	6.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	6.2
	424036	AA770688		H2A histone family, member L	6.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.2
40	450861	AI523898	Hs.17617	ESTs	6.1
	418821	AA436002	Hs.183161	ESTs	6.1
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	6.1
	432527	AW975028	Hs.102754	ESTs	6.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.1
45	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	6.1
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	6.1
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.0
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	6.0
	419647	AA348947	Hs.91816	hypothetical protein	6.0
50	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	6.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.9
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.9
	446416	AV658299	Hs.163959	ESTs	5.9
	407819	R42185		ESTs	5.9
55	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	5.9
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.9
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	5.8
	410240	AL157424	Hs.61289	synaptotagmin 2	5.8
60	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	5.7
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.7
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	5.7
65	433852	AI378329	Hs.126629	ESTs	5.7
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	5.6
	419440	AB020689	Hs.90419	KIAA0882 protein	5.6
	435706	W31254	Hs.7045	GL004 protein	5.6
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.6
70	442409	BE208843	Hs.129544	hypothetical protein MGC15438	5.6
	453171	R76472	Hs.65646	ESTs	5.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	5.6
	429638	AI916662	Hs.211577	kinecin 1 (kinesin receptor)	5.5
75	403046			NM_005656-Homo sapiens transmembrane pr	5.5
	447805	AW627932	Hs.302421	gemin4	5.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	5.4
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	5.4
80	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	5.4
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	5.4
	427308	D26067	Hs.174905	KIAA0033 protein	5.4
	409151	AA306105		SEC22, vesicle trafficking protein (S. c	5.4
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	5.4
	423242	AL039402	Hs.125783	DEME-6 protein	5.3
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	5.3

	415276	U88666	Hs.78353	SFRS protein kinase 2	5.3
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.3
	432435	BE218886	Hs.282070	ESTs	5.3
	417318	AW953937	Hs.240845	ESTs	5.3
5	429467	NM_004477	Hs.203772	FSHD region gene 1	5.3
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	5.3
	410076	T05387	Hs.7991	ESTs	5.3
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 28,	5.2
10	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	5.2
	436420	AA443966	Hs.31595	ESTs	5.2
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	5.1
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	5.1
	427176	AW381569	Hs.40334	ESTs	5.1
	450832	AW970602	Hs.105421	ESTs	5.1
15	448807	AI571940	Hs.7549	ESTs	5.1
	420568	F09247	Hs.247735	protocadherin alpha 10	5.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	5.0
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	5.0
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
20	452576	AB023177	Hs.29900	KIAA0960 protein	5.0
	431724	AA514535	Hs.283704	ESTs	5.0
	409757	NM_001898	Hs.123114	cystatin SN	5.0
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.0
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	5.0
25	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	5.0
	400301	X03635	Hs.1657	estrogen receptor 1	5.0
	426006	R49031	Hs.22627	ESTs	5.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
30	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.9
	444108	R55784	Hs.140942	ESTs	4.9
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.9
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.9
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.9
	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.9
35	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	4.9
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	4.9
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.9
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.9
40	442501	AA315267	Hs.23128	ESTs	4.8
	439735	AI635386	Hs.142846	hypothetical protein	4.8
	451752	AB032997		KIAA1171 protein	4.8
	423583	AL122055	Hs.129836	KIAA1028 protein	4.8
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	4.8
45	432363	AA534489		gb:mf76g11.s1 NCL_CGAP_Co3 Homo sapiens	4.8
	433313	W20128	Hs.296039	ESTs	4.8
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.8
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.8
	451982	F13036	Hs.27373	Homo sapiens mRNA: cDNA DKFZp564O1763 (f	4.7
	447574	AF162666	Hs.18895	tousled-like kinase 1	4.7
50	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.7
	420522	AW957137	Hs.98541	hypothetical protein	4.7
	417379	AA196390		gb:zfp99b10.s1 Stratagene muscle 937209 H	4.7
	411031	W37943	Hs.34892	KIAA1323 protein	4.7
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	4.7
55	441224	AU076964	Hs.7753	calumenin	4.7
	407813	AL120247	Hs.40109	KIAA0872 protein	4.7
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	4.7
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.7
60	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.7
	414922	D00723		glycine cleavage system protein H (amino	4.7
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.7
	438825	BE327427	Hs.79953	ESTs	4.7
	425174	D87450	Hs.154978	KIAA0261 protein	4.7
65	420380	AA640891	Hs.102406	ESTs	4.7
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.7
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.6
	436761	AI817776	Hs.236557	ESTs	4.6
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.6
70	404922			NM_003071:Homo sapiens SWI/SNF related,	4.6
	436556	AI364997	Hs.7572	ESTs	4.6
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	4.6
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.6
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.5
75	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.5
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.5
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	4.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.5
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.5
80	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.5
	453390	AA862496	Hs.28482	ESTs	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.5
	436873	NZ3874	Hs.50477	RAB27A, member RAS oncogene family	4.5

	408001	AA046458	Hs.95296	ESTs	4.4
	413950	AA249096	Hs.32793	ESTs	4.4
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	4.4
5	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	4.4
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	4.4
	433233	AB040927	Hs.301804	KIAA1494 protein	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.4
10	417958	AA767382	Hs.193417	ESTs	4.4
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	4.4
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.4
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
15	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	4.3
	452747	BE153855	Hs.61460	lg superfamily receptor LNIR	4.3
	429259	AA420450	Hs.292911	Plakophilin	4.3
	425092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	437967	BE277414	Hs.5947	met transforming oncogene (derived from	4.3
20	459284	AF155860	Hs.300496	mitochondrial solute carrier	4.3
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.3
	423453	AW450737	Hs.128791	CGI-09 protein	4.3
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.3
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	4.3
25	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	4.3
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	4.3
	450402	BE218027	Hs.89969	ESTs	4.3
	428055	AA420564	Hs.101760	ESTs	4.3
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	4.3
30	432675	AI791855		ESTs	4.2
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.2
	445707	AI248720	Hs.114390	ESTs	4.2
	410297	AA148710		tumican	4.2
	416737	AF154335	Hs.79691	LIM domain protein	4.2
35	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.2
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	4.2
	447620	AW290951		ESTs	4.2
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.2
40	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.2
	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	4.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	4.2
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.2
	427723	AI355260	Hs.279789	histone deacetylase 3	4.2
45	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	4.2
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	4.2
	428231	U17989	Hs.183105	nuclear autoantigen	4.2
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	4.1
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	4.1
50	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypothi	4.1
	408063	BE086548	Hs.42346	calcineurin-binding protein calcarsin-1	4.1
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	4.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.1
	427479	BE410092	Hs.178471	KIAA0798 gene product	4.1
55	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	4.1
	422072	AB018255	Hs.111138	KIAA0712 gene product	4.1
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	4.1
	449459	BE546846	Hs.195048	ESTs	4.1
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	4.1
60	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	412520	AA442324	Hs.795	H2A histone family, member O	4.0
	448663	BE614599		hypothetical protein MGC14797	4.0
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	4.0
	433647	AA603367	Hs.222294	ESTs	4.0
65	426030	BE243933	Hs.108842	zinc finger protein 22 (KOX 15)	4.0
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	4.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	4.0
	422634	NM_016010	Hs.118821	CGI-62 protein	4.0
	453469	AB014533	Hs.33010	KIAA0633 protein	4.0
70	418827	BE327311	Hs.47166	HT021	4.0
	446791	AI632278	Hs.195922	ESTs	4.0
	443884	N20617	Hs.194397	leptin receptor	4.0
	416857	AA188775	Hs.292453	ESTs	4.0
	401519			C15000476*:gij12737279[ref]XP_012163.1]	4.0
75	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.0
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.9
	408784	AW971350	Hs.63386	ESTs	3.9
	435655	AIW105663	Hs.6947	HSPC069 protein	3.9
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.9
80	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	3.9
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.9
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.9
	414869	AA157291	Hs.21479	ubimucin 1	3.9
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.9

	444190	AJ878918	Hs.10526	cysteine and glycine-rich protein 2	3.9
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.9
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.9
	435021	AA922192	Hs.73962	ESTs	3.9
5	412834	R77123	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.9
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	3.9
	408833	AW612232	Hs.254835	ESTs	3.9
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.9
	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.8
10	433345	AJ681545	Hs.152982	hypothetical protein FLJ13117	3.8
	421887	AW161450	Hs.109201	CGI-86 protein	3.8
	434614	AJ249502	Hs.29669	ESTs	3.8
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.8
	423270	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.8
15	413010	AA393273	Hs.76133	transcription factor 6-like 1 (mitochond	3.8
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.8
	439024	R96696	Hs.35598	ESTs	3.8
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.8
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.8
20	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	3.8
	422424	AJ186431	Hs.296638	prostate differentiation factor	3.8
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.8
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheri	3.8
25	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.8
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.8
	440695	AW088363	Hs.246240	ESTs	3.8
	429686	AJ871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.8
30	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	3.8
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.8
	426126	AL118747	Hs.26691	ESTs	3.8
	434263	N34895	Hs.44648	ESTs	3.8
	414407	AA147026	Hs.76704	ESTs	3.7
35	432426	AW973152	Hs.31050	ESTs	3.7
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	3.7
	432579	AF043244	Hs.278439	nuclear protein 3 (apoptosis repressor	3.7
	444101	R19175	Hs.169793	ribosomal protein L32	3.7
	432908	AJ861896		ESTs	3.7
40	432800	BE391046	Hs.278962	AIM-1 protein	3.7
	429966	BE081342	Hs.283037	HSPC039 protein	3.7
	419972	AL041465	Hs.182982	golgin-67	3.7
	410001	AB041036	Hs.57771	kallikrein 11	3.7
	432205	AJ806583	Hs.125291	ESTs	3.7
45	401197			ENSP00000229263*:HSPC213.	3.7
	420061	AW024937	Hs.29410	ESTs	3.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.7
	433577	AW007080	Hs.284192	ESTs	3.7
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.7
50	420805	L10333	Hs.99947	reticulon 1	3.7
	401886			Target Exon	3.7
	457183	H91882	Hs.118569	DNA-binding protein IDAX (inhibition of	3.7
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	3.7
55	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.7
	432388	X15218	Hs.2969	v-aki avian sarcoma viral oncogene homol	3.7
	438157	AW137011	Hs.49576	ESTs	3.7
	451945	BE504055	Hs.211420	ESTs	3.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.6
60	454229	AW957744	Hs.278469	lacrimal proline rich protein	3.6
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.6
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.6
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.6
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.6
65	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	3.6
	453049	BE537217	Hs.30343	ESTs	3.6
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLC	3.6
	408096	BE250162	Hs.83765	dihydrofolate reductase	3.6
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
70	450649	NM_001429	Hs.25272	E1A binding protein p300	3.6
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.6
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.6
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.6
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	3.6
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.6
75	427715	BE245274	Hs.180428	KIAA1181 protein	3.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	3.6
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.6
	403752			NM_002753*:Homo sapiens mitogen-activate	3.6
80	418559	AA225048	Hs.104207	ESTs	3.6
	438523	H56220	Hs.278177	ESTs	3.6
	438705	AJ049524	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.6
	443960	AJ093577	Hs.255416	hypothetical protein FLJ21986	3.5
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.5

	426695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.5
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.5
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	3.5
5	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.5
	433891	AA613792		gbcn097h03.s1 NCI_CGAP_Py2 Homo sapiens	3.5
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.5
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.5
	434672	AW294020	Hs.117721	ESTs	3.5
10	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.5
	434970	AW272262	Hs.225767	ESTs	3.5
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.5
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.5
	445943	AW898533	Hs.181574	ESTs	3.5
15	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.5
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.5
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.5
20	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.5
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.5
	436087	BE300296	Hs.5054	CGI-133 protein	3.5
	437898	W81260	Hs.43410	ESTs	3.5
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.5
25	439609	AW971945	Hs.293236	ESTs	3.5
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	3.5
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.5
	409960	BE261944		hexokinase 1	3.5
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.5
30	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.5
	442323	AW016669	Hs.29190	ESTs	3.5
	452707	AI093823	Hs.45070	ESTs	3.5
	421437	AW821252	Hs.104336	hypothetical protein	3.5
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.4
35	450628	AW382884	Hs.204715	ESTs	3.4
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.4
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	3.4
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.4
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.4
40	429922	Z97630	Hs.226117	H1 histone family, member 0	3.4
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.4
	434293	NM_004445	Hs.3796	EphB6	3.4
	414222	AL135173		sorbitol dehydrogenase	3.4
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
45	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	3.4
	411078	AI222020	Hs.182364	CocoaCrisp	3.4
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.4
	432302	AA345857	Hs.274307	KIAA1442 protein	3.4
	407944	R34008	Hs.239727	desmocollin 2	3.4
50	431674	AA098901	Hs.301642	G-protein coupled receptor	3.4
	408291	AB023191	Hs.44131	KIAA0974 protein	3.4
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.4
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.4
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.4
55	452295	BE379936	Hs.28866	programmed cell death 10	3.4
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.4
	439593	BE073597	Hs.124863	ESTs	3.4
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.4
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.4
60	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.3
	417315	AI080042	Hs.180450	ribosomal protein S24	3.3
	423392	AA195037	Hs.169341	HTPAP protein	3.3
	412652	AI801777		ESTs	3.3
	415172	AF079529	Hs.78106	phosphodiesterase 8B	3.3
65	418372	AA311833	Hs.84318	replication protein A1 (70kD)	3.3
	447958	AW796524	Hs.58644	Homo sapiens microsomal signal peptidase	3.3
	425010	T16837	Hs.4241	ESTs	3.3
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.3
	443181	AI039201	Hs.283316	ESTs	3.3
70	442064	AI422867	Hs.88594	ESTs	3.3
	431663	NM_016569	Hs.267182	TBX3-Iso protein	3.3
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	3.3
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	3.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	3.3
75	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypotheti	3.3
	436278	BE396290	Hs.5097	synaptogyrin 2	3.3
	424560	AA158727	Hs.150555	protein predicted by clone 23733	3.3
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.3
	418166	AI754416		Cdc42 effector protein 3	3.3
80	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.2
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	434747	AA837085		ESTs	3.2
	413125	BE244589	Hs.75207	glyoxalase I	3.2

	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.2
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	3.2
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	3.2
5	423396	AI382555	Hs.127950	bromodomain-containing 1	3.2
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	3.2
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	3.2
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypothell	3.2
	422173	BE385828	Hs.250619	phorbol-in-like protein MDS019	3.2
10	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	3.2
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.2
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.2
	407688	W25317	Hs.37616	Human D9 splice variant 8 mRNA, complete	3.2
	406214			NM_016371:Homo sapiens hydroxysteroid (1	3.2
15	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.2
	438714	AA814859	Hs.160074	ESTs	3.2
	433213	AW665130	Hs.137190	ESTs	3.2
	412170	D16532	Hs.73729	very low density lipoprotein receptor	3.2
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	3.2
20	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.2
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	3.2
	437179	AA393508		serologically defined colon cancer antig	3.2
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.2
25	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.2
	450546	AA010200	Hs.175551	ESTs	3.2
	409995	AW960597	Hs.129206	ESTs	3.2
	408739	W01556	Hs.44685	ESTs, Moderately similar to I38022 hypot	3.2
	438821	AA826425	Hs.192375	ESTs	3.2
	403532			NM_024638:Homo sapiens hypothetical prot	3.2
30	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	3.1
	414341	D80004	Hs.75909	KIAA0182 protein	3.1
	423044	AA320829	Hs.97266	protocadherin 18	3.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.1
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	3.1
35	423551	AA327598	Hs.89633	ESTs	3.1
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	3.1
	413550	W03011	Hs.306881	MSTP043 protein	3.1
	431933	AI187057	Hs.132554	ESTs	3.1
	439778	AL109729	Hs.99364	putative transmembrane protein	3.1
40	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.1
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.1
	421254	AK001724	Hs.102950	coat protein gamma-cop	3.1
	424339	BE257148		endoglycan	3.1
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	3.1
45	425320	U29344	Hs.83190	fatty acid synthase	3.1
	426170	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.1
	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.1
	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	3.1
	417622	AW298163	Hs.82318	WAS protein family, member 3	3.1
50	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	433036	AA574091	Hs.105964	ESTs	3.1
	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	3.1
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	3.1
	408380	AF123050	Hs.44532	diubiquitin	3.1
55	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	3.1
	445098	AL050272	Hs.12305	DKFZP566B183 protein	3.1
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	3.1
	437296	AA350994	Hs.20281	KIAA1700	3.1
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	3.1
60	448913	AA194422	Hs.22564	myosin VI	3.1
	415079	R43179	Hs.22695	hypothetical protein FLJ23548	3.0
	408157	AA047685	Hs.62946	ESTs	3.0
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	3.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.0
65	437546	AW074836	Hs.173984	T-box 1	3.0
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	3.0
	423932	T95633	Hs.189703	ESTs	3.0
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.0
	453293	AA382267	Hs.10653	ESTs	3.0
70	428171	AA489323	Hs.182825	ribosomal protein L35	3.0
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	3.0
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.0
	406627	T64904	Hs.163780	ESTs	3.0
	418259	AA215404		ESTs	3.0
75	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	3.0
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	3.0
	431416	AA532718		ESTs	3.0
	431631	AA548906	Hs.122244	ESTs	3.0
	409251	R10723	Hs.20573	ESTs	3.0
80	434974	AA778711		eukaryotic translation initiation factor	3.0
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	3.0
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.0
	433037	NM_014158	Hs.279938	HSPC067 protein	3.0

	411598	BE336654	Hs.70937	H3 histone family, member A	3.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	3.0
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.0
5	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	3.0
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	3.0
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	3.0
	432810	AA853400	Hs.23054	ESTs	3.0
10	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.0
	445696	R89543	Hs.12942	vesicle trafficking protein	3.0
	406670	W79632	Hs.256301	hypothetical protein MGC13170	3.0
	452779	AA418775	Hs.47234	ESTs	3.0
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.0
	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.0
15	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.9
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.9
	425920	AL049977	Hs.162209	claudin 8	2.9
	408927	T69981		gb:yc19d03.r1 Stratagene lung (937210) H	2.9
20	447881	BE620886		GCN1 (general control of amino-acid synt	2.9
	439584	AA838114	Hs.221612	ESTs	2.9
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.9
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.9
	422576	BE548555	Hs.118554	CGI-83 protein	2.9
25	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.9
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.9
	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.9
30	429351	AK001490	Hs.200016	hypothetical protein FLJ10628	2.9
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.9
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.9
	416439	AA180363	Hs.118769	ESTs	2.9
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
35	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.9
	428801	AW277121	Hs.254881	ESTs	2.9
	430462	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	2.9
	420552	AK000492	Hs.98806	hypothetical protein	2.9
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.9
40	418222	AI675881	Hs.86538	ESTs	2.9
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	2.9
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	2.9
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.9
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	2.9
45	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.9
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	2.9
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.9
	430375	AW371048	Hs.93758	H4 histone family, member H	2.9
	409650	T08490	Hs.288969	HSCARG protein	2.9
50	413588	AA971014	Hs.75432	IMP (inosine monophosphate) dehydrogenas	2.9
	412719	AW016610		ESTs	2.9
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.9
	439621	AI200281	Hs.123910	ESTs, Highly similar to B34087 hypothei	2.9
	437050	AA766420		ESTs	2.9
55	414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.9
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.9
	416941	BE000150	Hs.48778	niban protein	2.9
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.9
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.9
60	436823	AW749855		ESTs, Weakly similar to I38022 hypothei	2.8
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.8
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586i2022 (f	2.8
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	2.8
	457733	AW974812		ESTs	2.8
65	400860			Target Exon	2.8
	436165	AI373544	Hs.331328	Intermediate filament protein syncoilin	2.8
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	2.8
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.8
	421717	AF230924	Hs.107187	divalent cation tolerant protein CLTA	2.8
70	453912	AL121031		SWI/SNF related, matrix associated, acti	2.8
	435703	AW630133	Hs.83313	GK003 protein	2.8
	431108	AA991508	Hs.105317	ESTs	2.8
	451040	AA324743	Hs.40808	ESTs	2.8
	443837	AI984625	Hs.9884	spindle pole body protein	2.8
75	418196	AI745649	Hs.26549	KIAA1708 protein	2.8
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.8
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.8
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8
	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.8
80	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.8
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.8
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.8
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.8
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	2.8

	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.8
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.8
	423318	AW467064	Hs.5740	ESTs	2.8
5	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.8
	452827	AI571835	Hs.55468	ESTs	2.8
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypothe	2.8
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	2.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	2.8
10	419286	AA236005	Hs.128764	ESTs	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.8
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	2.8
	428054	AI948688	Hs.266619	ESTs	2.8
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.8
15	440080	AW051597		ESTs	2.8
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.8
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	2.8
	431525	AA506556	Hs.6185	KIAA1557 protein	2.8
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.8
20	433101	AW572317	Hs.12082	Homo sapiens mRNA: cDNA DKFZp566L203 (fr	2.8
	449052	AW029507	Hs.161102	ESTs	2.8
	418663	AK001100	Hs.41690	desmocollin 3	2.8
	442013	AA506476	Hs.10600	Human DNA sequence from clone RP11-353C1	2.8
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.8
25	453038	AW292415	Hs.20509	HBV pX associated protein-8	2.8
	419175	AW270037		KIAA0779 protein	2.8
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.8
	421091	W22821		ribosomal protein L26	2.8
	413435	X51405	Hs.75360	carboxypeptidase E	2.8
30	432651	AW973744	Hs.293100	ESTs	2.8
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.8
	454148	AW732837	Hs.42390	nasopharyngeal carcinoma susceptibility	2.8
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	2.8
	425491	AA883316	Hs.255221	ESTs	2.8
35	414556	AW975063	Hs.343443	ribosomal protein L36	2.8
	435126	AI393666	Hs.42315	p10-binding protein	2.8
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.7
	441128	AA570256		ESTs, Weakly similar to T23273 hypothe	2.7
40	440340	AW895503	Hs.125276	ESTs	2.7
	410339	AI916499	Hs.298258	ESTs	2.7
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.7
	406789	AI041403		ribosomal protein L29	2.7
	424130	AL050136	Hs.140945	Homo sapiens mRNA: cDNA DKFZp586L141 (fr	2.7
	449518	BE395253	Hs.30861	ESTs	2.7
45	410099	AA081630		KIAA0036 gene product	2.7
	422000	M30599	Hs.110637	homeo box A10	2.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	2.7
	415443	T07353	Hs.7948	ESTs	2.7
	432745	AI821926		gbn178f05.x5 NCL CGAP_Pr3 Homo sapiens	2.7
50	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.7
	424369	R87622	Hs.26714	KIAA1831 protein	2.7
	417831	H16423	Hs.82685	CD47 antigen (Rb-related antigen, integr	2.7
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	2.7
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypothe	2.7
55	400263			Eos Control	2.7
	435750	AB029012	Hs.4990	KIAA1089 protein	2.7
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothe	2.7
	421709	AA159394	Hs.107056	CED-6 protein	2.7
	421077	AK000061	Hs.101590	hypothetical protein	2.7
60	416359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA	2.7
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.7
	411605	AW006831		ESTs	2.7
	437133	AB018319	Hs.5460	KIAA0776 protein	2.7
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.7
65	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis, clone MA	2.7
	427657	AV652249	Hs.180107	polymerase (DNA directed), beta	2.7
	445636	AW105401		ribosomal protein L29	2.7
	443801	AW206942	Hs.253594	intron ottrichorhinophalangeal syndro	2.7
	420223	N27807		ribosomal protein L4	2.7
70	427515	T79526	Hs.179516	integral type I protein	2.7
	447673	AI823987	Hs.182285	ESTs	2.7
	411960	R77776	Hs.18103	ESTs	2.7
	433212	BE218049	Hs.121820	ESTs	2.7
	448244	BE613416	Hs.336425	Homo sapiens, clone MGC:17296, mRNA, com	2.7
75	441551	AA318224	Hs.296141	ESTs	2.7
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pompe disease,	2.7
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.7
	434851	AA806164	Hs.116502	ESTs	2.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.7
80	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.7
	432450	AI990739	Hs.158184	ORF	2.7
	426174	AA547959	Hs.115838	ESTs	2.7
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.7
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypothe	2.7

	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.7
	451558	NM_001089	Hs.26530	ATP-binding cassette, sub-family A (ABC1	2.7
	431615	AW295859	Hs.235860	ESTs	2.7
5	418649	AJ096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.7
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFp434N2412 (f	2.7
	438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.7
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.7
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
10	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.7
	412524	AA417613	Hs.44208	hypothetical protein FLJ23153	2.7
	435176	AA744875	Hs.189413	ESTs	2.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	2.7
	428013	AF151020	Hs.181444	hypothetical protein	2.7
15	441094	U33819	Hs.7647	MYC-associated zinc finger protein (puri	2.7
	451356	AA748418	Hs.164577	ESTs	2.7
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.7
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	2.7
	423476	AL035633		Human DNA sequence from clone RP5-1046G1	2.7
20	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	2.7
	404913			NM_024408: Homo sapiens Notch (Drosophil	2.7
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.7
	441054	AA913591		ESTs	2.6
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.6
25	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	2.6
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone H	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.6
	443666	AI458179	Hs.41528	ESTs, Weakly similar to neuronal thread	2.6
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	2.6
30	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.6
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.6
	421605	BE440108	Hs.106127	RNA polymerase I 16 kDa subunit	2.6
	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	2.6
	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	2.6
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibitor	2.6
35	430341	NM_006348	Hs.239631	golgi transport complex 1 (90 kDa subuni	2.6
	424956	AW198103	Hs.18724	ESTs, Weakly similar to granule cell mar	2.6
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	2.6
	408212	AA297567	Hs.43728	hypothetical protein	2.6
40	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypothetical pr	2.6
	425976	C75094	Hs.334514	NG22 protein	2.6
	448424	AW009892	Hs.31924	ESTs	2.6
	420164	AW339037	Hs.24908	ESTs	2.6
	443444	AW952619	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	2.6
45	412774	AA120865	Hs.23136	ESTs	2.6
	445922	AJ337316	Hs.147998	ESTs	2.6
	429925	NM_000786		cytochrome P450, 51 (lanosterol 14-alpha	2.6
	419222	AD001528	Hs.89718	spermine synthase	2.6
	417327	NM_004922	Hs.81964	SEC24 (S. cerevisiae) related gene famil	2.6
50	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.6
	408743	AL110246	Hs.47367	KIAA1785 protein	2.6
	434011	AW953437	Hs.5486	clone FLB5214	2.6
	434976	AI963821		ESTs	2.6
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.6
55	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6
	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.6
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFp5660134 (fr	2.6
	425017	AL119305	Hs.26409	ESTs	2.6
	440333	AI378424	Hs.288761	hypothetical protein FLJ21749	2.6
60	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.6
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.6
	409619	AK001015	Hs.55220	BCL2-associated atlanogene 2	2.6
	444550	BE250716	Hs.87614	ESTs	2.6
	446258	AI283476	Hs.263478	ESTs	2.6
65	440191	AI990417		tubulin, beta 5	2.6
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.6
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.6
	426841	AI052358	Hs.193726	ESTs	2.6
	435937	AA830893	Hs.119769	ESTs	2.6
70	425960	AW410645	Hs.164649	hypothetical protein DKFp434H247	2.6
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	2.6
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	2.6
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.6
	416751	T48130	Hs.5897	Homo sapiens mRNA; cDNA DKFp586P1622 (f	2.6
75	458946	AA009716	Hs.42311	ESTs	2.6
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.6
	449458	AI805078	Hs.208261	ESTs	2.6
	432409	AA806538	Hs.130732	KIAA1575 protein	2.6
	425184	BE278288	Hs.155048	Lutheran blood group (Aubergier b antigen	2.6
80	442336	AW340958	Hs.7572	ESTs	2.6
	445622	AF106697	Hs.12971	thioredoxin reductase beta	2.6
	440409	AW294316		ESTs	2.6
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.6
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	2.6

5	436972	AA284679	Hs.25640	claudin 3	2.6
	426809	BE313114	Hs.29706	ESTs	2.6
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.6
	457638	AI792670	Hs.144405	ESTs	2.6
	442821	BE391929	Hs.8752	transmembrane protein 4	2.5
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	2.5
	406764	AA429825	Hs.343443	ribosomal protein L36	2.5
	422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.5
10	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	2.5
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	2.5
	446091	AW022192		ESTs	2.5
	419848	AA251242	Hs.103238	ESTs	2.5
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	2.5
15	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	2.5
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.5
	447087	AW403870	Hs.301872	hypothetical protein MGC4840	2.5
	456050	R79445	Hs.76230	ribosomal protein S10	2.5
	426178	AA371409	Hs.105664	hypothetical protein FLJ22294	2.5
20	414528	AA148950	Hs.188838	ESTs	2.5
	426494	AL119528	Hs.170098	KIAA0372 gene product	2.5
	407656	AW747986	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f	2.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	2.5
	449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-like	2.5
25	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
	417386	AL037228	Hs.82043	D123 gene product	2.5
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalni	2.5
	408796	AA688292	Hs.170345	ESTs	2.5
	407627	AI419020	Hs.62620	chromosome 6 open reading frame 1	2.5
30	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synth	2.5
	415862	R51034	Hs.144513	ESTs	2.5
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	2.5
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	2.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypothi	2.5
35	449500	AW956345	Hs.12926	ESTs	2.5
	457090	AL080243	Hs.180920	ribosomal protein S9	2.5
	445389	NM_016831	Hs.12592	period (Drosophila) homolog 3	2.5
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	2.5
	452906	BE207039	Hs.306123	MAGEF1 protein	2.5
40	450341	N90956	Hs.17230	hypothetical protein FLJ22087	2.5
	419430	AI878942	Hs.90336	ATPase, H transporting, lysosomal (vacuo	2.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.5
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypothi	2.5
	431843	AA516420		ESTs, Weakly similar to I38022 hypothi	2.5
45	424795	AW102850	Hs.153177	ribosomal protein S28	2.5
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.5
	450704	H85157	Hs.40696	ESTs	2.5
	400262			Eos Control	2.5
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	2.5
50	418039	R06859	Hs.193172	ESTs, Weakly similar to I38022 hypothi	2.5
	429491	NM_012111	Hs.204041	chromosome 14 open reading frame 3	2.5
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.5
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	2.5
	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	2.5
55	424005	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	2.5
	429332	AF030403	Hs.199263	Ste-20 related kinase	2.5
	438572	BE267017	Hs.6315	acetylserotonin O-methyltransferase-like	2.5
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.5
	431188	W05656	Hs.169755	ESTs	2.5
60	408803	AF248953	Hs.24049	golgi autoantigen, golgin subfamily a, 2	2.5
	414482	S57498	Hs.76252	endothelin receptor type A	2.5
	437762	T78028	Hs.154679	synaptotagmin I	2.5
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.5
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.5
65	451585	AK001171	Hs.326422	hypothetical protein MGC4549	2.5
	424959	NM_005781	Hs.153937	activated p21cdc42hs kinase	2.5
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.5
	446054	AB014537	Hs.13604	KIAA0637 gene product	2.5
	452556	H78517	Hs.33905	ESTs	2.5
70	421026	AL047332	Hs.101067	GCN5 (general control of amino-acid synt	2.5
	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	2.5
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.5

TABLE 68B

75	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
80	Pkey	CAT Number	Accession	
	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236	
	429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259	

449625	249224_1	B1918168 AW779760 N48674 A1375997 AA235370 BG699146 A1913631 A1498402 A1016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 A1203107 R35004 F07491 R25094 R35360
412446	63467_1	BC021735 A1669212 A120184 A1769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908049 BE695424 BF908060 BF962832 BF952020 BF963134 B1035538 BF908052 BF908057 BF090026 BF943158 A1632924 BF512340 BF952021 BF960776 BF943437 BF942847 A1768015 F09778 F04816 F02721
433404	7392_1	AA102645 A1633838 AA617929 BF947001 B1035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815 BC022980 BF224081 BG149908 AW672842 BE670687 A1702161 AW341832 BE222503 N71836 A1026061 AW593116 AW083132 A1979261 AV725377 A1423298 A1640707 AW675518 A1032611 A1818044 A1299508 A1911386 A1270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433
453160	6028_5	BC009612 NM_003526 B1597616 AV761592 AV760377 A1601008 B1604131 BE645918 BG187760 BG181525 BG210634 BG192999 A1263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H07775 BF674991 BE769437 BG007856 AA037483 AW572535 A1143991 AA084581 AA033610 AV742510 AV735788 R08336
420218	191547_1	AW958037 R42557 A1337047 AA948360 A1638005 AA459950 A1624915 A1638047 A167856 A1521826 AA860305 A1932315 AW003092 AW271756 AW779380 AA609879 A1634791 A1493770 A1565211 Z41145 A1627952 AA303734 BE349457 AW196765 AA256627 BE089727
437124	59408_1	AL050013 BG939500 AW969191 AA769925 A1377973 A1625545 AA811365 AA521114 N24705 A1379579 AA424899 A1684571 AA829715 A1453010 N35401 AA677452 AA504340 A1209149 AA883574 A1379062 A1084455 A1280147 AA644327 BF432508 N27873 N47364 N34880 A1147024 T86860 A1219716 AA960926 H25544 B1857123 AW960489 AA599099 AA765246 AA328537 BG34703 AA890373 A1242765 AA824765 AA829886 N95742 A1218758 H25588 N36282 AA024987 N36687 B1919187 N49471 AA889970 AW166152 AA468546 A1262504 A1452782 AA554458 AA807080
438869	52134_1	AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 A1016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D61278 B1756812 AA508234 R49885 BF850422
428342	6712_1	AF075009 R63109 R63068 AK056315 A1015524 AA724079 B1713619 A1377728 AW293682 A1928140 A1092404 A1085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 A1332765 AW500888 AW576556 A1859571 AW499664 AW614573 AW629495 AW505314 W74704 A1356361 A1923640 AW070509 A1521500 A1042095 AA609309 AA761319 A1381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 A1392620 Z40708 A1985564 AW263513 AA913892 A1693486 AW263502 A1806164 AW291137 B1061872 B1059498 AA134476 AW084888 AA036967
450203	19009_1	AW370823 T55263 B1002756 AA489664 BF827261 W74741 BF963166 AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 A1819354 AW974068 A1393635 A1580846 A1024796 AW020098 B1491127 A1393644 N74993 AW472959 BM478854 B1597437 H12165 B1458612 BE543192
432586	6633_1	BC022881 A1150944 BG750783 AW754175 AW857737 A1911659 A1050036 AA554053 A1826259 AA568548 AB033091 A1520743 BE811813 N53332 N99716 A1561910 AA280655 BE710392 AV705100 AW293978 AW444566 AA281459 A1679751 A1873695 BG700891 B1553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 A1857643 A1768486 AW512118 AA479302 AW770384 AW072470 A1041596 A1049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 A1050294 BC010371 BF982270 A1042656 BF095732 AW812618 BF095731 BG212397 BF678765 B1038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 A1693720 AA743364 A1915793 N48185 A1573107 AA043474 A1351815 A1969490 A1910763 R50866 A1699181 N73808 H08164
436063	5483_1	AK000028 AA494483 A1298674 AA720773 AV761529 A1884670 A1936202 AW294235 D61652 BF881184 AV711384 N27154 A1926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593 NM_033445 BC001193 A1885781 BF794032 AA476620 AA810906 AA810905 A1291244 A1885097 A1359708 A1335629 H97396 A1344589 AA300377
424036	6226_1	AA457566 AW771833 BE465621 A1364068 A1364452 A1648505 A1918342 A1928670 AA866580 A1531029 AA866344 A1186419 BG329095 BM045465 A1531028 BG437151 BE868021 AA179427 AK056626 A1800896 BF939022 BE644718 A1954754 BE218177 BE348567 A1962406 AW293122 A1968798 A1457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185
407819	7392_2	NM_004892 AF047442 BE275338 BF724863 B1917206 BE276993 A1602308 AA306105 BM152505 BC001364 AW993411 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 A1902726 AA354813 B1092644 BG778400 B1260001 BG007325 A1267455 AA426574 A1160782 A172186 AA255500 AA34006 BG435520 A1356111 H00525 AV749060 BG944487 BG292031 AA902153 C04925 AA802160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R65855 R80136 AA484677
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A126014 AA778101 AA243218 AW498837 AA748311 A1754395 T15728 AA775369 AA858195 W73625 AA216784 AW513778 AW243958 A1061112 A1783806 AL569622 AA070466 BF229936 N58159 H80288 N32598 H80293 H80279 AL581253 AW571884 A1361698 AW073321 AA876464 H95640 T34421 AA331419 N99897 H80274 B1262120 AA205826 AA070716 AA653206 AA653483 BG389811 W20432 AA670295 AA653197 D51888 AA362527 BG056668 AW118162 AW073071 BE293868 BF792321 BF792258 BG107176 T56604 BM193566 H03238 AA618045 AA906004 B1085686 AA564566 A1221630 D52045 C14510 AA028390 W60153 H98743 A1682641 H28485 AA723093 A1081730 AA641309 AA687083 B1224818 AW204722 A1309186 A1215122 A1200785 BE467373 BM352502 A1304400 A193071 A1742483 AW003408 A1400201 A1656740 AW665173 A1215120 A1147599 A1803429 A1076110 A1754349 AW205103 A1262491 A1808243 A1281007 A1051273 A1004801 A1768918 AW103289 A1474637 A1264446 A1699509 BE704420 AA989278 AA918256 AA830956 AA989425 AA911929 AA262598 BE740563 BE727592 BE781003 BG030940 BE256750 W23528 AL517059 H95714 W00970 H74304 W32684 H38210 BE617658 AW593584 AA580593 H48653 N69544 AA181762 D20132 T55734 T60692 R76858 AA022948 AW770291 R50934 AA205918 R97811 H40328 R86252 AA936029 A1813809 AA933607 AA129695 AA548261 AA714393 AA775008 AA653439 AA983808 AA743251 AA401150 AA581651 AA555005 AA554408 D51494 C13991 D51478 D52007 AA489663 D52138 D51696 D55942 D52740 A1000118 AL516304 AL534259 N54940 AL579194 A1669399 A1342925 BE939201 AA633000 B1222963 A1619676 AW190306 BF035010 AW087897 A1864969 T57243 R48211 AA113880 R26594 C14467 C14444 A1195459 BE896346 BE270780 AL568073 BG389833 BE891549 B1223147 AW381001 AA448464 AW799744 AA412194 AA948107 AA927157 AA983841 BF752571 BE731304 A1380443 A1240179 AA977516 AA884643 AW079380 AW294316 A1913755 A1864320 A1685770 H25135 A1972654 A1538592 A1174783 R12271 R83569 A1274757 A1559500 AW022192 AW970134 AA516420 AA543007 BG057526 B1001430 A1498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60556 Z11692 X51466 NM_001961 M19997 B1224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 B1868669 BG337216 AW629935 BM016525 A1560409 AL562866 A1909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 B1261304 BG770095 B1033486 B1517580 BG876486 B1011828 A1313235 BG831724 BF869862 BG998348 B1011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 B1859287 BM016990 BG332369 BE933685 BE166758 BM452445 A1937808 AW026128 N23684 AW006041 A1337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 B1199487 BF761700 B1261519 BF944452 BF898506 A1038390 BM044934 AW381142 BG743618 BE769206 BE893973 B1015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 B1000274 BG255503 BG674499 BG774174 B1015084
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TABLE 68C

Pkey: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816, 119119-119244, 119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859, 56369-56511
404922	7341893	Plus	13248-13428
401519	6649315	Plus	157315-157950
401197	9719705	Plus	176341-176452
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833, 5708-5895
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401785	7249190	Minus	165778-165996, 166189-166314, 166408-16656
406214	7342036	Plus	86320-86523
403532	8076842	Minus	81750-81901
400860	9757499	Minus	151830-152104, 152649-152744
404913	7341740	Plus	97717-97976

Table 69A lists about 200 genes that are upregulated in human umbilical vein endothelial cells (HUVEC) compared to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 70A lists about 148 genes that are downregulated using the mean of vessels (veins and arteries) compared to the mean of HUVEC. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting relative level of mRNA expression.

TABLE 69A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of the mean of HUVEC AI's to the mean of the normal body tissue AI's

Pkey	ExAccn	UnigenelD	Unigene Title	R1
424806	AA382523	Hs.105689	MSTP031 protein	1.51
418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.94
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothet	1.60
442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.73
417944	AL077196	Hs.82985	collagen, type V, alpha 2	1.48
410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	1.91
452516	AA056630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.59
425139	AW630488	Hs.25338	protease, serine, 23	1.63
402463			NM_014624:Homo sapiens S100 calcium-bind	1.50
423798	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon	1.31
412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.53
419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (2.06
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	2.10
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	1.67
441457	AW996651	Hs.43838	ESTs	1.30
408296	AL117452	Hs.44155	DKFZP586G1517 protein	1.61
418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	1.87
413795	AL040178	Hs.142003	ESTs	1.64
441689	AI123705	Hs.289068	ESTs	1.44
412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	1.75
424432	AB037821	Hs.146858	protocadherin 10	1.65
432673	AB028859	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, membe	1.31
418683	U90908	Hs.87241	hypothetical protein from clones 23549 a	1.42
453085	AW954243		KIAA0251 protein	1.47
438887	R68857	Hs.265499	ESTs	1.49
436729	BE621807		transmembrane 4 superfamily member 1	1.91
400494			ENSP00000238970*:ClG30 (Fragment).	1.34
442506	BE566411		ESTs	1.54
425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	1.55
414476	AA301887	Hs.76224	EGF-containing fibulin-like extracellular	2.65
452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	1.62
422389	AF240635	Hs.115897	protocadherin 12	1.38
417124	BE122762	Hs.25338	ESTs	2.13
433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	1.31
419983	W55956	Hs.94030	Homo sapiens mRNA: cDNA DKFZp586E1624 (f	1.54
414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.51
450534	AI570189	Hs.25132	KIAA0470 gene product	1.43
449618	AI076459	Hs.15978	KIAA1272 protein	1.42
446098	AW072215	Hs.208470	ESTs	1.53
413281	AA861271	Hs.222024	transcription factor BMAL2	1.40
448674	W31178	Hs.154140	ovary-specific acidic protein	1.47
407061	X97748		gb:H.sapiens PTX3 gene promotor region.	1.33

	434846	AW295389	Hs.119768	ESTs	1.29
	408570	AL046406	Hs.103483	KIAA1798 protein	1.47
	436772	AW975688		metallothionein 1E (functional)	1.81
5	453789	AA628517	Hs.118502	ESTs	1.41
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	1.35
	441020	W79283	Hs.35962	ESTs	1.62
	401234			mitogen-activated protein kinase 8 inter	1.48
	420174	A1824144	Hs.199749	ESTs	1.75
10	445684	AK001696	Hs.13109	Ran binding protein 11	1.49
	418693	A1750878	Hs.87409	thrombospondin 1	1.89
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	1.77
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	2.02
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	1.64
15	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	1.26
	433376	A1249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	1.49
	422099	AA156022	Hs.111518	hypothetical protein	1.56
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	1.54
	445119	AF035121	Hs.12337	kinase insert domain receptor (a type II	1.40
20	438142	T90309	Hs.269651	ESTs	1.45
	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	1.44
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	1.42
	453459	BE047032	Hs.257789	ESTs	1.51
	442711	AF151073	Hs.8645	hypothetical protein	1.42
25	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xa	1.32
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.67
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.47
	407252	AA659037	Hs.163780	(AB075832) KIAA1952 protein [Homo sapien	1.76
	418825	AA228881	Hs.22394	hypothetical protein FLJ10893	1.40
30	417805	U38545	Hs.82587	phospholipase D1, phosphatidylcholine-spe	1.35
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	1.55
	415714	NM_002290	Hs.78672	laminin, alpha 4	1.90
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	1.71
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.88
35	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	1.75
	452298	A1039243	Hs.278585	NM_024756; Homo sapiens hypothetical pro	1.86
	434596	T59538		gb:gb65g12.s1 Stratagene ovary (937217)	1.52
	412351	AL135890	Hs.73828	T-cell acute lymphocytic leukemia 1	1.61
40	433374	A1821409	Hs.304471	EST	1.45
	429113	D28235	Hs.195384	prostaglandin-endoperoxide synthase 2 (p	2.14
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	1.50
	435705	AA782114	Hs.28043	ESTs	1.53
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	1.52
	453983	H94997	Hs.16450	ESTs	1.94
45	406506			Target Exon	1.97
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.32
	452924	AW580939	Hs.97199	complement component C1q receptor	2.38
	426696	AW363332	Hs.171844	NM_006505 Homo sapiens poliovirus recept	1.61
	418941	AA452970	Hs.239527	E1B-65kDa-associated protein 5	1.41
50	450152	A1138635	Hs.22968	intron of VEGFR	1.70
	437269	AA334384	Hs.149420	ESTs	1.60
	445279	R41900	Hs.22245	ESTs	1.59
	409509	AL036923	Hs.322710	ESTs	1.52
	410240	AL157424	Hs.61289	synaptotagmin 2	1.61
55	424711	NM_005795	Hs.152175	cathepsin receptor-like	1.96
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 6730	1.81
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	1.91
	410057	R66634	Hs.268107	mutimerin	1.85
	446727	AB011095	Hs.16032	KIAA0523 protein	1.67
60	412564	X83703		cardiac ankyrin repeat protein	1.51
	414786	A1246482	Hs.243010	Homo sapiens ras homolog gene family, me	1.71
	410276	A1554545	Hs.71832	angiotensin-2	1.91
	406627	T64904	Hs.163780	ESTs	1.78
	405025			Bone morphogenetic protein 6	1.69
65	422648	D86983	Hs.118893	Melanoma associated gene	2.33
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	1.78
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfamily	1.79
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	2.02
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	1.93
70	429276	AF056085	Hs.198512	G protein-coupled receptor 51	1.65
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.48
	448694	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	2.01
	434398	AA121098	Hs.3838	serum-inducible kinase	1.83
	416851	AW963951	Hs.85618	ESTs	1.65
75	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.69
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	1.71
	450689	A1369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	1.86
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural era	1.65
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	1.83
80	428206	AB020643	Hs.183006	KIAA0836 protein	1.77
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	2.00
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	1.94

5	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	1.74
	444409	A1792140	Hs.49265	ESTs	1.88
	421340	F07783	Hs.1369	decay accelerating factor for complement	1.74
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	2.18
	444009	A1380792	Hs.135104	ESTs	1.90
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.16
	416940	N75620	Hs.43157	ESTs	2.03
	418922	AW956580	Hs.42699	ESTs	2.09
10	431548	A1834273	Hs.9711	novel protein	1.81
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.14
	434558	AW264102	Hs.39168	ESTs	1.93
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	2.05
	428438	NM_001955	Hs.2271	endothelin 1	2.46
15	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	2.20
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.26
	439410	AA632012	Hs.188746	ESTs	1.93
	453467	AI535997	Hs.30089	ESTs	2.39
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	1.84
20	417933	X02308	Hs.82962	thymidylate synthetase	1.70
	436420	AA443966	Hs.31595	ESTs	1.97
	414430	A1346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.93
	412140	AA219591	Hs.73625	RAB6 interacting, kinesin-like (rabkines	1.80
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.03
25	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.58
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.81
	413745	AW247252	Hs.75514	nucleoside phosphorylase	1.99
	405121			mitogen-activated protein kinase 8 inter	2.99
30	425811	AL039104	Hs.158557	karyopherin alpha 2 (RAG cohort 1, impor	1.76
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	2.13
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	2.71
	421937	A1878857	Hs.109706	hematological and neurological expressed	1.65
	408669	A1493591	Hs.78146	platelet/endothelial cell adhesion molec	2.39
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.77
35	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.67
	408243	Y00787	Hs.624	interleukin 8	2.09
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.42
	407891	AA486620	Hs.41135	endomucin-2	2.34
	407891	AA486620	Hs.41135	endomucin-2	2.34
40	436032	AA150797	Hs.109276	latexin protein	2.24
	439382	BE247684	Hs.103070	ESTs	2.07
	419172	AW338625	Hs.22120	ESTs:similar to TRANSMEMBRANE 4 SUPERF	2.00
	442006	AW975183		ESTs, Weakly similar to S72482 hypothe	2.33
45	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	2.11
	432128	AA127221	Hs.296502	ESTs	2.27
	417426	NM_002291	Hs.82124	laminin, beta 1	2.11
	434217	AW014795	Hs.23349	ESTs	2.03
	439265	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	2.08
50	442923	AW248322	Hs.95835	ESTs, Weakly similar to unnamed protein	1.57
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.60
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.37
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	2.55
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.09
	449722	BE280074	Hs.23960	cyclin B1	1.76
55	413794	AF234532	Hs.61638	myosin X	2.01
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	2.15
	406964	M21305		gb:Human alpha satellite and satellite 3	3.08
	448231	A1701916	Hs.202509	ESTs	2.27
60	408989	AW381666	Hs.49500	KIAA0746 protein	1.43
	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	2.67
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	2.18
	418185	AW958272	Hs.347326	intercellular adhesion molecule 2	2.60
	417308	H60720	Hs.81892	KIAA0101 gene product	1.86
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	2.92
65	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.92
	400666			NM_002425:Homo sapiens matrix metallopro	2.59
	431728	NM_007351	Hs.268107	multimerin	2.72
	440086	NM_005402	Hs.288757	v-rel simian leukemia viral oncogene hom	2.25
70	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	1.76
	451979	F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	3.37
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	3.11
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	3.11
	444330	AI597655	Hs.49265	ESTs	3.08
	422424	A1186431	Hs.296638	prostate differentiation factor	2.96
75	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.84
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (Interstitial	11.91

TABLE 698

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey CAT Number Accession

453085	10017_1	BC017336 BG716430 BG501286 BI458528 AI582223 N98532 AI338138 AI273442 AW102617 AA831177 AA745842 AA412583 AA355375 BG547492 AW954243 BI766546 BG057641 AI192435 AI338935 AI312651 AI708679 AI191125 AI206832 AA676899 AI078010 AI888718 AA452830 BF445542 N69930 AA715017 BF446713 BE046852 AW771909 AA907729 AI143749 AI761290 AA890233 BF925759 AI783713 AI767267 AA814538 W56778 AA918481 BG743526 BE645242 AI025328 AI284436 AI290445 H27710 AI475034 BG740023 AI090348 AI340003 BI602481 W38495 AI183314 AI927418 BG397181 AA878310 W19369 W56507 C05751 AW380760 AW380770 AW380790 BF930729 H28425 AA037326 AA375805 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI698905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI79814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI590245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI288935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H08983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AI574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI282364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984522 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI736844 BE811458 BE773481 AI262930 AA948565 BE706942 BE158300 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545285 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL555586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BC541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 NM_002640 L40377 BG227962 AI925897 W60100 BG980023 AA853496 AA360401 AW956168 W61361 AI074846 AA373798 BG193973 BG499418 BF816267 AI675932 BG611734 BG777123 AW449485 BF912016 BE566411 BM068728 AW976385 AL121194 AI767324 BM054718 AW366882 AA156151 Z25109 C05177 AW975688 AA731063 N67084 AF147374 T59538 T59589 T59598 T59542 X83703 NM_014391 BC018667 AU139209 BE924924 BE924899 BE924977 BE924985 BE924947 BF229055 BE924917 BE924938 BE812621 BE924937 AA969184 BE924898 BF229056 BF229054 BF081177 BE924934 BF229040 BE925037 BE925011 BG943776 AA488072 AA486364 Z36249 AW455806 AW582753 BF081131 BE924910 BF229058 BF081172 BE924956 AW378093 BF081132 BF081168 BE812736 BE812738 BF081165 C04160 C04463 BF229048 AW975183 AA973583 AI365103 AI699495 AI301787
442506	29197_1	
436772	1239464_1	
434596	14701_1	
412564	18571_1	
442006	1239046_1	
45	TABLE 69C	
	Pkey: Unique number corresponding to an Eos probaset	
	Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.	
	Strand: Indicates DNA strand from which exons were predicted.	
	NL_position: Indicates nucleotide positions of predicted exons.	
50		
	Pkey Ref Strand NL_position	
	402463 9796896 Minus 8818-8952	
	400494 9714719 Plus 169845-170272	
55	401234 9929642 Plus 120173-120337	
	406506 7711374 Minus 6843-8077	
	405025 7107727 Plus 105267-105343, 106184-106294, 106387-10653	
	405121 8102330 Minus 35816-36004, 36587-36684	
	400666 8118496 Plus 17982-18115, 20297-20456	
60	TABLE 70A:	
	Pkey: Unique Eos probaset identifier number	
	ExAccn: Exemplar Accession number, Genbank accession number	
65	UnigeneID: Unigene number	
	Unigene Title: Unigene gene title	
	R1: Ratio of the mean of the vessel AI's to the mean of the HUVEC AI's	
70		
	Pkey ExAccn UnigeneID Unigene Title R1	
	428928 BE409838 Hs.194657 cadherin 1, type 1, E-cadherin (epitheli	0.99
	439180 AI393742 Hs.199067 v-erb-b2 avian erythroblastic leukemia v	1.06
	412636 NM_004415 Hs.199067 desmoplakin (DPI, DPL)	1.25
	426158 NM_001982 Hs.199067 v-erb-b2 avian erythroblastic leukemia v	1.36
75	414320 U13816 Hs.75893 ankyrin 3, node of Ranvier (ankyrin G)	1.50
	417878 U90916 Hs.82845 Homo sapiens cDNA: FLJ21930 fls, clone H	1.55
	414572 AU077174 Hs.288181 cathepsin H	1.64
	415314 N88802 Hs.5422 glycoprotein M6B	1.70
	431103 M57399 Hs.44 pleiotrophin (heparin binding growth fac	1.75
	406973 M34996 Hs.198253 major histocompatibility complex, class	1.88
80	456974 M12529 Hs.169401 apolipoprotein E	1.90
	430560 Z28942 Hs.243960 N-myc downstream-regulated gene 2	1.91
	406828 AA419202 Hs.84258 CD74 antigen (invariant polypeptide of m	1.97
	422048 NM_012445 Hs.288126 spondin 2, extracellular matrix protein	1.99

5	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	2.02
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.03
	413391	A1223328	Hs.75335	glycine amidinotransferase (L-arginine)	2.12
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	2.15
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.17
10	437536	X91221	Hs.144465	ESTs	2.21
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.26
	46945	A1193115	Hs.16611	tumor protein D52-like 1	2.27
	422639	A1929377	Hs.173724	creatine kinase, brain	2.29
	427451	A1690916	Hs.178137	transducer of ERBB2, 1	2.31
15	454042	H22570		hypothetical protein FLJ20093	2.37
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	2.38
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	2.39
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.41
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	2.43
20	427393	AB029018	Hs.177635	KIAA1095 protein	2.47
	414217	A1309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.49
	414063	H26904	Hs.75735	apolipoprotein D	2.50
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	2.51
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	2.51
25	410532	T53088	Hs.155376	hemoglobin, beta	2.56
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (2.58
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.58
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
30	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	427980	AA418305	Hs.303205	EST	2.59
	442695	AC002425	Hs.8603	p8 protein (candidate of metastasis 1)	2.62
	425751	T19239	Hs.1940	crystallin, alpha B	2.63
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	2.63
35	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.66
	453464	A1884911	Hs.32989	receptor (calcitonin) activity modifying	2.67
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.67
	452685	A1634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	2.67
	425869	AA524547	Hs.160318	FXD domain-containing ion transport reg	2.73
40	406643	N77976	Hs.347939	hemoglobin, alpha 2	2.73
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	2.74
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.80
	444195	AB002351	Hs.10587	KIAA0353 protein	2.81
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.86
45	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	2.92
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.93
	440820	AL031846		platelet 4	2.94
	429123	AB011099	Hs.196647	KIAA0527 protein	2.97
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.01
50	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	3.01
	425622	AW360847	Hs.16578	ESTs	3.01
	420195	N44348	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.04
	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	3.04
	407869	A1827976	Hs.24391	hypothetical protein FLJ13612	3.06
55	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.07
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	3.10
	412047	AA934589	Hs.49696	ESTs	3.12
	414840	R27319	Hs.23823	halcy/enhancer-of-split related with YRP	3.14
	424651	AW93206		ESTs	3.17
60	443932	AW888222	Hs.9973	tensin	3.18
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.20
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	3.20
	421834	BE543205	Hs.288771	DKFZP586A0522 protein	3.20
	423961	D13666	Hs.136348	periostin(OSF-2os)	3.24
65	447384	A1377221	Hs.40528	ESTs	3.24
	425383	D83407	Hs.155007	Down syndrome critical region gene 1-lik	3.25
	447023	AA356764	Hs.17109	Integral membrane protein 2A	3.25
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	3.25
	406972	M32053		gb:Human H19 RNA gene, complete cds.	3.26
70	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	3.27
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	3.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	3.29
	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.33
	410614	A1091195	Hs.65029	growth arrest-specific 1	3.35
75	451529	A1917901	Hs.208641	ESTs	3.35
	430310	U60115	Hs.239069	four and a half LIM domains 1	3.37
	424897	D63216	Hs.153684	frizzled-related protein	3.37
	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	3.38
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	3.41
80	421913	A1934365	Hs.109439	osteoglycin (osteoductive factor, mime	3.43
	451331	AK002039	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.44
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	3.46
	407938	AA905097	Hs.85050	phospholamban	3.48
	418005	A1186220	Hs.83164	collagen, type XV, alpha 1	3.51
80	452877	A1250789	Hs.32478	ESTs	3.52
	419577	L36531	Hs.91296	Integrin, alpha 8	3.52
	404277			NM_019111*Homo sapiens major histocompa	3.54

5	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	3.58
	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	3.64
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	3.68
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.70
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	3.71
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.73
	427818	AW511222	Hs.193765	ESTs	3.73
	433465	AV657778	Hs.3314	selenoprotein P, plasma, 1	3.75
10	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypothei	3.77
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	3.80
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	3.83
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	3.86
	428957	NM_003881	Hs.194679	WNT1 Inducible signaling pathway protein	3.89
15	434868	R50032	Hs.159263	collagen, type VI, alpha 2	3.90
	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	3.95
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.95
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3.97
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	4.01
20	449925	AI324293	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	4.03
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	4.07
	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3	4.09
	421823	N40850	Hs.28625	ESTs	4.17
	422550	BE297626	Hs.295049	microfibrillar-associated protein 4	4.25
25	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	4.26
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	4.29
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.34
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	4.37
	415165	AW887604	Hs.78085	complement component 7	4.37
30	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	4.41
	452114	N22687	Hs.8236	ESTs	4.43
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	4.43
	428411	AW291464	Hs.10338	ESTs	4.48
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	4.51
35	406849	AA454809	Hs.172928	collagen, type I, alpha 1	4.54
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	4.57
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactadin)	4.57
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.68
	421814	L12350	Hs.108623	thrombospondin 2	4.73
40	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	4.76
	414290	AI568801	Hs.71721	ESTs	4.98
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	5.13
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	5.14
	416784	AA334592	Hs.79914	lumican	5.20
45	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	5.50
	408221	AA912183	Hs.47447	ESTs	5.65
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	5.87
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	6.47
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.65
50	426408	AI742501	Hs.169756	complement component 1, s subcomponent	7.94
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	9.90
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev9)	9.91

TABLE 70B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
60	412636	1438_1
65		M77830 NM_004415 AF139065 BG681115 BG740377 BI712984 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI785807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149284 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW365566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI51766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW955615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068940 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AJ392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AG039975 AA946936 AA644381 BM314884 AA702424 AJ417612 AW190555 AJ220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AJ346078 W95070 AA149191 AA026864 AI830049 AW780435 AJ078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AJ205263 BF082491 AW021347 AI568096 BE939862 AA088865 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 NB4767 AA131077 H30148 BE714290 AE668689 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406

5	454042	30254_1	BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW17786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606553 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 AJ420458 AI018523 AA708686 BF949633 AL119553 BF945960 AI081305 AA041432 AI921013 AI684910 AI654847 AW874199 AI206120 AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350 W27787 H45331 BI549761 R53955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340813 R42410 AA707199 AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137298 AI366468 N64350 AA779107 AW025969 R49056 AA347011 R55722 AW771106 F04959 Z38381 F01659 H17396 BI493714 AJ880103 AW771447 AI202561 AA788851 AI494436 BF856114 H22570 AW964381 BG007409 BM314056 AA465642 T30661 T33111 Z42834 C04542 BF948152 BF944325 BF858895 AA935284 AI267350 N64249 W67500 F07962 AA322394 BI489987 BE644965 BM313782 AA910364 AI809246 AA836750 BF115228 AA829730 N27413 BM141766 AI742325 AA455261 AA938708 AI420241 AI130039 BF222341 BF941301 AA771807 Z41034 BF447457 BF447426 AW515347 T03874 F02360 F02302 N34898 AI678586 AA807824 AA948556 AW204638 BM142045 BF446775 AV648364 AI801368 AA971739 AI017351 AA760722 AI460007 AI458383 AI694152 AA226536 BE467282 N47808 BE348825 BE830581 BE830583 N53009 N59351 N41056 W67501 AA016246 H43293 F21282 R59121 R56280 BG435302 BM083687 AA904035 AA488889 W76175 AA761874 H28767 AA910081 AA837086 AI521825 BG986378 AI478562 AA743152 AA746092 H88863 BG986375 AA635644 AI493206 AA699979 BE245127 BG986430 BG986529 BF665873 BG030157 BG622575 AA766495
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TABLE 70C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
404277	1834458	Minus	91665-91946

TABLE 71A: 774 GENES UP-REGULATED IN EWING SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 1A lists 774 genes up-regulated in Ewing Sarcoma compared to normal adult tissues. These were selected from 35371 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" Ewing Sarcoma to "average" normal adult tissues was greater than or equal to 2.1. The "average" Ewing Sarcoma level was set to the 75th percentile amongst numerous Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	75th percentile of ewing sarcoma to 85th percentile of body map

Pkey	ExAccn	UnigeneID	Unigene Title	R1
104659	AW969769	Hs.105201	ESTs	70.3
101447	M21305		gbHuman alpha satellite and satellite 3	64.7
105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	50.5
115881	NM_005756	Hs.184942	G protein-coupled receptor 64	48.8
121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	46.7
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	46.6
110278	AF061573	Hs.19492	protocadherin 8	46.1
126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	41.4
116752	AL008583	Hs.91622	neuronal pentraxin receptor	40.9
119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	39.6
104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	36.9
110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	35.5
121362	AF050147	Hs.97932	chondromodulin I precursor	34.7
131291	NM_004350	Hs.170019	runt-related transcription factor 3	33.0
101063	D54745	Hs.80247	cholecystokinin	31.7
121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri	28.7
122651	AW975398	Hs.293836	ESTs	28.0
100299	D49493	Hs.2171	growth differentiation factor 10	26.5
129977	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	26.2
123619	AA602964		gbcno97c02s1 NCL CGAP_P12 Homo sapiens	26.1
124006	AI147155	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi)	23.1
116301	AW969706	Hs.293332	ESTs	22.6
121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	22.3
106533	AL134708	Hs.145998	ESTs	22.3
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabtkines	21.3
131313	R96290	Hs.75874	ribosomal protein L44	20.8
116790	AW161357		microtubule-associated protein tau	18.7
105316	AI671245	Hs.24835	hypothetical protein FLJ14594	18.2
102123	NM_001809	Hs.1594	centromere protein A (17kD)	17.8
126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13	17.8
119791	AA554907	Hs.58291	ESTs	16.7
113003	AW292215	Hs.7215	ESTs	16.3
102836	U94320	Hs.158330	neuropeptide Y receptor Y5	16.3
126799	AW753865	Hs.74376	olfactomedin related ER localized protei	16.3
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	15.5
107160	AA314490	Hs.27669	KIAA1563 protein	14.8
115313	AA808001	Hs.184411	albumin	14.6
123308	C14187	Hs.103538	ESTs	14.2

	126077	M78772	Hs.210836	ESTs	14.0
	100698	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	13.9
	106821	NM_006594	Hs.28298	adaptor-related protein complex 4, beta	13.9
5	110288	H40665	Hs.31564	ESTs	13.8
	106498	AJ221919		hypothetical protein FLJ10582	13.8
	112134	R41823	Hs.7413	ESTs;calyntenin-2	13.7
	115265	AA334274	Hs.18368	DKFZP564B0769 protein	13.4
	128639	AW582962	Hs.102897	CGI-47 protein	13.2
10	125698	AF078847	Hs.191356	general transcription factor IIH, polype	12.8
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	12.3
	119456	AA248897	Hs.48784	ESTs	12.2
	135155	AJ207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	12.1
	106614	AA648459	Hs.335951	hypothetical protein AF301222	12.0
15	131941	BE252983	Hs.35086	ubiquitin specific protease 1	12.0
	132968	AF234532	Hs.61638	myosin X	11.7
	132725	NM_005276	Hs.184167	splicing factor, arginine/serine-rich 7	11.7
	111353	W20090	Hs.6616	ESTs	11.4
	123289	AA495904	Hs.103316	ESTs	11.3
20	104968	AJ249502	Hs.29669	ESTs	11.1
	123532	AA608733		gb:ae56f06.s1 Stratagene lung carcinoma	11.0
	104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	10.7
	125556	AB033064	Hs.236463	KIAA1238 protein	10.7
	127240	AJ005683	Hs.86998	nuclear factor of activated T-cells 5, 1	10.6
25	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	10.6
	132315	AF091086	Hs.44563	hypothetical protein	10.5
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-link	10.5
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	10.4
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	10.4
30	110730	N67655	Hs.26411	ESTs	10.3
	119186	AJ979147	Hs.101265	hypothetical protein FLJ22593	10.3
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.3
	121916	AW117207	Hs.98523	ESTs	10.2
	131402	Y08890	Hs.113503	karyopherin (importin) beta 3	10.1
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	10.0
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	10.0
	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	10.0
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	9.9
	103446	X98834	Hs.79971	sal (Drosophila)-like 2	9.7
40	105091	AA148859	Hs.179909	hypothetical protein FLJ22995	9.6
	106146	W07288	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	9.5
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	9.5
	115414	AA662240	Hs.283099	AF15q14 protein	9.4
	117829	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	9.4
45	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	9.3
	121910	AJ204600	Hs.96978	hypothetical protein MGC10764	9.2
	130625	AF176012	Hs.260720	J domain containing protein 1	9.2
	129755	R42216	Hs.7759	Homo sapiens clone 24538 mRNA sequence	9.1
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	9.0
50	111109	AJ940675	Hs.20914	hypothetical protein FLJ23056	9.0
	120217	AA862257	Hs.66035	ESTs	9.0
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-link	8.9
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	8.8
	126262	AJ065153	Hs.143764	ESTs, Weakly similar to unknown [H.sapie	8.8
55	113903	AJ368034	Hs.36679	ESTs, Weakly similar to A46010 X-linked	8.7
	105253	AW997484	Hs.5003	KIAA0456 protein	8.6
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	8.6
	105172	AA187554	Hs.300496	mitochondrial solute carrier	8.6
	100380	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	8.6
60	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.5
	102725	AB026187	Hs.159156	protocadherin 11	8.5
	130298	AJ347487	Hs.132781	class I cytokine receptor	8.4
	132294	AB023191	Hs.44131	KIAA0974 protein	8.2
	118644	AA443241		ribosomal protein L44	8.2
65	106575	AW970602	Hs.105421	ESTs	8.2
	133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	8.1
	119499	AJ918906	Hs.55080	ESTs	8.1
	100248	NM_015156	Hs.78398	KIAA0071 protein	8.1
	114837	BE244930	Hs.166895	ESTs	8.0
70	107098	AJ823593	Hs.27688	ESTs	8.0
	123960	AW082862	Hs.287733	hypothetical protein FLJ23189	7.9
	105280	AA894638	Hs.14600	ESTs	7.9
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	7.9
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	7.9
75	133063	AJ654133	Hs.30212	thyroid receptor interacting protein 15	7.8
	106730	AW377314	Hs.5364	DKFZP564I052 protein	7.8
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	7.8
	107254	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	7.8
	134367	AA339449	Hs.82265	phosphoribosylglycinamide formyltransfer	7.8
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	7.7
80	125400	AL110151	Hs.128797	DKFZP566D0824 protein	7.7
	129413	AW377610	Hs.11123	DKFZP564G092 protein	7.7
	116766	AJ608657	Hs.95097	ESTs	7.7
	129075	BE250162	Hs.83765	dihydrofolate reductase	7.6

5	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti	7.6
	132438	AW363687	Hs.82916	chaperonin containing TCP1, subunit 6A (7.6
	118036	AJ471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	7.6
	131170	NM_014253		odc (odd Oz/ten-m, Drosophila) homolog 1	7.5
	104548	R39398	Hs.91559	ESTs	7.5
10	131495	AA812434		SMC2 (structural maintenance of chromoso	7.5
	132543	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.4
	124040	U23752	Hs.32964	SRF (sex determining region Y)-box 11	7.4
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous ri	7.3
	132559	AF119848	Hs.270863	hypothetical protein PRO1580	7.3
15	101050	AU077324	Hs.1832	neuropeptide Y	7.2
	111823	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	7.2
	116401	AW893940	Hs.59698	ESTs	7.1
	105127	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	7.1
	128478	AA708205	Hs.100343	ESTs	7.1
20	110456	H52348	Hs.36636	ESTs	7.1
	118846	AW295598	Hs.50895	homeo box C4	7.1
	120934	AA226198		gb:nc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	7.1
	128132	AA225632		gb:nc08a07.r1 NCL_CGAP_Pr1 Homo sapiens	7.0
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	7.0
25	106157	W37943	Hs.34892	KIAA1323 protein	6.9
	117852	AW877787	Hs.136102	KIAA0853 protein	6.9
	106213	N45018	Hs.8769	hypothetical protein DKFZp761J17121	6.9
	118013	AI674126	Hs.94031	ESTs	6.9
	120147	AJ917116		hemoglobin, beta	6.8
30	118267	N34905	Hs.44653	Homo sapiens cDNA: FLJ22669 fis, clone H	6.8
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	6.8
	120325	AA195651		AP-2 beta transcription factor	6.8
	133276	AW978439	Hs.69504	ESTs	6.8
	127742	AW293496	Hs.180138	ESTs	6.7
35	127664	AA806164	Hs.116502	ESTs	6.7
	108778	AF133123	Hs.90847	general transcription factor IIIC, polyp	6.6
	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associate	6.6
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.6
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.6
40	115197	R18656		ESTs	6.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	6.5
	103346	X87613	Hs.5464	thyroid hormone receptor coactivating pr	6.4
	126967	AA205976		gb:zq48a10.r1 Stratagene hNT neuron (937	6.4
	118499	N67274	Hs.50141	EST	6.4
45	105301	AW352357	Hs.7457	MAGE1 protein	6.3
	113617	AI869372	Hs.17207	Homo sapiens cDNA FLJ11922 fis, clone HE	6.3
	127968	AA830201	Hs.124347	ESTs	6.3
	134719	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	6.3
	110748	AW581992	Hs.301434	KIAA1387 protein	6.3
50	115844	AI373062	Hs.332938	hypothetical protein MGC5370	6.3
	121885	AA934883	Hs.98467	ESTs, Highly similar to AF257737 1 cilia	6.2
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	6.2
	130882	AA497044	Hs.20887	hypothetical protein FLJ10392	6.2
	132256	AI078645	Hs.431	murine leukemia viral (bmi-1) oncogene h	6.2
55	106383	AA447453	Hs.27860	Homo sapiens mRNA: cDNA DKFZp568M0723 (f	6.2
	135186	U73328	Hs.172648	distal-less homeobox 4	6.2
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	6.2
	109261	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	6.1
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	6.1
60	128501	AL133572	Hs.199009	protein containing CXXC domain 2	6.1
	109747	AI223001	Hs.22969	ESTs, Weakly similar to Z141_HUMAN ZINC	6.1
	128361	AW172570	Hs.14600	ESTs	6.1
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	6.0
	104689	AA420450	Hs.292911	Plekophilin	6.0
65	113575	AW138168	Hs.15671	ESTs, Weakly similar to KBF3_HUMAN NUCLE	6.0
	121830	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypotheti	5.9
	119298	NM_001241	Hs.155478	cyclin T2	5.9
	109841	H01052		gb:yj32h01.s1 Soares placenta Nb2HP Homo	5.9
	115622	AI088691	Hs.208414	Homo sapiens mRNA: cDNA DKFZp564D0472 (f	5.8
70	122969	AW821252	Hs.104336	hypothetical protein	5.8
	109872	R65841	Hs.28653	ESTs	5.8
	114208	AL049466	Hs.7859	ESTs	5.8
	113494	T91451	Hs.86538	ESTs	5.8
	127684	AA668631	Hs.159971	KIAA0379 protein	5.8
75	129300	W94197	Hs.110165	ribosomal protein L26 homolog	5.8
	127489	AA650250	Hs.272076	ESTs	5.8
	133479	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	5.8
	105909	AA195191		hypothetical protein FLJ20729	5.8
	101255	BE385864	Hs.149894	mitochondrial translational initiation f	5.8
80	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	5.7
	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	5.7
	126395	AI468004	Hs.278956	hypothetical protein FLJ12929	5.7
	130723	BE247676	Hs.18442	E-1 enzyme	5.7
	107230	AI034467	Hs.34650	ESTs	5.7
	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	5.6
	108699	AA121514	Hs.70832	ESTs	5.6
	128080	F12310		gb:HSC38D041 normalized infant brain cDN	5.6

	117357	N24829		gbyp98h12.s1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transpos	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
5	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
	126165	AI741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	5.5
	124370	AI243499	Hs.170552	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
10	106668	R49390	Hs.254129	KIAA1678	5.4
	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109605	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13675 fis, clone PL	5.4
	125186	AA610620	Hs.181165	major histocompatibility complex, class	5.4
15	131185	BE280074	Hs.23960	cyclin B1	5.4
	111227	T06701	Hs.12268	ESTs	5.4
	105516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.4
	116008	T79153	Hs.48589	zinc finger protein 228	5.3
20	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
	115121	AJ634549	Hs.325422	ESTs	5.3
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	5.3
	115596	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.3
25	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 femi	5.3
	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (5.3
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	105539	AB040884	Hs.109694	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	M41367	Hs.173002	ESTs, Weakly similar to I38022 hypothe	5.2
30	120830	AJ568170	Hs.96886	ESTs	5.2
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2
	103316	X83301	Hs.324728	SMA5	5.2
	116129	AF189011	Hs.49163	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
35	116680	AW902848	Hs.273829	ESTs	5.2
	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW161885	Hs.269745	ESTs	5.1
40	108301	AA069728	Hs.184582	ribosomal protein L24	5.1
	110799	AI089660	Hs.323401	dpy-30-like protein	5.1
	104899	AA054726	Hs.285574	ESTs	5.1
	125972	AJ927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107869	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypothe	5.1
45	121309	AA293834	Hs.97312	ESTs	5.1
	125321	T86652	Hs.178294	ESTs	5.1
	102627	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	5.1
	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79863	Hs.114243	ESTs	5.0
50	116814	H50834	Hs.77899	gbyp86a10.s1 Soares fetal liver spleen	5.0
	130622	AI582291	Hs.16846	ESTs, Weakly similar to O4HJ01 debrisocu	5.0
	110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	4.9
	127765	AA971146	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	108768	AF181721	Hs.61345	RJ2S	4.9
	120484	AA253170	Hs.96473	EST	4.9
55	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	4.9
	129012	R81936		ribosomal protein L44	4.9
	124973	AJ476066	Hs.102243	ESTs, Weakly similar to I78885 serine/th	4.9
	124548	AA249086	Hs.125034	hypothetical protein FLJ13340	4.9
	126904	AA948033	Hs.130853	ESTs	4.9
60	131526	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.9
	130637	AA356764	Hs.17109	integral membrane protein 2A	4.8
	126769	AA083456		gbczn09g08.r1 Stratagene hNT neuron (937	4.8
	126086	H75681		gbyp77g01.r1 Soares fetal liver spleen	4.8
65	100169	AL037228	Hs.82043	D123 gene product	4.8
	130262	D63216	Hs.153684	frizzled-related protein	4.8
	109260	AW978515	Hs.131915	KIAA0863 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocatio	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H86261	Hs.40568	ESTs	4.8
70	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	4.8
	105848	AW954064	Hs.24951	ESTs	4.7
	127987	AI022103	Hs.124511	ESTs	4.7
	129706	AA443241		ribosomal protein L44	4.7
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
75	126629	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	4.7
	111348	AA034922	Hs.9585	ESTs	4.7
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.178833	ESTs, Moderately similar to ALU5_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
80	123778	AW352149	Hs.102314	ESTs	4.7
	126521	AJ475110	Hs.203933	ESTs	4.7
	110343	AW136703	Hs.17268	ESTs	4.6
	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6

	113974	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bind	4.6
	133098	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	4.6
	109920	H05840	Hs.111323	ESTs	4.6
5	103487	AA743603	Hs.172108	nucleoporin 88kD	4.6
	125353	AB033043	Hs.149377	hypothetical protein DKFZp761L0424	4.6
	100893	BE245294	Hs.180789	S164 protein	4.6
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	4.6
10	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	4.6
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	4.5
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.5
	104912	AA813192	Hs.200596	KIAA0547 gene product	4.5
	110223	H19836	Hs.31697	ESTs	4.5
	113047	AI571940	Hs.7549	ESTs	4.5
15	101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.5
	113002	BE243513	Hs.7212	hypothetical protein PP1044	4.5
	105304	AW134924	Hs.190325	ESTs	4.5
	112386	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	4.5
20	108489	AA452054	Hs.119338	ESTs	4.5
	122792	AW188551	Hs.99519	hypothetical protein FLJ14007	4.5
	112651	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.5
	111346	AW970976	Hs.293653	ESTs	4.5
	123596	AA421130	Hs.112640	EST	4.5
25	125447	AI582222	Hs.128686	ESTs	4.5
	106178	AL049935	Hs.301763	KIAA0554 protein	4.4
	102250	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	4.4
	105868	AA378780	Hs.334842	tubulin alpha 1	4.4
	127496	AI031650		ESTs	4.4
	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	4.4
30	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	4.4
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.4
	129445	W52452	Hs.29797	ribosomal protein L10	4.4
	114721	D61939	Hs.103822	ESTs	4.4
	120922	AA481003	Hs.97128	ESTs	4.3
35	115167	AA749209	Hs.43728	hypothetical protein	4.3
	102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	4.3
	106111	AW875398	Hs.6451	PRO0659 protein	4.3
	123829	AF251237	Hs.112208	XAGE-1 protein	4.3
40	103616	NM_002647	Hs.32971	phosphoinositide-3-kinase, class 3	4.3
	100269	NM_001949	Hs.1189	E2F transcription factor 3	4.3
	112728	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.3
	135098	AW274526	Hs.277721	membrane component, chromosome 17, surfa	4.3
	106034	AW952005	Hs.14928	hypothetical protein FLJ12903	4.3
45	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	4.3
	106246	AL036917	Hs.288821	KIAA1638 protein	4.3
	125724	AL360190	Hs.318501	Homo sapiens mRNA full length insert cDN	4.3
	132206	AA425204	Hs.334721	hypothetical protein FLJ13391	4.3
	130227	BE397151	Hs.153003	serine/threonine kinase 16	4.3
50	129650	AF109298	Hs.118258	prostate cancer associated protein 1	4.3
	130382	NM_003450	Hs.155204	zinc finger protein 174	4.3
	106073	AL157441	Hs.17834	downstream neighbor of SON	4.2
	105403	AI473827	Hs.31793	ESTs	4.2
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.2
55	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	4.2
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	4.2
	106012	AI240665		ESTs	4.2
	116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.2
	130832	AW838006	Hs.20082	zinc finger protein 3 (A8-51)	4.2
60	125860	AI754693	Hs.145968	ESTs	4.2
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.2
	106232	AB037828	Hs.15370	KIAA1407 protein	4.2
	129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	4.2
	109929	AA773187	Hs.294027	ESTs	4.2
65	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	4.2
	101266	L36645	Hs.73964	EphA4	4.2
	132389	AA310393	Hs.190044	ESTs	4.2
	124320	H95749	Hs.102342	EST	4.2
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.1
70	116133	AW449597	Hs.313652	EST, Weakly similar to I38022 hypothetic	4.1
	129001	AA443323	Hs.107812	BPOZ protein	4.1
	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	4.1
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S.	4.1
	126107	H75477	Hs.93361	ESTs	4.1
75	115333	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	4.1
	100571	L14561	Hs.78546	ATPase, Ca ⁺⁺ transporting, plasma membra	4.1
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	4.1
	120150	BE005771	Hs.153746	hypothetical protein FLJ22490	4.1
	134470	X54942	Hs.83758	CDC28 protein kinase 2	4.1
80	129948	AI537162	Hs.263988	ESTs	4.1
	106882	AA149537	Hs.26994	hypothetical protein FLJ20477	4.1
	126199	AW088276	Hs.125829	ESTs	4.1
	112727	T91029	Hs.15069	ESTs	4.1
	118872	AI039201	Hs.283316	ESTs	4.1

5	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	4.0
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	4.0
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retrovira	4.0
	127153	AI732303	Hs.186518	hypothetical protein MGC2599 similar to	4.0
	124105	H11484	Hs.79133	ESTs	4.0
10	100031			AFFX control - DapX-M	4.0
	106897	AF039023	Hs.167496	RAN binding protein 6	4.0
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	4.0
	133928	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	4.0
	126965	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.0
15	103100	NM_005574	Hs.184585	UM domain only 2 (rhombotin-like 1)	4.0
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	4.0
	118751	N74210	Hs.50454	ESTs	4.0
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	4.0
	111387	AI244489	Hs.285724	ESTs	4.0
20	118676	N45312	Hs.46506	ESTs	4.0
	107348	AW973753	Hs.182426	ribosomal protein S2	4.0
	120528	AI923511	Hs.104413	ESTs	4.0
	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	4.0
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.0
25	115399	AF151534	Hs.92023	core histone macroH2A2.2	4.0
	133515	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4.0
	118129	N57493		gbvyy54c08.s1 Soares_multiple_sclerosis_	4.0
	126522	W31912	Hs.21168	gbztc76d03.s1 Pancreatic Islet Homo sapi	4.0
	131965	W79283	Hs.35962	ESTs	3.9
30	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	3.9
	126029	AA704253	Hs.169359	ESTs	3.9
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	3.9
	105808	AI133161	Hs.286131	CGI-101 protein	3.9
	134087	U51166	Hs.173824	thymine-DNA glycosylase	3.9
35	133195	AI434760	Hs.279949	KIAA1007 protein	3.9
	112996	BE276112	Hs.7165	zinc finger protein 259	3.9
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	3.9
	118967	AI668670	Hs.216756	ESTs	3.9
	127335	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.9
40	106636	AW958037	Hs.286	ribosomal protein L4	3.9
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	3.9
	102266	U29725	Hs.3080	mitogen-activated protein kinase 7	3.9
	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	3.9
	103080	AU077231	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomas	3.9
45	131971	BE567100	Hs.154938	hypothetical protein MDS025	3.9
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	3.9
	128895	AW467000	Hs.106985	ESTs	3.9
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	3.9
	112921	R91095	Hs.4276	KIAA1701 protein	3.9
50	120820	AA347417	Hs.96869	EST	3.8
	105459	AA789081	Hs.4029	glioma-amplified sequence-41	3.8
	114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.8
	105476	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.8
	122682	AA984531	Hs.159293	ESTs	3.8
55	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.8
	130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat	3.8
	115577	AA393167	Hs.41294	ESTs	3.8
	129785	H19006	Hs.184780	ESTs	3.8
	126127	N95428		gbzcb80d09.s1 Soares_senescent_fibroblas	3.8
60	109793	F13088	Hs.8040	heparan sulfate (glucosamine) 3-O-sulfot	3.8
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.8
	100154	H60720	Hs.81892	KIAA0101 gene product	3.8
	106140	AB006624	Hs.14912	KIAA0286 protein	3.8
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	3.8
65	103319	X83492	Hs.82359	tumor necrosis factor receptor superfami	3.8
	106319	W22335	Hs.7392	hypothetical protein MGC3199	3.8
	102391	AA296874	Hs.77494	deoxyguanosine kinase	3.8
	127262	AA828125		gb:od71a09.s1 NCL CGAP_Ov2 Homo sapiens	3.7
	126872	AW450979		gb:UI-H-B13-ala-a-12-0-UI.s1 NCL CGAP_Su	3.7
70	107315	AA316241	Hs.90691	nucleophosmin/nucleoplasmn 3	3.7
	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	3.7
	126962	R12014	Hs.20976	ESTs	3.7
	116203	AW137166	Hs.87306	ESTs	3.7
	123377	AW969183	Hs.271297	ESTs	3.7
75	122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.7
	107780	AA018927	Hs.269213	ESTs	3.7
	132733	AB020631	Hs.123654	PCF11p homolog	3.7
	120649	AA687322	Hs.192843	leucine zipper protein FKSG14	3.7
	131163	AA099524	Hs.23754	ESTs	3.7
80	126708	AW962593	Hs.135260	ESTs	3.7
	117417	AI241733	Hs.43871	ESTs	3.7
	106272	AW969731	Hs.323099	ESTs	3.7
	110834	AW273860	Hs.5759	ESTs	3.7
	123663	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.7
	124250	AA350256		EST, Weakly similar to 2109260A B cell g	3.7
	127038	AA233014	Hs.105965	ESTs	3.7
	107711	W96141	Hs.220687	ESTs	3.7

	130850	AB040922	Hs.20237	DKFZP566C134 protein	3.7
	119126	R45175	Hs.117183	ESTs	3.7
	125466	R08234	Hs.180461	ESTs	3.6
5	105150	AA631977	Hs.155995	KIAA05643 protein	3.6
	103163	AU077018	Hs.3235	keratin 4	3.6
	104495	AW975687	Hs.292979	ESTs	3.6
	107599	AW664072	Hs.60136	ESTs	3.6
	113577	AI300699	Hs.111334	PRO0470 protein	3.6
10	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.6
	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.6
	127563	AB035898	Hs.150587	kinesin-like protein 2	3.6
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.6
	114118	F01598	Hs.175930	ESTs	3.6
15	103937	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	3.6
	125174	W51835	Hs.231082	EST	3.6
	104799	AA029703		gbze95h08.s1 Soares_fetal_heart_NbHH19W	3.6
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	3.6
	135191	X16866	Hs.333497	cytochrome P450, subfamily IID (debrisoq	3.6
20	124367	AI683183	Hs.99348	distal-less homeo box 5	3.6
	113560	T91015		ESTs	3.6
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	3.6
	113988	W87536	Hs.36473	ESTs, Weakly similar to JC5238 galactosy	3.6
	115173	BE612940	Hs.88252	ESTs	3.6
25	126600	AA699949	Hs.191385	ESTs	3.6
	127256	AI738810	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN A	3.6
	123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.6
	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.6
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.6
30	132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
	115691	AW190215	Hs.62348	hypothetical protein FLJ11753	3.6
	134853	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle	3.6
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	3.6
	128468	T23625	Hs.150580	putative translation initiation factor	3.6
35	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	3.5
	133421	AF134160	Hs.7327	claudin 1	3.5
	135332	AW393883	Hs.98968	hypothetical protein FLJ23058	3.5
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	3.5
40	125562	AI494372	Hs.98968	hypothetical protein FLJ23058	3.5
	126996	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.5
	125558	R59305		gb:yh16c10.r1 Soares infant brain 1N1B H	3.5
	117265	AA451966		RAB9-like protein	3.5
45	130215	BE301883	Hs.152707	glioblastoma amplified sequence	3.5
	109482	AI002238	Hs.11482	splicing factor, arginine/serine-rich 11	3.5
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	3.5
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	3.5
	117613	AW029507	Hs.161102	ESTs	3.5
	100944	L07518		mucin 6, gastric	3.5
50	105226	R59958	Hs.26608	hypothetical protein MGC15880	3.5
	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	3.5
	123720	AA609734	Hs.112755	EST	3.5
	128846	AA730767	Hs.285753	SCG10-like-protein	3.5
	116443	AW962196	Hs.339808	LBP protein 32	3.5
55	128770	AB015982	Hs.143460	protein kinase C, nu	3.5
	106918	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.5
	131244	AI638429	Hs.24763	RAN binding protein 1	3.5
	128765	AF073310	Hs.143648	insulin receptor substrate 2	3.5
	111223	AA852773	Hs.334838	KIAA1866 protein	3.5
60	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	3.5
	105395	AI580880	Hs.268149	putative methyltransferase	3.5
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	3.5
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.5
	106367	AA504747	Hs.136102	KIAA0853 protein	3.5
65	103392	X94563		gb:Hsapiens dbi/acbp gene exon 1 & 2.	3.5
	101086	AA382524	Hs.250959	histatin 1	3.5
	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	3.5
	117714	N45226	Hs.46495	EST	3.5
	110986	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	3.5
70	114096	AF060219	Hs.27007	chromosome condensation 1-like	3.4
	117147	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	133347	BE257758	Hs.71475	acid cluster protein 33	3.4
	132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	3.4
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.4
75	109734	AI927212	Hs.3734	ESTs	3.4
	132786	BE083422	Hs.56851	hypothetical protein MGC2668	3.4
	106685	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.4
	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.4
	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	3.4
80	108687	BE544475	Hs.54347	ESTs	3.4
	113115	AI141426	Hs.8706	ESTs	3.4
	107234	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.4
	123110	AA486256	Hs.193510	EST	3.4
	131019	W28614		chorionic somatomammotropin hormone 1 (p	3.4

	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	3.4
	111122	N63753	Hs.16492	DKFZP564G2022 protein	3.4
	103934	BE278111	Hs.134200	DKFZP564C186 protein	3.4
5	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory su	3.4
	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	3.4
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	3.4
	120149	AA227609	Hs.94834	ESTs	3.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	3.4
10	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	3.4
	122365	AA813546	Hs.99034	GTP-binding protein Rho7	3.4
	134455	BE378152	Hs.83530	hypothetical protein	3.4
	115506	AB037756	Hs.45207	hypothetical protein KIAA1335	3.4
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	3.4
15	106691	AA443164	Hs.23259	hypothetical protein FLJ13433	3.4
	105169	BE245294	Hs.180789	S164 protein	3.4
	120120	BE547267	Hs.59791	hypothetical protein MGC13183	3.4
	126638	AA649257	Hs.86998	ESTs	3.4
	128531	H03721	Hs.63236	ribosomal protein S15a	3.3
20	106650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f	3.3
	108859	AL121500		ESTs	3.3
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypotheti	3.3
	125693	H23989	Hs.169743	Homo sapiens clone 25121 neuronal effact	3.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	3.3
25	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.3
	124691	R05835	Hs.110153	ESTs	3.3
	112511	AW970420		dynactin 2 (p50)	3.3
	132985	AL045579	Hs.62113	KIAA0717 protein	3.3
	125743	H17151	Hs.7416	gb:ym37a05.r1 Soares infant brain 1NIB H	3.3
30	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	3.3
	107908	AF087999		ESTs	3.3
	105312	BE613348	Hs.211579	melanoma cell adhesion molecule	3.3
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	3.3
	132073	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	3.3
35	107090	AW809208	Hs.183297	DKFZP566F2124 protein	3.3
	105463	AA825974	Hs.32646	hypothetical protein FLJ21801	3.3
	109592	AI198059	Hs.26370	ESTs	3.3
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	3.3
	103898	AA248884		gb:3517.seq.F Human fetal heart, Lambda	3.3
40	116439	AA251594	Hs.43913	PIBF1 gene product	3.3
	129535	AA397972	Hs.112603	chimerin (chimaerin) 1	3.3
	113283	T66813	Hs.12947	EST	3.3
	128992	H04150	Hs.107708	ESTs	3.3
	133160	N54968	Hs.66309	hypothetical protein MGC11061	3.3
45	134076	AF086215	Hs.78980	gb:Homo sapiens full length insert cDNA	3.3
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	3.3
	127728	AW404061		protein kinase C, beta 1	3.3
	126516	R95872	Hs.117572	chemokine binding protein 2	3.3
	127506	T61039	Hs.76067	ribosomal protein L10a	3.3
50	104769	AA025887	Hs.293943	hypothetical protein MGC11266	3.3
	126666	AA648886	Hs.151999	ESTs	3.3
	130453	U00735	Hs.173854	PAX transcription activation domain inte	3.3
	107131	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.3
	130422	AW160614	Hs.180034	cleavage stimulation factor, 3' pre-RNA,	3.3
55	121292	AA401807		gb:zv65f11.s1 Soares_tetal_fetus_Nb2HF8_	3.3
	123284	AA488988	Hs.283796	ESTs	3.3
	130734	AW137091	Hs.18624	KIAA1052 protein	3.3
	105400	AF198620	Hs.10283	RNA binding motif protein 8A	3.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC0	3.3
60	114988	AA251089		gb:zs04f05.s1 NCL_CGAP_GCB1 Homo sapiens	3.3
	132867	AF226667	Hs.58553	CTP synthase II	3.3
	124169	BE079334	Hs.271630	ESTs	3.3
	114652	AI521936	Hs.107149	novel protein similar to archaeal, yeast	3.3
	113876	AI799751	Hs.5635	ESTs	3.3
65	111520	AI985369	Hs.301134	ESTs	3.3
	121748	BE536911	Hs.234545	hypothetical protein NUF2R	3.3
	106834	AL044182	Hs.28070	KIAA0753 gene product	3.3
	128869	AA768242	Hs.80618	hypothetical protein	3.3
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	3.3
70	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	3.3
	116734	AW900992	Hs.93796	DKFZP586D2223 protein	3.3
	100253	D38024	Hs.157425	double homeobox, 2	3.3
	130999	AA326683	Hs.21992	likely ortholog of mouse variant polyade	3.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.3
75	128284	AA318224	Hs.296141	ESTs	3.3
	119127	AA708035	Hs.12248	ESTs	3.3
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	3.3
	132664	AI740461	Hs.54542	ESTs	3.3
	118397	BE139479	Hs.161492	ESTs	3.3
80	107003	AW138437	Hs.24790	KIAA1573 protein	3.3
	126735	M69113	Hs.226795	glutathione S-transferase pi	3.2
	130847	AI672483	Hs.20220	lipase protein	3.2
	101186	AA020956	Hs.179881	core-binding factor, beta subunit	3.2
	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	3.2

5	121782	AW452957	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.2
	119863	AA081218	Hs.58608	Homo sapiens cDNA FLJ14205 fis, clone NT	3.2
	106103	BE620779	Hs.12094	mitochondrial ribosomal protein L30	3.2
	123808	AA620552		gb:aa58g11.s1 Stratagene lung carcinoma	3.2
	133761	AF041430	Hs.75922	brain protein I3	3.2
10	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.2
	115239	BE251328	Hs.73291	hypothetical protein FLJ10881	3.2
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.2
	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	3.2
	129673	D38552	Hs.1191	KIAA0073 protein	3.2
15	105154	AA307279	Hs.35947	methyl-CpG binding domain protein 4	3.2
	126722	N66148	Hs.11125	HSPC033 protein	3.2
	109966	H09103	Hs.30897	EST	3.2
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	3.2
	109517	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.2
20	105252	AB039670	Hs.9728	ALEX1 protein	3.2
	101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.2
	110384	H45282	Hs.268798	ESTs	3.2
	134118	BE336680	Hs.182877	KIAA0116 protein	3.2
	134869	AL157518	Hs.90421	PRO2463 protein	3.2
25	100780	BE561958	Hs.293441	immunoglobulin heavy constant mu	3.2
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	3.2
	129794	AF161399		hypothetical protein FLJ13433	3.2
	129056	AI769958	Hs.108336	ESTs, Weakly similar to ALUE_HUMAN IIII	3.2
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.2
30	103038	AA926960		CDC28 protein kinase 1	3.2
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1	3.2
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	3.2
	132305	AI806090	Hs.44344	hypothetical protein FLJ20534	3.2
	131136	AB033099	Hs.23413	KIAA1273 protein	3.2
35	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.2
	117639	AA377165	Hs.44833	ESTs	3.2
	127076	AI422951	Hs.146162	ESTs	3.2
	126153	H85692	Hs.40730	ESTs	3.2
	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypothei	3.2
40	104946	AW242407	Hs.73848	carcinoembryonic antigen-related cell ad	3.2
	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	3.2
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	3.2
	109442	AW286134	Hs.86999	ESTs, Weakly similar to S66657 alpha-1C-	3.2
	100474	NM_000699	Hs.300280	amylase, alpha 2A, pancreatic	3.2
45	115536	AK001468	Hs.62180	anillin (Drosophila Scrapie homolog), act	3.2
	119651	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.2
	127211	AA305520	Hs.108812	hypothetical protein FLJ22004	3.2
	134964	AI803516	Hs.272891	hippocalcin-like protein 4	3.1
	105551	AW005822	Hs.25292	ribonuclease HI, large subunit	3.1
50	119750	AI538880	Hs.94812	ESTs	3.1
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	3.1
	104590	AW373062		nuclear receptor subfamily 1, group I, m	3.1
	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	3.1
	116429	AF191018	Hs.279923	putative nucleotide binding protein, est	3.1
55	133915	AA815092	Hs.77554	Homo sapiens cDNA FLJ14957 fis, clone TH	3.1
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.1
	128538	R44214	Hs.101189	ESTs	3.1
	129179	AW969025	Hs.109154	ESTs	3.1
	108793	AA129395	Hs.71139	ESTs	3.1
60	108807	AI652236	Hs.49376	hypothetical protein FLJ20644	3.1
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	3.1
	132571	AW674699	Hs.5169	suppressor of G2 allele of SKP1, S. cere	3.1
	134937	AI251449	Hs.171939	ESTs	3.1
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	3.1
65	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	3.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	3.1
	128179	AW293689	Hs.127116	ESTs	3.1
	117121	H95044	Hs.321386	EST	3.1
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	3.1
70	128403	AI908008	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.1
	127930	AA809672	Hs.123304	ESTs	3.1
	114250	AI914699	Hs.13297	ESTs	3.1
	108828	AK001693	Hs.273344	DKFZP564O0463 protein	3.1
	105225	AA211777		gb:cn57d02.s1 Stratagene muscle 937209 H	3.1
75	117997	N52090	Hs.47420	EST	3.1
	104558	R56678	Hs.88959	hypothetical protein MGC4816	3.1
	124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	106035	N35568	Hs.5245	hypothetical protein FLJ20643	3.1
	127521	AW297208	Hs.164018	ESTs	3.1
80	120215	AF109219	Hs.108787	phosphatidylinositol glycan, class N	3.1
	119403	AL117554	Hs.119908	nucleolar protein NOPS/NOP58	3.1
	105024	AA126311	Hs.9879	ESTs	3.1
	123485	AJ308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
	109416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	3.1
	132490	NM_001290	Hs.4980	UIM domain binding 2	3.1
	115348	AA281562	Hs.768	ESTs	3.1
	117297	AW779829		gb:cn88a05.x1 NCI_CGAP_Jd11 Homo sapien	3.1

5	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.1
	107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	3.1
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	3.1
	132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.1
	115188	AK000219	Hs.88367	hypothetical protein FLJ20212	3.1
	129707	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	3.1
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.1
	106472	AI207162	Hs.3815	stathmin-like-protein RB3	3.0
10	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.0
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	3.0
	105522	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	133650	D84294	Hs.118174	tetratricopeptide repeat domain 3	3.0
	134624	AF035119	Hs.8700	deleted in liver cancer 1	3.0
	112435	NM_013255	Hs.288791	muskelin 1, intracellular mediator conta	3.0
15	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	3.0
	106651	AA460421	Hs.30875	ESTs	3.0
	109597	AA989362	Hs.293780	ESTs	3.0
	132342	AW162758	Hs.341729	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.0
20	106057	BE614474	Hs.289074	F-box only protein 22	3.0
	106378	AA824298	Hs.21331	hypothetical protein FLJ10036	3.0
	128560	AA011597	Hs.177398	ESTs	3.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	3.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	3.0
25	125219	AI804331	Hs.99423	ATP-dependent RNA helicase	3.0
	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	3.0
	133966	BE280478	Hs.182695	hypothetical protein MGC3243	3.0
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A	3.0
	131586	AA460352	Hs.26966	KIAA1171 protein	3.0
30	100237	D30715		Human PAP (pancreatitis-associated prote	3.0
	105515	T24968	Hs.23038	HSPC071 protein	3.0
	123073	AA485061	Hs.105552	ESTs	3.0
	111375	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.0
	130724	AK001507	Hs.44143	Homo sapiens clone FLB6914 PRO1821 mRNA,	3.0
35	129928	AI338993	Hs.134535	ESTs	3.0
	118922	AW206193		hypothetical protein DKFZp76182423	3.0
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	3.0
	125165	W45350		gb:cc81h08.s1 Pancreatic Islet Homo sapi	3.0
	122219	AA436002	Hs.183161	ESTs	3.0
40	132195	BE018717	Hs.42124	ESTs	3.0
	102298	AA382169	Hs.54483	N-myc (and STAT) interactor	3.0
	103286	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	3.0
	130168	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.0
	126997	AI377150	Hs.150914	ESTs	3.0
45	128902	AA036637	Hs.107052	ESTs	3.0
	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-II	3.0
	108711	BE390125	Hs.143187	hypothetical protein	3.0
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	3.0
50	135029	H58818		hydroxysteroid (17-beta) dehydrogenase 7	3.0
	112003	AW978731	Hs.301824	hypothetical protein PRO1331	3.0
	106735	R77698	Hs.337778	ESTs	3.0
	126628	N49776	Hs.170994	hypothetical protein MGC10946	3.0
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
55	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	3.0
	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	3.0
	129601	AB032964	Hs.115726	KIAA1138 protein	3.0
	123423	AA598484		gb:aa38f04.s1 Gessler Wilms tumor Homo s	3.0
	128695	NM_003478	Hs.101299	cullin 5	3.0
60	123470	AW303285		Human DNA sequence from clone RP11-110H4	3.0
	109252	BE440157	Hs.85944	ESTs	3.0
	101445	M21259		gb:human Alu repeats in the region 5' to	3.0
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	3.0
	116475	AA733050	Hs.334612	small nuclear ribonucleoprotein polypept	3.0
65	106573	AA223447	Hs.12835	A kinase (PRKA) anchor protein 7	3.0
	103106	W27172	Hs.1857	phosphodiesterase 6G, cGMP-specific, rod	3.0
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	3.0
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	3.0
	125887	H20832		gb:ym48d03.s1 Soares infant brain 1N1B H	3.0
70	117960	AA310417	Hs.47044	ESTs	3.0
	133626	AW836130	Hs.75277	hypothetical protein FLJ13910	3.0
	113179	BE622021	Hs.152571	ESTs, Highly similar to IGF-II mRNA-bind	3.0
	109568	H09232	Hs.26484	HIRA-interacting protein 3	3.0
75	125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	2.1

TABLE 718

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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5	108451	13766_27	5	AA079195 AA084955 AA126308 AA084956
	107908	46987_1		AF087999 N25296 AI928858 AA846757 N02229 AAD26894 D08634 AW388923 AW388802 AW388957 AW571771 AW388839
	123619	371681_1		AI686662 AW389079 AA602099 AW134567 AW517843 AI682674 AI474874 AA374167
10	131495	142008_1		AA602964 AA609200
	101445	1650_5		AA812434 AI831542 AA766261 AI769894 N63376 AA214392 AA135833 AW605017 AA135965 AW450072 H04812 AA446459
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	116790	19864_1		AW172843 W19794 N21460 AI743862 AW130622 AA991348 AI204553 AA992664 N80848 AA699329 AI824676 R26624 R49653
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25				AL121500 AW291763 AI732432 AA129708 AA133309 AI733750 AI225224
				W45350 W45406
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30				AA476718 AW772454 AI807703 R44253 AA976667 AI985186 AI650254 H38942 R84829 AA018724 AA010000 H85934 AA019126
				H85609 AA017000 AA333355 AW950556 D51397 AA213981 BE548002 AI056359 AA001560 AW952113 AA317769 AI857477
				AI857475 AW249771 AW162661 H38943 AA018628 R85885 AI984613 AI934765 AI796172 AW157488 AI929191 R85523 D51221
35				D53851 H85610 AI749674 F21582 AA323145 AA019127 AA687444 T06745 AI699293 H29532 AA214029 AA223656 NM_016834
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				H17335 R37659 R42802 R46242 R60936 R59731 H28993 AA479907 R44570 AI890696 AA308884 AA507078 R41274 AI365507
40				T16348 AI660453 F03259 F04722 T16312 AA016081 AW073061 BE314824 W28930 R44098 R51045
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55				AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336680
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75				AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752
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				AA248884
				AA083456 AA127026 AA084934 AA120972 AA085317
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				F12310 T66402 H07020
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				BE467708 AW243400 AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984
				AI922204 N98343 BE174213 AA845571 AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768
				AI004723 AW087420 AI565133 N49464 AI268939 AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019
				AA757598 X56196 AA902959 AI334784 AI860794 AA010207 AW890091 AW513771 AI951391 AI337671 T52499 AA890205
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				AA195651 AW235123
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				AI360184 BE205945 AI761796 AI185049 R94506 AI343947 AI565814 AI341735 AI749190 AW269588 AI393145 AI620080
				AW003752 AI750035 AI624837 AI797658 AA679066 N87192 AI937537 AW003753 R72610 R7274 AI757401 AA553744 AA460166
				AA535727 AW304422 R68273 AW027615 C01651 AI090327 AI538258 AW003744 AA938372 AW051486 AA055513 BE466452
				AA931719 AI174548 AW182752 T84462 R11149 AI767627 BE218556 BE217986 BE222697 AI762382 BE299599 AA987212
				AI767136 AI268928 AA090761 AA329280 AI700593 AA460766 BE222710 BE550651 R11148 AI979278 AW235819 AW874095
				AW196492

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Table 72A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigene Title for all of the sequences in Table 73.

80	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigene number
	Unigene Title:	Unigene gene title

Seq ID No: Seq ID number correlation for those sequences in Table 73

Pkey*	ExAccon	UnigeneID	Unigene Title	Seq ID No
5	103080	AU077231	Hs.82932	Seq ID No B1 & B2
	410102	AW248508	Hs.279727	Seq ID No B3 & B4
	101104	AW862258	Hs.169266	Seq ID No B5 & B6
	447761	AF061573	Hs.19492	Seq ID No B7 & B8
	428183	AW969726	Hs.98381	Seq ID No B9 & B10
10	439221	AA737106	Hs.32250	Seq ID No B11 & B12
	121619	AA528339	Hs.178062	Seq ID No B13, B14, & B15
	104659	AW969769	Hs.105201	Seq ID No B16
	105782	H09748	Hs.57987	Seq ID No B17 & B18
	129977	NM_000399	Hs.1395	Seq ID No B19 & B20
15	100299	D49493	Hs.2171	Seq ID No B21 & B22
	116301	AW969706	Hs.293332	Seq ID No B23 & B24
	106533	AL134708	Hs.145998	Seq ID No B25-B27
	131313	R96290	Hs.75874	Seq ID No B28 & B29
	105316	AI671245	Hs.24835	Seq ID No B30 & B31
20	113003	AW292315	Hs.7215	Seq ID No B32
	102836	U94320	Hs.158330	Seq ID No B33 & B34
	102745	AW753865	Hs.74376	Seq ID No B35-B40
	123308	C14187	Hs.157208	Seq ID No B41 & B42
	120147	AI917116		Seq ID No B43
25	123049	BE047680	Hs.211869	Seq ID No B44 & B45
	119082	AF252297	Hs.91546	Seq ID No B46 & B47
	105301	AW352357	Hs.7457	Seq ID No B48 & B49
	128478	AA708205	Hs.100343	Seq ID No B50-B53
	106111	AW875398	Hs.6451	Seq ID No B54 & B55
30	131307	NM_000025	Hs.2549	Seq ID No B56 & B57
	120830	AI568170	Hs.96886	Seq ID No B58 & B59
	127654	AA806164	Hs.116502	Seq ID No B60
	102725	AB026187	Hs.159156	Seq ID No B61 & B62
	132520	AA257992	Hs.50651	Seq ID No B63 & B64
35	130637	AA356764	Hs.17109	Seq ID No B65 & B66
	117602	N35020	Hs.44685	Seq ID No B67 & B68
	128797	NM_002975	Hs.105927	Seq ID No B69 & B70
	129703	BE388665	Hs.179999	Seq ID No B71 & B72
	125770	AA143045	Hs.81665	Seq ID No B73 & B74
40	414761	AU077228	Hs.77256	Seq ID No B75 & B76
	420462	AF050147	Hs.97932	Seq ID No B77 & B78
	410268	AA316181	Hs.61635	Seq ID No B79 & B80
	104691	U29690	Hs.37744	Seq ID No B81 & B82
	416836	D54745	Hs.80247	Seq ID No B83 & B84

Table 72B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
131307	3138_1	NM_000025 X72861 X70811 M29932 X70812 S53291 AW015148 AW581776 AI276134
131313	93372_1	R96290 H02411 C18327 AA367588 AA367557 H96332 C17954 AA568860 AI752983 AA699451 H04260 AI128118 AW193364 N94503
55		AA029995 T40536 AA368746 AI189909 BE047384 AA747591 R22855 AI032539 AI151343 AA148534 H63941 T49595 AA694405 H74226
		AJ200363 R79731 AA702947 AI400076 AI088494 C17938 AA599478 H02962 R77665 C17370 R65618 H73711 R58545 D79189 AW265710
		R77664 T52101 AW953745 AW953739 D79107 AA029105 AW953738 AA456487 R67000 AA156623 AA368336 H63662
	116301	52669_2 AW969706 AA456258 AA491881 BE501639 D62113 AW969710 AI591236 AI379869 AW969897 AA040053 AI807206 AW663917 AA454645
		AA489238 BE241958 AA743491
60	103080	17092_1 AU077231 AA852219 M74092 X59798 M64349 NM_001758 AA226806 M73554 BE409154 AA160096 BE384352 AA160820 BE382880
		BE261734 AA113821 BE407745 AA156380 BE390287 BE390020 AA100854 AA127152 AW794066 AW367101 AW367093 U47703 AI347077
		W05266 AI824103 AI499061 AA642944 AI042556 AA906539 W60380 AI571777 AL135581 AA112340 N75459 AA592829 AI085348 AI278890
		AA126942 AI023701 AI873252 AA156319 AI190622 W60289 AI274886 R81309 AA100801 AA227161 AI568929 AA160603 AI074344 AI344561
		AI150778 AA852218 AA158286 N20142 AA622148 AA864225 AA576367 AW182124 T89175 AI758455 AA780573 N71757 R81200 AI659595
65		AI674613 AA642544 AW503909 AA128851 W39350 N40420 AA113072 BE168116 AI620604 AI298125 BE075272 N40078 BE075109 BE080779
		AI918938 BE168117 BE087369 AW995539 BE080949 BE080727 BE075271 BE075108 BE080955 BE089655 BE081115 AW750304 H66084
		AI146884 BE075154 AW992247 AI186525 AI752230 AW263140 W03329 N26056 AA948080 AA113073 H99284 AA227101 AA631077
		AA148042 AI740837 BE082728 AA149570 W44495 BE089351 AA375044 N26775 H27771 AA064705 BE091204 R89337 N32676 N27141
		BE164704 H98049 W67603 AA425549 W31090 AA807411 BE173280 BE000178 T09020 W23852 AA062709 BE167894 AA076515 R97329
70		BE541980 N42086 AA102307 AA113772 BE276181 H20622 W44436 W67604 W46412 AW771113 AI700678 AA502628 AA133137 BE274186
		BE396090 BE813371 BE612645 W46650 W95203 W29251 AI087288 R76299 AW604781 N55320 AI912334 AA403248 AW169156 H24970
		AW298822 AW080962 AI073747 W24123 AA577596 H21715 H27925 H26436 AI288304 AA148043 AA204678 BE047090 W46631 AA908347
		AA599485 AI276505 AI953979 AA563710 H25674 H51747 AA425389 AA516104 AI095335 T77237 AA151696 T92084 AI689037 AI624162
		W49709 AW514883 AA100676 AI366087 AA069474 AA525859 AW771076 AA029402 AA941114 AI351505 AW770816 AI333594 AI289794
75		AI346589 AA487700 AI081104 AA613344 AI377520 AI284911 AI311390 AA622062 AI055890 AI650881 AI366117 AA403090 AI272818
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		AI168564 AA918965 AI066484 AI123599 AI921518 W94586 AA535600 AA064665 AA705388 AA064623 AA962503 AI924926 AW131206
		AW275281 AI280632 T29597 W48728 AW954336 W38317 W94768 AI084717 W46567 AI245645 AW302501 W72201 AW510563 AW079132
		AA207064 AI143740 AW440672 AA632154 AI290286 AI350704 AI271377 AA025369 AI864756 T77451 H97348 AA852165 AI932951 N98526
80		AA487486 R92970 AA934071 AI080448 AA063257 C05786 N99099 R42969 AA887065 AA62686 AA539333 AA662304 H51748 BE539444
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		AW372354 AI094358 R37210 AA948510 AA226909 BE172527 AI086652 BE408324 AW292848 AI768962 BE540703 BE409478 AA931692

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	129703	64196_1	BE388665 AA740614 A1394542 AA484451 AW070675 AA877654 A1360981 A1475799 BE349560 A1037351 N29437 A1246453 AW083444 AA844441 A1150871 A1440477 A1889061 AA682422 AA680053 AA740212 A1588728 AA490589 AW243692 A1249450 A1304448 AA534421 A1500317 A1273337 AW027729 A1979132 C06120 A1860916 AW591923 A1803174 A1559264 BE250500 AW675522 AA883284 T71033 A1346838 A1066754 A1197913 AA931979 AA427599 A104730 A1285159 A1273325 A1038450 A1033760 N74972 AA136517 A1304446 A1262652 AA401348 AW514617 A1361795 AW514389 N30307 N39439 AA190775 BE349902 A1342114 A1186831 AA039628 H74242 A1914825 A1955761 A1343851 AA693856 T71096 A1498539 AA778995 AA084278 A1274678 A1022673 AW339621 AA704929 AW089735 AA041252 AA161337 A1185333 AW189397 A1160990 A1082392 A1935848 A144404 A1141633 AA447987 AA646241 A1342103 AW026118 AA834025 AW664459 AA603777 AA630752 AA115450 N49944 AW166071 AW769795 AA991877 AA873609 AW083441 H89130 AA910638 AA486199 AW083358 AA151767 A161193 N54945 AA180193 A1423477 A1188387 A1608747 N58900 A1038449 AA136852 AA565913 AA180502 H61741 AA701125 A1127678 AA278541 R76523 AA666187 H85083 F24755 R77729 AA135137 BE250395 R76239 AW794625 AW794404 H61957 AA308197 AW995031 AA345524 N52726 AA354360 AA179785 N57375 R16447 AA160645 W21481
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Table 73: Sequences

Seq ID NO: B1 DNA sequence
Nucleic Acid Accession #: NM_053056.1
Coding sequence: 210..1097

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	AAACCATCCG	CCGCGCGTAC	CCCGATGCCA	ACCTCCTCAA	CGACCGGGTG	CTGCGGGCCA	300
	TGCTGAAGGC	GGAGGAGACC	TGCGCGCCCT	CGGTGTCTTA	CTTCAATGT	GTGCAAGAGG	360
15	AGGTCTGTGC	GTCCATGCGG	AAGATCGTCG	CCACCTGGAT	GCTGAGAGTC	TGCGAGGAAC	420
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	TGGAGCCCGT	GAATAAGAGC	CGCTGCGAGC	TGCTGGGGGC	CACCTGCAATG	TTCTGTGCGC	540
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	CCATCCCGCC	CGAGGAGCTG	CTGCAAAATG	AGCTGCTCCT	GGTGAACAAG	CTCAAGTGA	660
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	GCCTTCTCTC	CGAGGTGATC	AAGTGTGACC	CAGACTGCCT	CCGGGCTGAC	CAGGAGCAGA	960
25	TGGAAGCCCT	GCTGGAGTCA	AGCTCGCGCC	AGGCCACGCA	GAACATGGAC	CCCAAGGCCG	1020
	CCGAGGAGGA	GGAAGAGGAG	GAGGAGGAGG	TGGAACCTGC	TTGCACACCC	ACCGACGTGC	1080
	GGGAGCTGGA	CATCTGAGGG	CGCCAGGCAG	GCGGGCGCCA	CCGCCACCCG	CAGCGAGGGC	1140
	GGAGCCGCGC	CCAGGTGCTC	CCCTGACAGT	CCCTCCTCTC	CGGAGCATTT	TGATACCAGA	1200
	AGGGAAAGTG	TCATTCTCTC	TGTTGTGGT	TGTTTTTTCC	TTTGCTCTTT	CCCCCTTCCA	1260
30	TCTCTGACTT	AGCAAAAGA	AAAAGATTAC	CCAAAAACTG	TCTTTAAAG	AGAGAGAGAG	1320
	AAAAAAGAAA	TAGTATTGTC	ATAACCCCTGA	GCGGTGGGGG	AGGAGGGTGT	TGCTACAGAT	1380
	GATAGAGGAT	TTTATACCCC	AATAATCAAC	TGTTTTTTAT	ATTAAATGAT	TTGTTTCTCT	1440
	GTGTGAAGAA	TAGGCATTAA	CACAAAGGAG	GCGTCTCGGG	AGAGGATTAG	GTTCATCTCT	1500
	TTACGTGTTT	AAAAAAAGC	ATAAAACAT	TTTAAAAACA	TAGAAAAAAT	CAGCAAAACCA	1560
35	TTTTTAAAGT	AGAAGAGGGT	TTTAGGTAGA	AAAACATATT	CTTGTGCTTT	TCCTGATAAA	1620
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	ACTTTATAAG	TCATTGTATG	TTATTATATT	CCGTAGGTAG	ATGTGTAACC	TCTTCACTTT	1740
	ATTCTATGCT	GAAGTCACCT	CTTGTTTACA	GTAGCGTAGC	GTGGCCGTGT	GCATGTCTCT	1800
	TGCGCGCTGT	ACCACCAACC	CAACAAACCA	TCCAGTGACA	AACCATCCAG	TGGAGGTTTG	1860
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	CCATTTCCAA	GCATTTTCAG	TCCAATAGGT	GTAGGAATA	GCGCTGTTTT	TGTTGTGTGT	2160
45	GCAGGGAGGG	CAGTTTTCCTA	ATGGAATGTT	TTGGGAATAT	CCATGTACTT	GTTTGCAGGC	2220
	AGGACTTTGA	GGCAAGTGTG	GGCCACTGTG	GTGGCAGTGG	AGGTGGGGTG	TTTGGGAGGC	2280
	TGCGTGTGCT	TCAAGAGAGA	AAAGGTTTGC	ATTCTCACAT	TGCCAGGATG	ATAAGTTCTT	2340
	TTCTTTTCTT	TAAAGAAAGT	TGAAGTTTAG	GAATCCTTTG	GTGCCAAGTG	GTGTTTGAAA	2400
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50	TCACACCGGA	AGGTTTTTAA	ACACTAAAAT	ATATAATTTA	TAGTTAAGGC	TAAAAAGTAT	2520
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	GATGAATTC	TATCCCTGCG	CCCTTCTCTT	AAAAAACTTA	GTGACAAAT	AGACAATTTG	2880
	CACATCTGG	CTATGTAATT	CTTGTAAATT	TTATTTAGGA	AGTGTGAAG	GGAGGTGGCA	2940
	AGAGTGTGGA	GGCTGACGTG	TGAGGGAGGA	CAGGCGGGAG	GAGGTGTGAG	GAGGAGGGTC	3000
	CCGAGGGGAA	GGGCGGTGCG	CCACACCGGG	GACAGGCGCG	AGCTCCATTT	TCTTATTGCG	3060
60	CTGCTACCGT	TGACTTCCAG	GCAAGGTTTG	GAATATTTCA	CATCGCTTCT	GTGTATCTCT	3120
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	ATGTACTAGT	TTTAGTTTTT	TCTTAGAACA	TTGTATTACA	GATGCCCTTT	TTGTAGTTTT	3240
	TTTTTTTTTT	ATGTGATCAA	TTTTGACTTA	ATGTGATTAC	TGCTCTATTC	CAAAAAGGTT	3300
	GCTGTTTCAC	AATACCTCAT	GCTTCACTTA	GCCATGTGGG	ACCCAGCGGG	CAGGTTCTGC	3360
65	CTGCTTTGCG	GGGCAGACAC	GCGGGCGCGA	TCCCACACAG	GCTGGCGGGG	GCCGGCCCCG	3420
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	TTCCCTGCGC	CTGTGATGCT	GCGCACITCA	TCTGATCGGG	GGGTAGCAT	CATAGTAGTT	3540
	TTTACAGCTG	TGTTATTCTT	TGCGTGTAGC	TATGGAAGTT	GCATAATTAT	TATTATTATT	3600
	ATTATAACAA	GTGTGCTCTA	CGTGCCACCA	CGCGGTTGTA	CCTGTAGGAC	TCTCATTCGG	3660
70	GATGATTGGA	ATAGCTTCTG	GAATTGTTC	AAGTTTTGGG	TATGTTTAA	CTGTTATGTA	3720
	CTAGTGTCT	GTTTGTGTTT	GTTTTGTAA	TTACACCATA	ATGCTAATTT	AAAGAGACTC	3780
	CAAACTCTCA	TGAAGCCAGC	TCACAGTGCT	GTGTGCCCGG	GTCACTAGC	AAGCTGCCGA	3840
	ACCAAAAGAA	TTTGCACCCC	GCTGGCGGGC	CACGTGGTTG	GGGCCCTGCC	TGGCAGGGT	3900
	CATCCTGTGC	TGCGAGGCCA	TCTCGGGCAC	AGGCCCAACC	CGCCCAACCC	CTCCAGAACCA	3960
75	CGGCTCACCG	TTACCTCAAC	CATCTGGGCT	GCGGGTCTG	TCTGAACAC	GCGGGGGCCT	4020
	TGAGGGACGC	TTTGTCTGTC	GTGATGGGGC	AAGGGCACAA	GTCTGATG	TTGTGTGTAT	4080
	CGAGAGGCCA	AAGGCTGGTG	GCAAGTGCAC	GGGGCACAGC	GGAGTCTGTC	CTGTGACGGG	4140
	CAAGTCTGAG	GCTCTGGGCG	GCGGGCGGCT	GGGTCTGTGC	ATTCTGTGTT	GCACCGCGCG	4200
	GCTTCCGAGC	ACCAACATGT	AACCGGCATG	TTTCCAGCAG	AAGACAAAAA	GACAAACATG	4260
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Seq ID NO: B2 Protein sequence
Protein Accession #: NP_444284.1

1 11 21 31 41 51
797

5
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 Coding sequence: 1..1576

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 Protein Accession #: KP_044166.2

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5 Seq ID NO: B5 DNA sequence
Nucleic Acid Accession #: NM_000909.1
Coding sequence: 209..1363

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Seq ID NO: B6 Protein sequence
Protein Accession #: NP_000900.1

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65 CVSITVSIFS LVLLAVERHQ LIINPRGWRP NNRHAYVGLA VIWVLAVASS LPFLIYQVMT 180
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70 Seq ID NO: B7 DNA sequence
Nucleic Acid Accession #: NM_002590.2
Coding sequence: 204..3416

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Seq ID NO: B8 Protein sequence
Protein Accession #: NP_002581.2

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Seq ID NO: B9 DNA sequence
Nucleic Acid Accession #: AL121939.12
Coding sequence: 185..1426

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30     TTGCCTCTGG ATTCAGGGA ACGATGCCAA TTGTGCTTAC GGCTAACAGA GACCTGAAAC 1440
AGGCGGTGT ATCATCTAAA TCACAGAGAA AACCAGCTCT GCTTACCGTA GTGAGATCAC 1500
TTCATAGGTT ATGCTGAGC TTGAACCTCT TCAATAGCAT TTCACATTT TTCAAATCA 1560
GGAGATTTTC GTCCATTAA AAAATGTATA GGTGCAGATA TTGAAACTAG GTGGGCATT 1620
CAATGCCAAG TATATCTCT TCTTATCATG GTGATGAGTT TCATTGTAG AAAAAATTTG 1680
35     TTGCCTCTCT TTAATTTAGA CACACTTAA ACCTTCAAAC AGGTATTATA AATAACATG 1740
GACTCCTTAA TGGACTTATT CTCAGGGTCC TACTCTAAGA AGAATCTAAT AGGATGCTGG 1800
TTGTGTATTA AATGTGAAT YGCATAGATA AAGGTAGATG GTAAAGCAAT TAGTATCAGA 1860
ATAGAGACAG AAGTTTACA CACAGTTTGT ACTACTCTGA GATGGAYCCA TTCAGTCTAT 1920
GCCCTCAATG TTTATATTGT GTTATCTGTT GGGTCTGGGA CATTTAGTTT AGTTTTTTTG 1980
40     AAGAAATACA ATTCAGAGAA AAAAGCAAGC ATTATAACA AACTAATAA CTGTTTACT 2040
GCTTTAAGAA ATAACAATTA CAATGTGTAT TATTTAAAAA TGGGAGAAAT AGTTTGTCT 2100
ATGAATAAAA CTTAGTTTAG AAATAGGGAA GCTGAGACAT TTTAAGATCT CAAGTTTTTA 2160
TTAACTAAT ACTCAAATA TGGACTTTTC ATGTATGCAT AGGGAAGACA CTTCAAAAT 2220
TATGAATGAT CATGTGTTGA AAGCCACATT ATTTTATGCT ATACATTCTA TGTATGAGT 2280
45     GCTACATTTT TAGGACAAAG AATTCTGTAA TCTTTTCAA GAAAGAGTCT TTTTCTCTT 2340
GACAAATACC AGCTTTTGTA TGAGGACTAT AGGGTGAATT CTCTGATTAG TAATTTTAGA 2400
TATGTCTCTT CTAAATAATG AATAAAATTT ATGAATATGA CTTAAAAAAA AAARWCGAG 2460
CGGCCGCGAA TTTAGTAGTA GTAGTCGACC CGGGAATTCC GGACCGGTAC CTGCAGGCGT 2520
50     ACCAGC
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Seq ID NO: B10 Protein sequence
Protein Accession #: CAC35071.1

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55     1      11      21      31      41      51
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MENMLLWLIF FTPGWTLDIG SEMEWDFMWH LRKVPRIVSE RTFHLTSPAF EADAKMMVNT 60
VQGISQKEL PTPSLELED YLSYETVFEN GTRTLTRVKV QDLVLEPTON ITTKGVSVRR 120
KRQVYGTDSR FSILDKRFLT NFFPSTAVKL STGCSGILIS PQHVLTAACH VHDGKDVKG 180
60     SKKLRLVLLK MRNKGSGIKR RGSKRSRREA SGGDQREGTR EHLRERAKGG RRRKSGRGQ 240
RIAEGRPSPQ WTRVKNTHIP KGWARGGMD ATLDYDYALL ELKRAHKKY MELGISPTIK 300
KMPGGMIHFS GFNDRADQL VYRFCVSUDE SNDLLYQYCD ABSGSTSGSV YLRKDPDKK 360
NWKRIIAVY SGHQWVDVHG VQRDYNVAVR ITPKYAQIC LWHGNDANC AYG
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Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: NM_002035.1
Coding sequence: 108..1106

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CGCGCGCGCC CGCGCGCGCC GCTCGGCGCC CCTGGCCCGG CGAGCGATG CTGCTGCTGG 120
CTGCGCCCTT CCTCGTGGCC TTCTGTCTGC TGCTGTACAT GGTGTCTCCG CTCATCAGCC 180
CCAAGCCCCC CGCCCTGCCC GGGGCGCATG TGGTGGTTAC AGGAGGTTCC AGTGGCATCG 240
75     GGAAGTGCAT TGCTATCGAG TGCTATAAAC AAGGAGCTTT TATAACTCTG GTTGACAGAA 300
ATGAGGATAA GCTGCTGCAG GCAAGAAAG AAATGGAAT GCATCTTATT AATGACAAAC 360
AGGTGTGTCT TTGCATATCA GTTGATGTAT CTCAGACTA TAACCAAGTA GAGAATGTCA 420
TAAACAAGC ACAGGAGAAA CTGGGTCCAG TGGACATGCT GGTAAATGTG GCAGGAATGG 480
CAGTGTGAGG AAAATTTGAA GATCTTGAAG TTAGTACCTT TGAAGGTTA ATGAGCATCA 540
80     ATTACCTGGG CAGCGTGTAC CCCAGCGGG CGTGATCAC CACCATGAAG GAGCGCCGGG 600
TGGCGAGGAT CGTGTGTTG TCCTCCACAG CAGGACAGTT GGGATTATTC GGTTCACAG 660
CCTACTCTGC ATCCAGTTT GCCATAAGGG GATTGGCAGA AGCTTTGCAG ATGAGAGTGA 720
AGCCATATAA TGTCTACATC ACAGTTGCTT ACCCAACAGA CACAGACACA CTGGCCTTTG 780
CGAAGAAAA CAGAACAAAG CTTTGGGAGA CTCGACTTAT TTCAGAGACC ACATCTGTGT 840
GCAACACAGA ACAGGTGGCC AAACAAATTG TTAAGATGCT CATACAAGGA AATTTCACAA 900
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5 GTTCCCTTGG CTCAGATGGG TACATGCTCT CGGCCCTGAC CTGTGGGATG GCTCCAGTAA 960
CTTCTATTAC TGAGGGGGCTC CAGCAGGTGG TCACCATGGG CCTTTTCCGC ACTATTGCTT 1020
TGTTTTACCT TGAAGGTTTT GACAGCATAG TTCGTGCTG CATGATGCAG AGAGAAAAAT 1080
CTGAAAATGC AGCAAAACT GCCTAATCTT CTTACCCCTT GGAAGAAGAC TGTTTCCAAA 1140
TAATTTGAAC AGCTTGCTGC TAAATGGGAC CCAATTTTTG GCCTATAGAC ACTTATGTAT 1200
TGTTTTCGAA TAGCTCAGAT TGGACCATG CTCTTCAGGA ATGTGGCTGC AAGCAAGGG 1260
CTAGAAGTTC ACCTCTGAC AGTATTATTA ATACTATGCA AATATGGAAT AGGAGACCAT 1320
TGATTTTCT AGGCTTTGTG GTAGAGAGGT GAAGGTATGA GAATTAATAG CGTGTGAACA 1380
AAGTAAAGAA CAGGATTCOA GAATGATCAT TAAATTTGTT TCTATTATT CTTTTTGCC 1440
10 CCCTAGAGA TTAAGTCCAG AAATGTACTT TCTGGCAGT AAAGAAATCT TGAGGACTTT 1500
GTTTAAACCT TCCATAAAAA AACAAATTTT GGTTCCTCG GTTCTCTCTC TCTGTCTCTC 1560
TGCTCTCTG TCTCTCTGTC TCTCTGTCCT TCTCTCTCTC TCTCTTCTT TCTTTGTGTA 1620
TTTTATTCAA GATGAGTTGG ACCCAATGCC AGTGAGTCTG AATGTCACTG ACAGCCCTGT 1680
15 GTTGTGCTCA GGACTCCTC TGCTGCTGGT GGAAACTCAT GGCTTCTCTC TCTCTTGAT 1740
CCCATAAAGC TACGAGGGGG ACGGGAGAGG GCAGTGCAAT GGAAGTAAA GAGATATTTT 1800
CCAGTAGGAA AAGCAATGCT TTCTGTCTT TAGACTCAAA TGCTTAGGGA ACCTTTCATT 1860
TCTCAATCAT GGGGAAAGCG AGCCTCCTTA AATGTTTCT GAAGAGCGGT AAAATCTAGA 1920
AGCTTAAAG TTTACAGTTC CTTCAATAAC CATGATGACC TGAAGTTCAC CTATCCCAT 1980
20 TTAGCATCTA CTGTTTTTTC CCATCTCTTC CTTTCCAATT TTGCTTATAC TGCTGTAATA 2040
TTTTTGTAAA AAAAAAAGAA AAGGAAAAAA AAGACCAAGT AAAATTTTCG ACTTGACTTT 2100
TTAACTTAAC TCATGAATTA ATTAAGACAA ATGAAAAAAT TAAAAAGTGT GACTTTTTCT 2160
CGGAGCATAT ATGTAGCTTT TAGGAAAGGC TGATGATGGT ATAAAGTTTG CTCATTAAGA 2220
AAAAAGACA AGGCTGATTT TGAAGAGAGT TGCTTTTGAA ATAAATGAT CA

25 Seq ID NO: B12 Protein sequence
Protein Accession #: NP_002026.1

30 1 11 21 31 41 51
MLLLAAAFV AFVLLLYMVS PLISPKPLAL PGARVVVTGG SSGIGKCAI ECYKQGAFIT 60
LVARNEKLL QAKKEIEMHS INDKQVVLCT SVDVSQDYNQ VENVIKQAQE KLGPDVMDLVN 120
CAGMAVSGKF EDLEVSTFER LMSINYLGSV YPSRAVITM KERRVGRIVF VSSQAGQLGL 180
FGFTAYSASK PAIRGLAEAL QMEVKPYNVY ITWAYPPDID TPGFAEENRT KPLETRLISE 240
35 TTSVCKPEQV AKQIVKDAIQ GNFNSSLGSD GYMLSALTGC MAPVTSITEG LQQVVTMGLF 300
RTIALFLYLS FDSIVRRMCM QREKSENADK TA

Seq ID NO: B13 DNA sequence
Nucleic Acid Accession #: CAT Cluster

40 1 11 21 31 41 51
CTTGGGATGC ATTATATATT GCATTATATT TGCCGGTAAA ACTCGGTAAA TTTTAAAAAT 60
CGGCAAAATA TTGGTGCCTT TCCCGAAATT TGGTCCCGGG CTCCTTATA GGATAATTGG 120
45 TTGGATTTGG TTAAGTCCAA TTATTAAATG CTGCGGTTTC AAATTCACAG CTGGAAGGAC 180
CACCATTTA AAAACTTCAG AAGGCAGGAT CCTGCTCAAT TTATAAGGCT TTGGAAAATT 240
CCAGGCATTG GTTTGACATA TTTCCAGAGC TCAAACTGTC AGTGTTCAC ATGCACATAC 300
AAGATCCAGA GTCTCATGTT AAAATCACTT ACATACCCAG AAAGACCACC ACTTTGCAGG 360
TATAATATTG TACTTAAAGA CAGAGAGGAA GTGTTTCTTA ATCCAAACAC ATGTACACCA 420
50 AAGAACACAT AAGATGCCTT CTTCATCAA ATGCACCTGC TTGTGAATTA ATGGACTTGT 480
AAATGAACA ATGCAATCAG TCTTTTATAA TGCACTGTTT AATTGAGAT TCAAGTATTT 540
CTATTTCTTG GAAAAAATTT TAAGAAATCA AAATAAAGAA AATAAAAAGT GCATACAGTT 600
AAACATTCCA AAAAAAAGAA AA

55 Seq ID NO: B14 DNA sequence
Nucleic Acid Accession #: XM_086767.1
Coding sequence: 276..611

60 1 11 21 31 41 51
CTTGTTCATG GCATCTTTAG AAACAAACTG CAATTTTATT TCATTTCCTT GTCGTTTATA 60
CAAAGATTAC AAGACTAGCT TATGTGTGGA CTGTGACTGT TTTAAGGAAA AATCATGTCC 120
TCGGCTGGGT TATCAAGCCA AGCTATTAA AGGTGTTTAA AAAGAAAGGA TGGAAAGGAAG 180
65 ACCCTCTAGG ACCACTGTGT TTTTGGATAC AAGTGGTACA TATCCATTCT GTAGCCTATT 240
ATTTTGTCT CAGTATAATT GTTCCAGATA AAACATGAT GGATGGCTCG TTTTCATTTA 300
AATTATTAAT TCAGCTTGGG ATGATTGAAG AGCCAAAGCT TTATGAAAG AACAAACCAT 360
TTTATAAAT TCAAGAAAGT AAGATTCCTG CTCAATTTTA TAATGACTTT GTAAATATTT 420
CAAGCATTTG TTTGACATAT TTCCAGAGCT CAAATCTGCA GTGTTCACA TGACATACA 480
70 AGATCCAGAG ACTCATGTTA AAATCACTTA CATACCCAGA AAGACCACA CTTTGCAGGT 540
ATAATATTGT ACTTAAAGAC AGAGAGGAAG TGTTCCTTAA TCCAAACACA TGTACACCAA 600
AGAACACATA AGATGCCCTC TTCCATCAAA TGCACTTGCT TGTGAATTA TGGACTTGTA 660
AATGAACATA TGCAATCAGT CTTTATAAAT GCACGTGTC AATTGAGATT CAAGTATTTT 720
TATTTCTTGG AAAAAATTTT AAGATCAAA AATAAAGAAA ATAAAAATG CATACAGTTA 780
75 AACATTCC

Seq ID NO: B15 Protein sequence
Protein Accession #: XP_086767.1

80 1 11 21 31 41 51
MMDGFSFSLK LNQLGMIEEP RLYEKNKPFY KLQEVKILAQ FYNDFVNIS IGLTYFQSSN 60
LQCSTCTYKI QRLMLKSLTY PERPFLCRVN IVLKDRBEVP LNPNTCTPKN T

Seq ID NO: B16 DNA sequence

Nucleic Acid Accession #: CAT cluster

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5	TTTTTTTTT	TTTTTTTTT	TTAAATGCAA	AGGAGCAACA	AAATTTATTG	ACTGAATTAA	60
	ACACACAGT	AAAATGGCAG	TGTTGTAATT	TCATTTTCAG	ATGTTTGAAT	GGAAACAAGAA	120
	AAGTGCTATT	AGCCCAAGCT	TCTTACATTC	ATTAAAAGAG	TGACTATCAA	AAACAGCAAC	180
	ATGCACAATG	GTACATATGC	ACAAAATGGA	ATTATATCAA	CAAAATATACA	AAATACCCAA	240
10	AATAAAATAT	TTACAGGTTT	AAAAATATAA	ACATTGATTC	CTCTATCCCA	TTAAACCATT	300
	GGAGTGGAGA	AAGGAGGAAA	GACCCATATTG	CTATTTAGAA	TCCTTTTTAA	AACAAGTTTT	360
	TAAAAATAG	AATTAGTTCT	AGGAGACAAT	TTTTGATGTT	TTTCAGGGGT	TTAACATTCT	420
	ATTATAAAAA	TAACATCTAT	AAACCTACTA	ACAATTTTCC	TCCTGTGCAC	AAAAATAATA	480
	CTGCCAAAAC	CTGTCTCAA	AGACATGCCT	GACTTTCAGG	AAAGCTAATT	ATGGAATG	540
15	AGTTTCTCGT	TTGGGTTATC	TTTGTACTA	TTTTCAATA	ACCAGCAACT	CCCTATATTA	600
	CACGTAGATA	CTTTATATAA	ATAACGTGGG	CGAAACCTGA	AGTTCACAAT	GAGCCTGCTA	660
	GGTAGCTGCT	GTCAAGTACA	AATGATAGGA	ATTGACTTTG	CCAACAACAT	CAAAAGCATT	720
	TTCCCTGATA	TTCCGTATAG	ACCTACCACT	ATCAGATCCT	CCATATTCAA	TAAGATTAT	780
	CCTGGAGCA	ATGAAATGT	TAAATATTAC	TTTGCTAGAG	TTTCTCTCC	TTTATTAGA	840
20	AATAAATGTG	TAGTGGGGAC	CAGTGGTGTG	AATGTAGATA	CTTGAGAAGT	TTCAATTGATT	900
	CCTTCAGACC	CATGCCG					

Seq ID NO: B17 DNA sequence

Nucleic Acid Accession #: NM_022898.1

Coding sequence: 268..2739

25	1	11	21	31	41	51	
	TTTTCTTGCT	TTTCTTCCCT	TTTTTTTCTT	TTTGCAAAACA	AAACAAAAAA	CAGCATAGAA	60
	GAAAGAGCAA	AATAAAGAAG	AAGAAGAGGA	GGAAGAGAGG	GAAAGAGAGG	AAGGGAAAAA	120
30	AAACACCAAC	CCGGGCGAGG	GAGGAGGTGC	GGCGGCGCGG	GGCGGCGCGG	CAGCGCGCGG	180
	AGCGGCGCGG	CGGGGCTCG	GACCCCTCC	CCCGGCTCCC	CCCATCAGTG	CAGCTCTCCG	240
	GGCGATGCCA	GAATAGATGC	CGGGGCAATG	TCCCGCCGCA	AACAGGCAAA	CCCGCAGCAC	300
	TTGTCCCGA	GGGAGCTCAT	CACCCAGAG	GCTGACCATG	TGGAGGCGCG	CATCTCTGAA	360
	GAAGACGAGG	GTCTGGAGAT	AGAGGAGCCA	AGTGGCTTGG	GGCTGATGGT	GGGTGGCCCC	420
35	GACCCCTGACC	TGCTCACTGT	TGGCCAGTGT	CAAATGAATC	TCCCTTTGGG	GGACATCTCT	480
	GTTTTTATAG	AGCACAAGAG	GAAGCAGTGT	GGCGGCGAGT	TGGGTGCTTG	CTATGACAAG	540
	GCCCTGGACA	AGGACAGCCC	GCCACCTTCC	TCACTGCTCC	AGCTCAGGAA	AGTGTCCGAG	600
	CCGCTGGAGA	TCCGGATCCA	AGTCAACCCC	GACGAAGATG	ACCACCTGCT	CTCACCCACG	660
	AAAGGCATCT	GTCCCAAGCA	GAGAAACATT	GCAAGTAAAG	ATGAGCTTTC	CAGCTACATT	720
40	TGCACAACAT	GCAAGCAGCC	CTTCAACAGC	GGTGGTTTCC	TGCTGCAGCA	CGCGCAGAAC	780
	ACGCAAGGCT	TCCGCATCTA	CCTGGAGCCC	GGGCGGCCCA	GCAGCTCGCT	CACGCGCGGG	840
	CTCACCTATCC	CGCGCGGCTT	CGGGCGGAG	GCCTGGCGCG	AGTCCCGGCT	CATGAATTTT	900
	CTGGCGGACA	GCAAGCCCTT	CAACCTGCTG	CGCATGAOOG	GCCTCATCTT	CGGGGACCCAC	960
	CCGGGCTTGG	GGGAGGGCGG	CCTGCGGGGC	AOCGCGGCTC	TCTTCAGTCC	CCGCGCGGCG	1020
45	CACCACTTGG	ACCGGCACCG	CCTCAGTGCC	GAGGAGATGG	GGCTCGTGCG	CCAGCACCCC	1080
	AGTGCCTTGG	ACCGAGTCAAT	CGGCTGTAAC	CCCATGGCCA	TGCACTCGCC	CGCCATGAC	1140
	TTCTCGGGCG	GGCTCGCGGA	GCTGGCGGGC	AACAGCTCCA	CGCGCGCGCC	CGTGTCCCGG	1200
	GGCGCGGCGA	CCCTATGCA	CGGGCTCTGT	AAACCCCTTCC	AGCCCGAGCC	CAAGTCCCCG	1260
	TTCTTGAGCA	CGCGCGGCTT	CGCGCCCATG	CCCCCTGGCG	GCAGCGCGCC	CCCGCAGCCG	1320
50	CCAGGCCAGA	GCAAGTCTGT	CGAGTTCTGC	GGCAAGACCT	TCAAGTTCCA	GAGCAATCTC	1380
	ATCGTGCAAC	GGCGCAGTCA	CACGGGCGAG	AAGCCCTACA	AGTGCCAGCT	GTGCGACCCAC	1440
	GGCTGCTGCG	AGGCGAGCAA	GCTCAAGGCG	CACATGAAGA	CGCACATGCA	CAAGGCGCGC	1500
	TGCTGCGGCG	GCCGCTCGGA	CGACGGGCTC	TGGCGCGCCA	GCTCCCCCGA	GCCCGGCACC	1560
	AGCGAGCTGG	CGGGCGAGGG	CCTCAAGGCG	GCGGACGGTG	ACTTCCGCCA	CCAAGAGAGC	1620
55	GACCCGTGCG	TGGGCCACGA	GCGGAGGAG	GAGGACGAGG	AGGAGGAGGA	GGAGGAGGAG	1680
	GAGCTGCTAC	TGGAGAAOGA	GAGCGGGCCC	GAGTGGAGCT	TCAGCATGGA	CTCGGAGCTG	1740
	AGCGCGAACC	GGGAGAACGG	CGGTGGTGGG	GTGCGCGGGG	TCCCGGGCGC	GGGGGGCGGC	1800
	GCGGCGAAGG	CGCTGGCTGA	CGAGAAGGCG	CTGGTGTCTG	GCAAGGTCAT	GGAGAACTGT	1860
	GGCCTAGGCG	CAGTCCGCGA	GTACGGGAG	CTCCTGGCGG	ACAAGCAGAA	GCGCGGCGCC	1920
60	TTCTTGAGGC	GTGCGGCGGG	CGGCGGGGAC	GCGGGGCGAG	ACGACGACGC	GGGCGGCTGC	1980
	GGGGAAGCGG	GCGCGGCGGG	CGCGGTCAAC	GGGCGCGGGG	GCGGCTTCGC	GCCAGGCAAC	2040
	GAGCCCTTCC	CGGGCTCTT	CCCGCGCAAG	CCCGCGCGCG	TGCCAGCCCG	CGGGCTCAAC	2100
	AGCGCGGCGA	AGGCATCAA	GGTGGAGAAG	GACCTGGAGC	TGCGCGCGCG	CGCGCTCATC	2160
	CGTTCGAGA	ACGTGTACTC	GCACTGGCTG	GTGGGCTACG	CGGCGTCCCG	GCACTTCATG	2220
65	AAGGACCCCT	TCTTGGGCTT	CACGGACGCA	CGACAGTCCG	CCTTGGCCAC	GTGCTCCGAG	2280
	CACCTGTCGG	AGAAACGGCG	CCTGCGCTTC	TCCACGCGCG	CGGGGACCTT	GCTGGAAGGC	2340
	GGCCTCTGGG	GCGCGAGCGG	CACGGCCAGC	GGAGGCAGCA	CCCGCACCCT	GGGCGGCGCG	2400
	GGCCCGGGCG	GGCCAGCTCT	CAAGGAGGGC	CGCGCGAGCG	ACAAGTGGCA	GTAATGCGGC	2460
	AAGGTGTGCA	AGAACTGCGG	CAACTTGACG	GTGCAACGCG	GGAGCCACAC	CGCGGAGCGG	2520
70	CCTTACAAGT	GCGAGCTGTG	CAACTACGCG	TGCGCGCAGA	GCAGCAAGCT	CACGCGCCAC	2580
	ATGAAGACCG	ACGGGAGGAT	CGGCAAGGAG	GTGTACCGCT	GGGACATCTG	CCAGATGCCC	2640
	TTACAGGCTT	ACAGCACCTT	GGAGAAACAC	ATGAAAAGT	GGCAGGCGGA	GCACTTGTCT	2700
	ACTAACGAGC	TCAAAATGGA	GCAGGCGGAG	AGGAGCTAAG	CGCGCGGGCC	CGGCGGCCCC	2760
	GCACCTGTAC	AGTGGAAACG	TTGCCAACCG	AGAGAATGCT	GACCTGACTT	GCCTCCGTGT	2820
75	CACGCGCACG	CGGCAACCGG	CGTGTCCCGG	GGGCGGAGGG	GAGGCGGCGC	TCCAACCTAA	2880
	CCTGTGTCTG	CGAAGTCTTA	TGGAAACCGG	AGGGTTGATT	AAGGCACTAC	AAATGTGGA	2940
	GCCTTTTAAC	TGTGCAATAA	TTTCTGTATT	TATTTGGTGT	TGTAATTTTT	TTGGCATGTG	3000
	CAGGTACTTT	TTATTATTAT	TTTTTCTGTT	TGAATTCCTT	TAAGAGATT	TGTGGGTAT	3060
	CCATCCCTTC	TTTGTTTTTT	TTTTAACCGG	GTAGTAGCCT	GAGCAATGAC	TGCAAGCAA	3120
80	TGTTAGAGGG	GAGCATATAT	TTTTAAATTA	TAATTTGGGG	GGAGGGGTGG	TGCTGCTTTT	3180
	TTGAAATTTA	AGCTAAGCAT	GTGTAATTTT	TTGTGAAGAA	GCCAACTCTC	AAATGACTTT	3240
	TAAAGTTGTT	TACTTTTCTA	TTCTTCTCTT	TTTTTTGTCT	TGAAATAAAA	AGTGGCATGC	3300
	AGTTTTTTTT	TTAATTTATT	TTTAATTTTT	TTTTTGGTGT	TTGTTTTTGG	GGTGGGGGGT	3360
	GTGGATGTAC	AGCGGATAAC	AATCTTTCAA	GTGTAAGCAC	TTTGTTCAG	AACCTGAATG	3420

5 GAGATGTAGC ACTCATGTGG TCCCGAGTCA AGCGGCCCTTT TCTGTGTTGA TTTCGGCTTT 3480
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 GCGCCGAGAG ATAGGGTTTT TGGAGGGCTC CTCTGGGAAA TGGCCCGACA GCATTCTGAG 3600
 GTTGTGCATG ACCAGCAGAT ACTATCCTGT TGGTGTGCC TGGGTGCCA TGGCTGCTAT 3660
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 10 TCTCATTTAA TGCACACTGA TGATATTGTA GGGATGGGTG GGGTGGGGAT CTTGCAAAAT 3960
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 15 GTTAAACTGT AAGGGACAGC TGAGATTGAG TGTCAATATT GCTAAGCGTG GCATTACAA 4260
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 20 AGATAGAGGA TATGAAATGC CATAAGACCC AATCAATGA AGAAATAAAC CCAGCACAA 4560
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 25 GGTAAAAAAA AAATTGTGTG TATGTGTGTT GGAGCGATCT TTTTTTTTCA AAGTTTGCTT 4860
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 35 TAAGCTGTGC CTTTAAAGG GATTAAATGT ACCTTTTGT TAGTGAATTT GGAATAAAA 5460
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 40 TCAATTAGT TATATATT TTTGCGGAA TTGGCTACA CAGAGAACCG TCGTGTGG 5700
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 45 AGAGAGCGAG AGAACATCTT CCTCTCTAC CATCACTCCT GTGGCGGTCA CCACACAC 5940
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 55 TAATCTCTA TTTTATTTT ATTTTGTGTA AAGCCAGTA GCTTTAAGT AAAGTGGTGG 6420
 TCTTTTGGAT GAGGGAATAA TGCAATTTTA AATAAATAC CAATATCAGG AAGCCATTT 6480
 TTAATTCAGG AATGTAAGA AACCATTATT TCAGGTATG AAAGTATAAC CAAGCATCCT 6540
 TTTGGGCAAT TCCTTACCAA ATGCAGAAGC TTTCTGTTT GATGCACTCT TTCCTCTTG 6600
 CCACCTACCT TTGCAAGTTT AAAAAAAGG GGGGAGGGA TGGGAGAGAA AGCTGAGATT 6660
 TCAGTTTCTT ACTGCAGTTT CCTACCTGCA GATCCAGGG CTGCTGTTGC CTTTGGATGC 6720
 60 CCCACTGAGG TCCTCAGAGT CCTCCAGGGT GGTCTTCTG TAGTCATAAC AGCTAGCCAG 6780
 TGCTCACAGC CTACACAGAT TGCCAGGACT AAGCCATCCC AAGCACAAG CATGTGTGT 6840
 CTCTGTGACT GCAGAGAAGA GAGAAATTTT CTCTGTTTT GTGTTTAAAA AACCAACAG 6900
 GAAGCAGATG ATCCGAGAG AGAGGCTCT AGCATGGGTG ACCCAGCCGA CCTCAGGCCG 6960
 65 GTTTCGACAC TGCCACAAC TTTGTTCAAAG TTGCCCCCA TTTGAACTG CACTTGGCA 7020
 TTAGAGGGTC TTTTATGGG AGAGAAGGAG ACTGAATTAC TCTAAGCAAA ATGTGAAAAG 7080
 TAAGGAATC AGCTTTTCAT CCCGTCCTA AGTAAOCGT AGCCGAAGGT CTCGTGGAAC 7140
 ACAGGCAAC CCGTGAATTT GGTGCTCCTT GTAACCTCAG CCTGCAAGC AAAGTCCCAT 7200
 70 TGATTTAAGT TGTGTCATT TGTACTGGCA AGGCAAAATA TTTTATTAC CTTTCTATT 7260
 ACTTATTGTA TGAGCTTTT TTTTACTT GAGGTTTGT TCTTTTACTA CAAGTTTGA 7320
 ACTATTATT ATTGCTTGT ATTGTGCTC TGTTTAAGAA ACAGGCACTT TTTTATT 7380
 TGGATAAAT GTTGAGATGA CAGGAGGTCA TTTCAATATG GCTTAGTAAA ATATTATTG 7440
 TTCTTTATT CTCTGTACAA GATTTTGGG CTCTTTTTT CTTAATGTC ACAATGTTGA 7500
 GTTCAGCATG TGTCTGCCAT TTTATTGTA CGCTGTGTTA AAACCAAGTT TGTCTGGTT 7560
 TCAAGTTATA AAAATAAAT GGACATTAA CTGTATCTCC AAA

Seq ID NO: B18 Protein sequence
 Protein Accession #: NP_075049.1

75 1 11 21 31 41 51
 MSRRKQGNPQ HLSQRELITP EADHVEAAIL EDEGLEIEE PSGLGLMVGQ PFDLLTCGQ 60
 QQMNFPLGDI LVFIEHQRKQ CGGSLGACYD KALDRDSPPP SSRSELKRVK EPVEIGIQVT 120
 PDEDDHLLSP TKGICPKQEN IAGKDEPSSY ICTCKQPFN SAWFLQHAQ NTHGFRIYLE 180
 80 PGPASSSLTP RLTIPLPLP EAVAQSPLMN FLGDSNPFNL LRMTGPILED HPGFGEGRLP 240
 GTPPLFSPPP RHHLDPHRLS AEEMGLVAQH PSAFDRVMRL NPMADSPAM DFRRLRELA 300
 GNSSTPPPVV PGRGNPMHRL LNFQFSPKPS PFLSTPPLPP MPPGGTTPPPQ PPAKSKSECF 360
 CGKTFKQSN LIVHRRSHITG EKPYKQQLCD HACSQAQSLK RHMKTHMHKA GSLAGRSSDDG 420
 LSAASSPEPG TSELAGEGLK AADGDFRHHE SDPSLGHEPE EDEDEDEDEE EELLLENESR 480

5 PESSFSMDSE LSRNRENGGG GVPGVPGAGG GAAKALADEK ALVLGKVMEN VGLGALPQYG 540
ELLADKQKRG AFLKRAAGGG DAGDDDDAGG CGDAGAGGAV NGRGGGFAPG TEPFPGLEFR 600
KPAPLPSPGL NSAAKRIKVE KDLELPPAAL IPSENVYSQW LVGYAASRHF MKDPFLGFTD 660
ARQSPFATSS EHSSENGSLR FSTPPGDLLD GGLSGRSGTA SGGSTPHLGG PGPGRPSSKE 720
GRRSDTCBYC GKVPKNCNL TVHRRSHTGE RPYKCELCNY ACAQSSKLTR HMKTHGQIGK 780
EVYRCDICQM PFSVYSTLEK HMKKWHGEHL LTNDVKIEQA ERS

10 Seq ID NO: B19 DNA sequence
Nucleic Acid Accession #: NM_000399.2
Coding sequence: 339..1769

1 11 21 31 41 51
15 TAACTGAGCG AGGAGCAATT GATTAATAGC TCGGCGAGGG GACTCACTGA CTGTTATAAT 60
AACACTACAC CAGCAACTCC TGGCTTCCCA GCAGCCGAA CACAGACAGG AGAGAGTCAG 120
TGGCAATAG ACATTTTCTT TATTTCTTAA AAAACAGCAA CTGTGTTGCT ACTTTTATTT 180
CTGTGATT TTTTCTCTG GTGTGTGTGG TGGTTGTTT TAAGTGTGGA GGCAGAAAGG 240
AGATACCATC CCAGGCTCAG TCCAACCCCT CTCCAAAACG GCTTTCTGTA CACTCCAGGT 300
AGCGAGGGAG TTGGGTCTCC AGGTTGTGCG AGGAGCAAAAT GATGACCGCC AAGGCCGTAG 360
20 ACAAANTCCC AGTAACCTC AGTGGTTTTG TGCACCAGCT GTCTGACAA ATCTACCCGG 420
TGGAGGACCT CGCCGCCAGG TCGGTGACCA TCTTTCCCAA TGCCGAACTG GGAGGCCCT 480
TTGACCATGAT GAACGGAGTG GCCGGAGATG GCATGATCAA CATTGACATG ACTGGAGAGA 540
AGAGGTGCTT GGATCTCCCA TATCCAGCA GCTTTGCTCC CGTCTCTGCA CCTAGAAACC 600
AGACCTTCAC TTACATGGGC AAGTCTCTCA TTGACCTCA GTACCTGTGT GCCAGCTGCT 660
25 ACCCAGAAGG CATAATCAAT ATTGTGAGTG CAGGCATCTT GCAAGGGGTC ACTTCCOCAG 720
CTTCAACAC AGCCTCATCC AGCGTCACTT CTGCTTCCCC CAACCCACTG GCCACAGGAC 780
CCCTGGGTGT GTGCACCATC TCCAGACCC AGCCTGACCT GGACCACTG TACTCTCCG 840
CACGCTCTCC TCCTCTCTAT TCTGGCTGTG CAGGAGACCT CTACCGAGAC CTTCTGCGT 900
30 TCTGTGTCAG AGCCACCACT TCCACCTCTT CCTCTCTGGC CTACCCACCA CCTCTTCTCT 960
ATCCATCCCC ACGGACCCAG ACGGACCCAG GTCTCTTCCC AATGATCCCA GACTATCCCT 1020
GATTCTTCC ATCTCAGTGC CAGAGAGACC TACATGTGAC AGCTGGCCCA GACCGTAAGC 1080
CCTTTCCCTC CCACTGGAG ACCCTGCGGG TGCCCTCTCC ACTCACTCCA CTCTCTACAA 1140
TCCGTAACCT TACCTTGGGG GCGCCCACTG CTGGGGTGAC CGGACCAAGG GCCAGTGGAG 1200
35 GCAGCGAGGG ACCCGGCTG CCTGTGAGCA GCTCAGCAGC AGCAGCAGCC GCCGCGCGCG 1260
CCGCTATATA CCAACACCACT CTGCCACTGC GGCCTATTCT GAGGCTGCG AAGTACCCCA 1320
ACAGACCCAG CAAGACCGCG GTGCACGAGA GGCCTACCC GTGCCAGCA GAAGGCTGCG 1380
ACCGGGGTT TCCTCGCTCT GACGAGCTGA CACGGCACAT CGAATCCAC ACTGGGCATA 1440
AGCCCTTCCA GTGTGCGATC TGCATGCGCA ACTTCAGCG CAGTGACCAC CTCACCAACC 1500
40 ATATCCGAC CCACACCGGT GAGAAGCCCT TCGCCTGTGA CTACTGTGGC CGAAAGTTTG 1560
CCCGGAGTGA TGAGAGGAAG CGCCACACCA AGATCCACCT GAGACAGAAA GAGCGGAAAA 1620
GCAGTGCCCC CTCTGCAATG GTGCCAGCCC CCTCTACAGC CTCTGTCTCT GGGGGGTGTC 1680
AGCCTGGGGG TACCTGTGTC AGCAGTAACA GCAGCAGTCT TGGCGAGGG CGCTCGGCC 1740
CTGTCTCTCT TGGACCCGG ACACCTTGAG ATGAGACTCA GGCCTGATCA CCAGCTCCCA 1800
AAGTCCCGG AGGCCCTTTG TCCACTGGAG CTGCACAACA AACACTACCA CCCTTTCCTG 1860
45 TCCTCTCTCT CCTTTGTTGG GCAAAGGGCT TTGGTGGAGC TAGCACTGCC CCTTTCAC 1920
CTAGAAGCAG GTTCTTCTTA AAACCTAGCC CATTCTAGTC TCTCTTAGGT GAGTTGACTA 1980
TCAACCAAG GCAAAGGGGA GGCTCAGAAG GAGGTGGTGT GGGGATCCCC TGGCCAGAG 2040
GGCTGAGTCT TGACCTCTCT TTAAGGGTGT GTTTGACTAG GTTTTGCTAC CCCACTTCCC 2100
CTTATTTTGA CCAATCAGAG GTTTTGTACC CTGGATGTCA GAGTTGATCT AAGACGTTTT 2160
50 CTACATAGG TTGGGAGATG CTGATCCCTT CAAGTGGGA CAGCAAAAG ACAAGCAAAA 2220
CTGATGTGCA CTTTATGGCT TGGGACTGAT TTGGGGGACA TTGTACAGTG AGTGAAGTAT 2280
AGCCTTTATG CCACACTCTG TGGCCCTAAA ATGGTGAATC AGAGCATATC TAGTTGTCTC 2340
AAACCTTGAA GCAATATGTA TTATATACTC AGAGAACAGA AGTGCAATGT GATGGGAGGA 2400
ACGTAGTAC ATCTGCTCTT TTTGAGTTG TTTGAGAAAT GTAGGCTATT TTTTCAGTGT 2460
55 ATATCCCTC AGATTTTTGT TATTTTGTAT GTACCCACAC TGTCTCTTAA ATTCTGAATC 2520
TTTGGGAAAA AATGTAAAGC ATTTATGATC TCAGAGGTAA ACTTATTTAA GGGGATGTA 2580
CATATTCTCT GAAACTAGGA TGCAATGCAAT TGTGTGGGAA GTGTCTTGTG TCGCCTTGTG 2640
TGATGTAGAC AAATGTITACA AGGCTGCATG TAAATGGGTT GCCTTATTAT GGAGAAAAAA 2700
ATCACTCCCT GAGTTTAGTA TGGCTGTATA TTTATGCCTA TTAATATTTG GAATTTTTTT 2760
60 TAGAAAGTAT ATTTTGTAT GCITTTGTTT GTGACTTAAA AGTGTACCT TTGTAGTCAA 2820
ATTTAGATA AGAATGTACA TAATGTTACC GGAGCTGATT TGTGTGGTCA TTAGCTCTTA 2880
ATAGTTGTGA AAAAATAAAT CTATCTAAC GCAAAACCAC TAACTGAAGT TCAGATATAA 2940
TGATGGTTT GTGACTATAG TGTAATAAAA TACTTTTCAA CAAT

65 Seq ID NO: B20 Protein sequence
Protein Accession #: NP_000390.2

1 11 21 31 41 51
70 MMTAKAVDKI PVTLSGFVHQ LSDNIYPVED LAATSVTIFP NAEELGGPFDQ MNGVAGDGM 60
NIDMTGEKRS LDLPYPSFFA PVSAPRNQTF TYMGKFSIDP QYPGASCYPE GIINIVSAGI 120
LQGVTSFAST TASSSVTSAS FNPLATGPLG VCTMSQTQPD LDHLYSPPPP PPPYSGCAGD 180
LYQDPSAFLS AATTSSTSSL AYPPPPSYPS PKPATDPLGF PMIPDYPGFF PSQOQDLH 240
75 TAGPDRKPFP CPLDTRLVPP PLTPLSTIRN FTLGSPSAGV TGPASGGSE GPRLPSSSSA 300
AAAAAAAAY NHPHLPLRPI LRPRKYPNRP SKTPVHERPY PCPABGCDRR FSRSDLTRH 360
IRHTGKFF QCRICMRNFS RSDHLTTHIR THTGEKPFAC DYCGRKFPARS DERKRTKIH 420
LRQKERKSSA PSASVPAPST ASCSGGVQPG GTLCSSNSSS LGGGLAPLCS SRTTTP

80 Seq ID NO: B21 DNA sequence
Nucleic Acid Accession #: NM_004962.2
Coding sequence: 457..1893

1 11 21 31 41 51

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CACACACGGG CGCACGCACA CGGCAGCCGG GCCAGGGACG ACCCTGTGAC CTGCAGCCCC 60
 AGAGGTCOCG GCGCGGCAGC CGGGTCCOCT CGAGGGGSCA GCCGGCCGCC CCGCCCCGCC 120
 CCTCGAAGAA GCGCGGGCCG GCGCGCAGTG GGCTACAAAC TTTCGACGCG CGAGTCCGCC 180
 AAGGCAGCGC GCGGACTCGG GCTCGGCTCG GCTCTGCGCT GCTCGGACG GCTGTGACCG 240
 CTGGCCGGGG GCTCGGGCCG CCGGTACCCA CGGACCGCGC GCCCGGGTGC CTGCTCCGCT 300
 AAGCCCTCTG CCGCGCGCGG ACCTCGGTAT CCAGCGCCCT GCTGCCCGGG CTCTCCCGCG 360
 GCGCCCTACT GCGCGGAGGT CAGTCCGCAG CCTCGGTCG GCCAGCGCTC GCCTTCTCTC 420
 TCCTGGACTT CCGCCCTTTG CCGCCCTCAC CAGCCCATGG CTCTGTCCC CGCTCGGACC 480
 AGCCCGGGAC CCGGGCCCCA GCTGCTGCTG CTGCTGCTGC CGTTGTTTCT GCTGTTGCTC 540
 CGGATGTGGG CCGGACGCCA CAGGGCCCCC GCCTGGTCCG CACTGCCCGC GGCGGCGAC 600
 GGCTCGCAGG GGGACAGGGA TCTCCAGCGG CACCTCGGGG AGCGGCGCGC CAGTTGGGGC 660
 CCCAGCGCCC AGGACATGGT CGCTGTCCAC ATGCACAGGC TCTATGAGAA GTACAGCCGG 720
 CAGGGCGCGC GCGCGGGAGG GGGCAACACG GTCGCGAGT TCAGGGCCAG GCTGGAAGTG 780
 GTCGACCAGA AGGCGGTGTA TTTCTTCAAC CTGACTTCCA TGCAAGACTC GGAATGATC 840
 CTTACGSCCA CTTTCCACTT CTACTCAGAG CCGCCTCGGT GGCTCGAGC GCTCGAGGTG 900
 CTATGCAAGC CCGCGGCCAA GAAACGCTTCA GGCGCGCCGC TGCCCTCGGG CCGGCCCA 960
 GCGCAGCACC TGCTCTTCGG CAGCCTCTCG CAGAACACGG CCACACAGGG GCTACTCCGC 1020
 GGGGCCATGG CCTCGGCGCC CCCACCGCGC GGCTGTGGC AGGCCAAGGA CATCTCCCC 1080
 ATCGTCAAGG CCGCCCCCGG GGGATGGCGAG CTGCTCCTCT CCGCCGAGCT GGATTCTGAG 1140
 GAGAGGGACC CCGGGGTCGC CCGGCCAGC CCCTATGCGC CCTACATCCT AGTCTATGCC 1200
 AACGATCTGG CCATCTCGGA GCCCAACAGC GTGGCAGTGA CGTGCAGAG ATACGACCCC 1260
 TTCCCTGCCG GAGACCCCGA GCCCGCGCA GCCCCAACA ACTCAGCGGA CCGCGCGTG 1320
 CGCGAGCCG CGCAGGCCAC TGGGCCCTTC CAGGACAACG AGCTGCCGGG GCTGATGAG 1380
 AGGCGCGCCG GCGCCACGCG ACAGCACTTC CACAAGCACC AGCTGTGGCC CAGCCCCCTC 1440
 CGGCGCTGA AACCCCGGCC AGGCGCGAAA GACCGCAGGA AGAAGGGCCA GGAGGTGTT 1500
 ATGCGCGCCT CCGAGGTGCT GGAATTTGAC GAGAAGACGA TGCAGAAAGC CCGGAGGAAG 1560
 CAGTGGGATG AGCCGAGGCT GTGCTCCCGG AGGTACCTGA AGGTGGAATT CGCAGACATC 1620
 GGCTGGAATG AATGGATAAT CTCACGAAA TCTTTTGATG CCTACTACTG CGCGGGAGCA 1680
 TGTGAGTTCC CCATCGCTAA GATCGTTTCT CCATCCAAAC ATGCCACCAT CCAGAGCATT 1740
 GTCAGGGCTG TGGGCTCATC CCTGGCATC CCAGAGCCCT GCTGTGTTCC CGATAAGATG 1800
 AACTCCCTTG GGGTCTCTT CCTGGATGAG AATCGAATG TGGTCTGAA GGTGTACCC 1860
 AACATGTCCG TGGACACCTG TGCGTCCCGG TGAGACCACT CCAGGCTGGA AAGAAGCCAC 1920
 GCCCAGCAGA GCTGCTTCTC CGGAGCCTTC TGCAACACAG ACTGTGGTG CAGCTGCAGA 1980
 CACAGAGCAC AGCTCATGGG CAACATCACT GGGGCCCAA GAGAGCTGTC CGCCAGTGCA 2040
 TCATTAGGGG GTCTTTTCA TCTAGTACT AGCCCTTAA ATGCCAGCT GAGTACCTGA 2100
 AGGAATCTGG GAATTAGCCC TGGCCTGAAA GTGGCCATC ATTCTATACC ACTGTTCTGA 2160
 AGGCTTGAAA ACAAAACATA TCCACAACAT TGGCTTGATG TGATCATCAT CTCATACTG 2220
 AGCAAGAAGA CTATGCAAAAT CTTAGGGGCG TOGCTCCCTG CACACGGAAG GAACTCTGTT 2280
 TAAATGCTCA GTTCAGAAC CTTTGGGCCA CATAGTGATT TTGGAACAA GGATAATCGT 2340
 GGTGTAAATG AGTGTTCCT TCAAAAGTCC ACTGCAGAGC TTTTATCCAT ATGGTATGCA 2400
 CATGTAGCCA ATATTGGTTT CTTTTCTTA ATATATATAT TTTATTTTAA AACACAAAA 2460
 AGGAGGGGCG TTGACACCAT TCCCCACAGA GATAGTCACT CTGAGTGTGG GTTGTTTTAA 2520
 CATGCATATT GAAATACAC ATATAGTAAC GTGGGAATAC TAAAAAATA CCAAGATTTT 2580
 ATATTTTGT AAATTACTT TCTATACTG TAGATTGTG ATGTTATGAG TTTTATGGA 2640
 AAGCTAATA ATTAAGGTA CAGTGTATC TTGA

Seq ID NO: B22 Protein sequence
 Protein Accession #: NP_004953.1

50
55
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1 11 21 31 41 51
 MAHVPARTSP GFGPQLLLLL LPLFLLLLRD VAGSHRAPAW SALPAAADGL QGDRDLQRHP 60
 GDAATLGPS AQDMVAHVMH RLYEKYSRQG ARPGGGNTVR SFRARLEVVD QKAVYFFNLT 120
 SMQDSEMITL ATFHFYSEPP RWPRALEVLK KPRAKNASGR PLPLGPPTRO HLLFRSLSON 180
 TATQGLLRGA MALAPPPRGL WQAKDISPIV KAARRDGELL LSAQLDSBER DPGVPRPSPY 240
 APYILVYAND LAISEPNSVA VTLQRYDPPF AGDPEPRAAP NNSADPRVR AAQATGPLQD 300
 NELPLGDERP PRARAHQPHK HQLHPSPPFA LKPRPGRKDR RKGQGEVFMA ASQVLDPDEK 360
 TMQKARRKQW DEPRVCSRRY LKVPDFADIGW NEWIISPKSF DAYYCAGACE FPMPIKVRPS 420
 NHATIQSIVR AVGIIPGIPE PCCVPDRMNS LGVPLDENR NVVLKVPYPM SVDTACAR

Seq ID NO: B23 DNA sequence
 Nucleic Acid Accession #: AK026322.1

65
70
75
80

1 11 21 31 41 51
 ATTCTTTAAA TACTTAAACA TGGTTATAAC AGCTGTGTTT TAAGCTCCTT GTCTGTTAAT 60
 TCCATCATCT GTCATTTTGG CATCTGTTTT TATTGACTAA CTTTCTTCTT CATCATGGTC 120
 ACATATCCCTT GCTTCTTCCC ATATTAGTA AAGTTTAGTT GGATGCTGGA TTGTTTAAAT 180
 TTAGCATTTT GGAGTGACTG CTTTGGCACT TGCCCTTAAA AGTATTGGAC TTGTTTGA 240
 TAGTTGAAT ACTTGCAAAAT CAGCTTGATC ATCTGAGAC TTGTTTAA CTTTGTGCA 300
 AAAGGCTATG CTACTTCAAG TATAATAAAA OCTAGTTTGA GTTTTATCCT ATAACATAAG 360
 CATGTGTTC AATTGAATGT CTCCAACCTT GTGTGAACCT TGAATATTGT TCAGCTCCCA 420
 ATTTGCGAGT AATTTTTTTT GTTCAGCCTT GCACTCTCAT CTAATCAAG TGTGGCTCTG 480
 TATCCAACAA CAGTCTTGGG GATCTCATGA AGATTCTGA AACTTTTGTCT CTGCAGGATA 540
 CCTTCTTCTT TGGTTATGTT CCTGAAAC TCACGCTCC GTGTCTTCAA TTCAGTGA 600
 CTACTACTCT GCTTGGATTG CCTCTTATA CAATGGTCTA CCAAGTGA CTGCAACAGAA 660
 ATCTAAGGGA ATTTTCAGGAG TCACCTCATT TATTTTCTTT TTTTTCAGGG ATTATAGTAG 720
 TACTATACCA CCGTTCAGCC AATGTGTGAG AATGGTGGTT TCATACATTT TCTCCAATTC 780
 TTTCTTGTTA CAGGAGCCTC CATTACTTTT CAAACAGTAA TGCAGTTGCA GTTGCTCTCT 840
 CTTTCTTCTT TTAGTGTGTT ATCTCTGGCA GTTTGAGCCA AGAGAGGGCA CGGAGAAGTA 900
 CAATGACTAG AGAGCACTTC TGTGAGGCT CATTCAATGA CCCCTACCCC AGTCTTTTAT 960
 GAATGTGTGC TGCAGATGTC ATACAGCATC ACAGCTTCTT CTCTAATTTA TGAGCCATAA 1020
 TTTTCTTTT TGTATTTTGA TTGTATTACC TGCTTGGTTG CAAGAGGATG ATGAGGAGGA 1080
 CTACTATAGG ATAAATTTGT TTTTATAGAG CAATTCTCA TGGGTACAGA GGGATAGTAC 1140

TCCATTTTCC TCACGTATAT CGGCTTGATC ATCTGAGTCA GTGGGCTCAT TGTGGAACA 1200
 TATGGAATCC TTTATGCTTT TTCTCAGGCT GCTTCGTGA CATGAATAA AGCCAGAGTT 1260
 GATTGTGAAA AAAAAAAAAA AAAA

5

Seq ID NO: B24 DNA sequence
 Nucleic Acid Accession #: cat cluster

	1	11	21	31	41	51	
10	TGTATACATT	CCTTTCAAA	AAAGACCTTG	AGAAAAACAGC	AGAGCCCAAGT	GAAGATCACC	60
	TAAAGAACTT	TGTGGCTAAT	TTTACTTCA	TGTAGTAGCA	GTGGGTACTG	GGCAGGGTCT	120
	CTTTCCCACT	CTGATGATTT	GTGCTCTTAT	TTTTCTTAGA	TTTACCTCAT	CTAGGGCATA	180
	TTCTTTTCCC	TCTTCTCTTT	TACCTTTTCT	GGTCTGATC	CCTCTGTAAT	CAGTTCCCTT	240
	AAATTATTGG	ACTACAACT	AAATATACTAG	AAAAGCATAC	ACTTATTTTA	TTTGAATGCA	300
15	GAATGCTAT	CTATCAGTAT	ATATACATAA	GAATGTATAT	TACAGTATAT	CTATATATAC	360
	TTAACACTGT	AACTTTTCA	ATCCCCAGT	TAGCGTACCT	AACTCTCCTG	TGGGTATATG	420
	TAATTCCTAT	TAGACTACTA	GAGAAAAACC	AACTGGCAGT	TTGCTAAGCA	TATCTACTGG	480
	TGTTGTCTCT	GCGCCTCTT	TTGGCTAATT	GATGTAATTA	TACTGGCTCT	AAAGATTTAC	540
	TGCCCAATAA	GTAAATAGTA	TAGCCACATT	CTGAACATAT	CAAAAGTACA	AACTTAGGAG	600
20	GAGTGTATGT	ACAAAATGT	AAAATTTTAT	GAAAATGAAC	ATGTTTTTAT	GATGTTATTT	660
	CTAGTTCATA	AGAATGTGAT	GACTGCTTTG	CTTCATTAT	GTACGTTCCC	ATTATATTCT	720
	TGCTGTCAAT	CAATACACAA	TTTATATCAG	ATTAGGATAA	ACTAAGCCAT	TTTATGTATT	780
	TTATTTTAAA	CCTTATTTTG	GCAGAGTAAT	TCCTTAGAAT	TGGAAGAGCT	GTTACTTTGA	840
	AATTACCAAT	TTATTACAAA	ACATAGAAAT	GTATTGTAGC	TACAAAGACA	ACCAAGCATT	900
25	TTCTGTGTTT	TAATGAATAT	CTAAAAAAT	ACATTIAGTT	TATTTTACTC	AGTTTTGAAA	960
	TGATTTTTTT	ACTGGCTCTA	TTGCCTTAAA	ATAACTAAGA	GATTAAATGAT	TCITTTGTATA	1020
	ATTTTCTTTT	TCTTTGTCTT	TTTTTTTACA	TTTGCAGAG	TTATATCTAT	AGTTTTTAGTA	1080
	ACAAATTTCT	ATGTATTCTG	GATAACTGAA	AACAATAAAA	GGTGTGGGCG	ATTAGAAAAT	1140
	AATGTGAGC	AGTAAGATTA	CTGATGTAAT	ATGTATGTTG	GACTGAAGTA	TTTCTTTATA	1200
30	AACATTCTAT	TTGATTTTAA	GCAAAATGTA	TGTTAAAGCA	TGTTTTTACA	TCAGTAAAGT	1260
	CATTGTGCGA	CCTTCTGGAA	ATGAAAGGTT	TTTACCTAGA	TACTGTAAAT	TACACCTCCT	1320
	TAACAATCAT	ATTTGTCAAT	GTGTTTTTCT	GCAAAACAAA	ATGTTTATGG	GCTTCAATGA	1380
	GGCTTAAAGT	TGTAGGCAAA	AATGGACTGA	GTTTCAAGAC	CTTCAAGCAG	TAGGCATTCA	1440
	GTTACAGAGC	AGTTGGTACT	TTGTAAACCA	GACTTACAGT	TTAAAAATAT	CAAGTTAGCT	1500
35	GATGTTTCTA	TATATAAATA	ATACTATTTT	GCTTAAGAGT	TGTATTACAA	ATATTGTGTC	1560
	TTAACATTAG	AAATAGCTGT	TTTAAATTGT	AGTTAACATA	TTAACTTTTT	CAGAAAAAAA	1620
	GCATGGTTTA	TTTTTAATAA	TGAAATAGAG	AACATAATAC	GTAATGTTCA	GTATAACAGC	1680
	TGAGTTAAAA	CATCTGCCAG	GATTAACATC	AGTGGTTTTT	TGCCAATGCA	TAGAGGCATT	1740
	TTTCTCTAAG	TATGATGGCT	AATGATAACT	ATTCTTTGTT	ACACATTCAA	GTCACCTCCA	1800
40	TCAAGTAAC	TATGGGGTGA	TATGTTTCAC	TCCAAGGGT	GTATTAATTC	TGAATGCTAA	1860
	TCATGAAGAC	TTAAGTTAGG	ACRACACTTC	AAACCAGGAA	GTGTGAACGT	ATTTA	

Seq ID NO: B25 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1144

45

	1	11	21	31	41	51	
50	ATGGAGCGCG	GGATGCACTT	CGGTGCAGCG	GCGGCGGGCG	AGGACGACCT	CTTCTCTCAC	60
	AAGAGCTCTA	GCGCTCCAC	CTCCAAGCGC	TTGGAAGCGG	CTTTCCGCTC	CACGCCCCCG	120
	GGCATGGACC	TGTCTCTGGC	GCGGCGGCGC	CGGGAAGCGC	CGGGCTCTCT	CTCTCTGTCT	180
	CCCTGGGCTG	GCTTGGAGCC	GGCTGACCCC	GAGGGGGCAG	GGCTGCTGTT	GCGGCGGCGT	240
	GGAGGAGGGG	GCGGCGGCGC	GCGGCGGAGT	GCGGCGGCGG	GCGGCGGCGG	GGTGGGTGTC	300
55	CCCGGGCTGC	TAGTAGGTTT	AGCCGCGGTT	GGGGGCGACC	CTAGCCTAAG	CAGCCTCGCG	360
	GCGGGGGCGG	CCCTTTGGCT	CAAGTAGCGC	GAAAGCGCGA	GCCGGGGCTC	GGTGGGCGAG	420
	AGCAGCGCGG	GCGAGCAGAG	CCCGGCGGAC	GACAGCGAGG	GTGCTGCGA	GCTGCTGCTG	480
	GCGGCGGCGG	TAGCGGACCC	GCGGGGCTCC	CCGGGAGCGG	GAGGTGTTGG	CGCGAAGGCA	540
	GCGAGGGGCT	GCTTCAATGC	CCACCTCCAC	GGGCGGCGCA	GCGTCCCGCC	GGGGGGGCTG	600
	GGGCGGCGGG	GCGGCGGGGG	TAGCAGCAGC	GGTAGCAGTG	GCGGCGGTTG	CGGTAGCGGT	660
60	AGCGGCGAGG	GCGGCGGCGG	CAGCAGCAGC	AGCAGCAGCA	GCAAGAAATC	CAGAGAGCAA	720
	AAGGCGCTGC	GGCTTAACAT	CAATGCCCGA	GAGGCGCGGC	GGATGCAAGA	CCTGAACGAC	780
	GCGCTGGAAG	AGCTGCGGCG	GGTGATCCCC	TACGCGCACA	GCCCTCTGGT	GCGAAAGCTC	840
	TCCAAGATGC	CCACGCTGCT	GCTGCGCAAG	AACTACATCC	TCATGCAGGC	GCAGGCGCTG	900
	GAGGAGATGC	GCGGCTAGT	CGCCTACCTC	AAACAGGGCC	AGGCCATCTC	GGCTGCTCTC	960
65	CTGCCAGCT	GCGGCGTGC	AGCGGCGAGC	GCTGCTGCCC	TGCACCGGCG	GCTCGGGGCG	1020
	TACGAGCAGG	CAGCGGCTA	CCCGTTTACG	GCGGCGGCTC	CCCGGCGCTC	CTCTGCGCGG	1080
	GAGAGTGGG	CCCTGTTTAA	CAGGCTCTCC	TCCAGGCTCT	GCAACAGTGT	CACGGAGAAG	1140
	CCTT						

70

Seq ID NO: B26 Protein sequence
 Protein Accession #: FGENESH predicted

75

	1	11	21	31	41	51	
75	MERGMHLGAA	AAGEDDLFLH	KSLASASTSKR	LEAPRSTPP	GMDLSLAPPP	RERPASSSSS	60
	PLGCFEPADP	EGAGLLLP	GGGGGGSAGS	GGGGGGGVGV	PGLLVGSAGV	GGDPSLSLPP	120
	AGAALCLIKY	ESASRGVVAE	SSGGEQSPDD	DSGRCLELVL	RAGVADPRAS	PGAGGGGAKA	180
	AEGCSNAHLH	GGASVPPGGL	GGGGGGGSSS	SSSGGGGGSG	SGSGGSSSSS	SSSSSKSKEQ	240
	KALRLININAR	ERRRRHDLND	ALDELRAVIP	YAHSPSVRKL	SKIATLLAK	NYILMQAQL	300
80	EBMRRLVAVL	NQGQIAAAS	LPSSAAAAAA	AAALHPALGA	YEQAAGYFFS	AGLPPAAACP	360
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Seq ID NO: B27 DNA sequence
 Nucleic Acid Accession #: cat cluster

	1	11	21	31	41	51	
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	TAGATACACA	TACAAATGGT	CGTACATAGC	TGTCATAGTC	TGATTGACCT	ATTTAATATA	120
	TATATCATTC	TTTACACATC	CAAAACCCGC	CAACAGATCC	ATCAGAGCTC	CCAACCTCAC	180
	ATCCAACCTG	ACAAACTGAA	TTTGTATTAT	CTGCAAGGAG	TGGAAAATAG	CAGGACTCCA	240
	TTTTTAAAAA	AGATTTTCTT	GATTTTCATA	GGGCGGAAAG	GCAGTCAAAAC	AGCCATGCAA	300
10	AACATAAACT	GAAAGCTCAC	TTTGGGTAAA	TAGCTTCTTG	TTCTTCCTTA	GTTTTCTTTC	360
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15	AGTCCCTTTT	CAAAAAAGAG	ATCAATTTCAT	TCATCAATTA	AGAATACACC	TTTCTGTAA	660
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	CTTGTTGGCA	AATAAACCTT	TAAACACTTG	GCACACAGCA	TAAGTAATCT	ATAAAACAAT	840
	TTTAGAGGCA	TTAAAAAAT	CTGCACATAA	GACCCATGAC	TTTAACACAT	GATAAATACT	900
20	GTGTAGTGG	AAGGTCATT	GAAGAATAAC	AAATAAATAC	CATGAATTGT	TAATACATCA	960
	TTGCAGAGTA	GAAAGTAACA	AGGTGCACAT	AAATATTTTT	AAATGCAATT	TTTCAGCCA	1020
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	CAGAGCAAT	AAAAAATACA	AGTCTTTCAT	AGTAACATGT	TCTCTCTCTC	TCGCTCTGGG	1140
	TTTTATTTCC	CCCTCACTTA	AGTCAACATT	TCAAGTTTTT	CTCTGGCTC	AGAATCAAAA	1200
25	TTTATTTTCA	AGTGCCCTTT	CTGATTTGTC	TGAATGAATA	TTCCATCTCT	CATGTACCCG	1260
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Seq ID NO: B28 DNA sequence
Nucleic Acid Accession #: NM_002581.2
Coding sequence: 368..5251

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	CAAAGGTGGG	GAGAGTGGAG	CACACACCTT	GAGGAGGAAA	GOGAGAAAGA	AAAGAAAAAA	240
	GCAAGTGAAG	GGGGGCTCGC	CCAAGAAGGG	TGAAGAAGCG	AAGAAAGTCG	AGGCGCCGAG	300
	GCTCCCAAAG	TGCGCAGCTC	CGGGTGGCGG	TGCAGGGGCG	AAGGGGGGGG	CGGGGGGAAC	360
40	GTCCGACATG	CGGCTCTGGA	GTGCGGTGCT	GCACCTGGGG	CTGCTGAGCG	CCGCGCTGGG	420
	CTGCGGGCTG	CGCGAGCGTC	CCCGCCGGGC	CCGAGAGAGC	CCGCGGGCCG	GCGAGCCGCC	480
	GCGCCCGGCC	GCGCGCCCGG	CCAAGTGGCG	CACCGCGCGC	CCGCGGGCCG	CGCGCTCGCG	540
	CGCGCGCGCC	GCGCGCGCGG	GGCGTGCCTG	GGAAGCGGTG	CGCGTCCCGC	GGCGCGCGCA	600
	GCGCGCGGAG	GCGAGGGGCG	CCACCGAGGA	GCGAGCGCCG	CCGAGCCGGG	CGCTCTATTT	660
45	CAGCGGGCGA	GCGAGCAGCG	TGCGAGTCTC	CCGGGCGGAC	CTCGAGCTGC	CCCGGGAAGC	720
	GTTCACGCTG	CAAGTGTGGC	TGCGAGCGGA	GGGGGGCCAG	AGGTCCTCCG	CAGTGATCAC	780
	AGGGCTGTAT	GACAAATGTT	CTTATATCTC	ACGTGACCGA	GGATGGGTGG	TGGGCATTCA	840
	CACCATCAGT	GACCAAGACA	ACAAAGACCC	ACGCTACTTT	TTCTCCTTGA	AGACAGACCG	900
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	CACCAATGTC	ACTCAGACTT	GCTTTGACCC	CGACTCTCCA	CACAGAGCCT	ACTTGGATGT	1860
65	TAATGAGCTG	AAGAACAATC	TTAAATTGGA	TGGATCAACA	CATCTCAATA	TTTTCTTTGC	1920
	AAAATCCTCA	GAGGAGGAGT	TGGCAGGAGT	AGCAACTTGG	CCATGGGACA	AGGAGGCCCT	1980
	GATGCACTTA	GGTGGCATTG	TCTTGAACCC	ATCTTCTCTA	GGCATGGCTG	GGCACACCCA	2040
	CACCATGATC	CATGAGATTG	GTCAACAGCT	GGGCTCTCTA	CACGTCTTCC	GAGGCATCTC	2100
	AGAAATCCAG	TCTCTGAGTG	ACCCCTGCAT	GGAGACAGAG	CCCTCCTTGG	AGACTGGAGA	2160
70	CCTCTGCAAT	GATACCAACC	CAGCCCTTAA	ACACAGTCC	TGTGGTGACC	CAGGGCCAGG	2220
	AAATGACACC	TGTGGCTTTC	ATAGCTTCTT	CAACACTCCT	TACAACAACT	TCATGAGCTA	2280
	TGCAGATGAC	GACTGTACGG	ACTCCTTCAC	GCCCAATCAA	GTGCGCAGAA	TGCATGTGTA	2340
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	CCCCCAAGTT	CTGGGCCACA	CAACGGACTC	TGTGACACTG	GAGTGGTTCC	CACCTATAGA	2460
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	CCTGGTGCAG	TATGCTTCCA	ACGCTTCCCT	CCCAATGCCG	TGCAGCCCAT	CAGGACACTG	2580
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	CACCTGGAGC	CCAAATPTCAG	CTGTCAACCC	ACACAAGGTT	CCTCCAGCCT	GCCCTGAGCC	2700
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	GGATGAGCAC	CTGAGATGCG	ATGCTGCCAT	GTGACCTCC	ACTGCAGACA	CCCCACTCTG	3000
	TCTACAGTGT	AAGCCCTCTG	AGTATAAGGT	GGTCCGGGAC	CCTCTCTCTC	AGATGGATGT	3060
	GGCTCTCATC	CTACATCTCA	ATAGGAAATT	CGTAGACATG	GATCTAAATC	TTGGCAGTGT	3120

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Seq ID NO: B29 Protein sequence
Protein Accession #: NP_002572.1

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LQVWLRABEG QRSFAVITGL YDKCSYISRD RGVVVGHTI SDQDNKDPFY PPSLKTDRAR 180
QVTTINAHRS YLPGQWVYLA ATYDQFMKL YVNGAQVATS GEQVGGIFSP LTQKCKVLM 240
GGGALNNHYR GYIEHFSLWK VARTQREILS DMETHGAHTA LPQLLLQENW DNVKHAWSPM 300
KDGSSPKYEF SNAHGFLDIT SLEPPLCGQT LCDNTEVIAS YNQLSSFRQP KVVRYRVVNL 360
YEDDHKNPTV TREQVDFQHR QLAEAFKQYN ISWELDVLEV SNSSLRRLRI LANCDISKIG 420
DENCDPECNH TLTHGHDGDC RHLRHPAFVK KQHNGVCOMD CNYERFNPFG GECCDPEITN 480
VTQTCFDPDS PHRAYLDVNE LKNILKLDGS THLNIFFAKS SEELAGVAT WPDWKEALME 540
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Nucleic Acid Accession #: NM_032808.1
Coding sequence: 61..1008

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35 Seq ID NO: B31 Protein sequence
 Protein Accession #: NP_116197.1

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 55 AACCAGGACC CTGCTCCCA GCCCAGAGGT GGAGGAGGAC GGTACAGGTTG GGGTCTACAG 240
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 GAAAGTGGCC GGGGTGCTCC TTGGAAACA GTTGGGCTGT TCTTGGCAGG AATTAGTGAC 360
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Seq ID NO: B34 Protein sequence
 Protein Accession #: NP_006165.1

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 MDLELDEYNN KTLATENNTA ATRNSDFPVN DDYKSSVDDL QYFLIGLYTF VSLLGFMGNL 60
 LILMALMKKR NQKTTVNPLI GNLAFSDLV VLFCSPTTLT SVLLDQWMPG KVMCHIMEPL 120
 QCVSVLVSTL ILISIAIVRY HMIKHPISNN LTANHGYFLI ATVWTLGFAI CSPLPVFHSN 180
 VELQETFGSA LLSSRYLCVE SWPSDSYRIA FTISLLLVQY ILPLVCLTVS HTSVCRSISC 240
 GLSNKENRLE ENEMINLTLH PSKSGSPQVK LSGSHKWSYS FIKKHRRYS KKTACVLPAP 300
 ERPSQENHSR ILPENFGSVR SQLSSSKFKI PGVPTCFEIK PEENSVDVHEL RVKRSVTRIK 360
 KRRSRVFYRL TILILVFAVS WMLHLFHVV TDFNDNLISN RHPKLIVYIC HLLGMMSCCL 420
 NPILYGLNN GIKADLVSLI HCLHM

Seq ID NO: B35 DNA sequence
 Nucleic Acid Accession #: NM_014279.1
 Coding sequence: 286..1689

1 11 21 31 41 51
 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCGCG CCAGCCCAGC 60
 CCTGCCCCAGC CCTGCCCGGA GGCAGACGCG CGGGAACCGG GACGCGATAA ATATGCAGAG 120
 CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGTGTCTGAA TCAGGCGGTG 180
 GGGACACGAG CCGGGCGCGG CCGCGGAGGC CAGCGGAGCC GGGGCCAGAG CGGAGCGCGG 240
 TCCGCGTCCA CGCAGCCGCC GGC CGGCCAG CACCCAGGGC CTGCGATGCC AGGTGCTGG 300
 AGGTGGCAGC GAGACATGCA CCCGCCCCGG AAGCTCTCTCA GCCTCCTCTT CCTCATCTG 360
 ATGGGCACTG AACTCACTCA AGTGTCTGCC ACCAACCCCTG AGGAGAGCTG GCAGGTGTAC 420
 AGCTCTGCCC AGGACAGCGA GGGCAGGTGT ATCTGCACAG TGTGCGCCCC ACAGCAGACC 480
 ATGTGTTCAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540
 ATGTCTCAAT CCATAGAGGT CTGTGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600
 AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCA 660
 AAGCAACACC TGGCCAGGCA GTTTAAGGCG ATAAAGCGA AAATGGATGA ACTTAGGCCT 720
 TTGATACCTG TGTGGGAAGA GTACAAGGCC GATGCCAAAT TGTGATTGCA GTTTAAAGAG 780
 GAGGTCCAGA ATCTGACGTC AGTGCTTAAC GAGCTGCAAG AGGAAATTGG CGCCTATGAC 840
 TACGATGAAC TTCAGAGCAG AGTGTCCAAT CTGGAAGAAA GGCTCCGTGC ATGCATGCAA 900
 AAATAGCTT GCGGGAAGTT GACGGGCATC AGTGACCCCG TGACTGTCAA GACCTCCGGC 960
 TCGAGGTTCG AATCCTGGAT GACAGACCCCT CTGCGCCCTG AAGGCGATAA CCGGTGTGG 1020
 TACATGGAGC GCTATCACAA CAACCGCTTC GTACGTGAGT ACAAGTCCAT GGTGTGACTC 1080
 ATGAACACCG ACAATTTTAC CTCCCACCGT CTCCCCCACC CCGTGTGGG CACGGGCGAG 1140
 GTGGTCTACA ACGGTCTTAT CTACTTCAAC AAGTTCAGG GCCACATCAT CATCAGGTTT 1200
 GACCTGAAGA CAGAGACCAT CCTCAAGACC CGCAGCCTGG ACTATGCCGG TTACAACAAC 1260
 ATGTACCACT ACGCCTGGGG TGGCCAATCG GACATCGACC TCATGGTGA CGAGAGCGGG 1320
 CTGTGGGCGG TGTAGCCAC CAACCAAGAC GCTGGCAACA TCGTGTTCAG TAGGCTGGAC 1380
 CCGGTGTCCC TGCAGACCTG GCAGACCTGG AACACGAGCT ACCCCAAGCG CAGCGCGGG 1440
 GAGGCTTCA TCATCTGCGG CAOGCTGTAC GTCAACCAAG GCTACTCAGG GGGTACCAAG 1500
 GTCCACTATG CATACAGAC CAATGCTCTC ACCTATGAAT ACATGACAT CCCATTCCAG 1560
 AACAAATACT CCGCATCTC CATGCTGGAC TACAACCCCA AGGACCGGGC CCGTATGACC 1620
 TGAACAACG GCCACCATG CCTCTACAAC GTGACCTCT TCCAAGTCAT CCGCTCCGAC 1680
 GAGTTGTAGC TCCTCTCTCC TGAAGGCCAA GGGGCCAAGT CCTCACCACA AAGGGACTCC 1740
 TGTGAATCG CTGCCAATAA GATACCAATA ACCTAACCA TACGATCTT GAAAAATCAT 1800
 CAGCAGTGGC GATTCTGAGA TCGAGGGATG GCATTACCTC CGTGTCTTC CTTTCCGAGC 1860
 CCGCGGGCCA CAGGCTGGG AAGAAATCC CGTATTGCA GCTGGAAGT CAGCCCAAG 1920
 CGCCCCGGTT TTCTCCCGG CCCTGTCCCT CTCTGGTCAA ACAACATACT AAAGAGGCGA 1980
 GGCAATGACT GTTGGCCAGT TCTCACCGGG GAAAAACCA CTGTTAGGAT GGCATGAACA 2040
 TTCTCTTAGA TCGTGGTCAG CTCGAGGAA TGTGGCGTCC AGGCTCTTTG AGAGCCATGG 2100
 GCTGCACCGG GCGTAGGCT AGTGAATC GCATCCCAT GCAGTGGCGT TCTTGTACTG 2160
 TGTGTCTGTC TCTTAGATTA ACGTGTCTGA GGCTCCCAT AGCTCTTGA CCTGTGTCTA 2220
 GTACATACCTG AAGCGATGGT CAGAGTGTGT AGAGTGAAGT TGCTGTGCCC ACAATGTTG 2280
 AACTCGCGTA CCGGTAGAT ACATTGTGCA ACGTCTCTCT GTTATTCCCT TGAGGTGGTA 2340
 ACTTGTATG TTCAGTTTAT GCGATGATTG TTGTAAATGC AATGCCGTAG TTTGGATTAA 2400
 TAAGTGGATG GTTTTGTGTT CTAATAAGAA AAAAAAATC AGTGTTCACC CTTATAGAGA 2460
 CATAGTCAAG TTCATGTTGA TAATAATCAA AGGAATTACT CTCTCTTGT TAAATTAGCT 2520
 AAATCATGTA ACGGCAGATA GGAAGGGCTC ACCTGGGGAA ACTCTGGTTT COGATGGGAC 2580
 AGGAAAGTCA TACGGGCAAC AGTATGCGGA AAGTACGTTT TTTTAAGTAA AAAACAAAGG 2640
 CAACTTTGT ACTATCCAGT TATCTAAGGA ACAATAAAAA CATTAGGAGA AAAAAAAGG 2700
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A

Seq ID NO: B36 Protein sequence
 Protein Accession #: NP_055094.1

1 11 21 31 41 51
 MPGRWRWRQD MHPARKLLSL LFLILMGTEL TQVLPTNPKE SQVYSSAQD SEGRICITVV 60
 APQQTMCSDR RQTKQLRQLL EKVQNMSSQI EVLDRRTQRD LQYVEKMNQ MKGLESKFKQ 120
 VEESHKQHLA RQPKAKAKM DELRLPLV LQYKADAKLV LQPKVEQNL TSVLNELOEE 180
 IGAYDYDELQ SRVSNLEERL RACMQKLACC KLTGISDPVT VKTSGSRFGS WMTDPLAPEG 240
 DNRVWYNDGY HNNRFVREYK SMVDFMNTDN FTSRLPHPW SGTGQVYVNG SIYFNKQFSH 300
 IIRFDLKTE TILKTRSLDY AGYNNMYHYA WGGHSDIDL M VDESLWAVY ATNQNAAGNIV 360

VSRLDPVSLQ TLQWNTSYP KRSAGEAFII CGTLYVTNGY SGGTKVHYAY QTNASTYEYI 420
DIPFPQNKYSH ISMLDYNPKD RALYAWNNGH QILYNVTLPH VIRSEDEL

Seq ID NO: B37 DNA sequence
Nucleic Acid Accession #: NM_006334.1
Coding sequence: 286..693

1 11 21 31 41 51
| | | | | |
10 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
CCTGCCCCAGC CCTGCCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG 180
GGGACACGAG CCAGGCGCGC CGCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
TCCGCGTCCA CGCAGCGCCG GCGCGGCCAG CACCCAGGGC CCTGCATGCC AGGTCGTTGG 300
15 AGGTGGCAGC GAGACATGCA CCGGGCCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCTTG 360
ATGGGCACTG AACTCACTCA AGTGTCTGCC ACCAACCCCTG AGGAGAGCTG GCAGGTGTAC 420
AGCTCTGCCC AGGACAGCGA GGGCAGGTGT ATCTGCACAG TGGTCGCCCC ACAGCAGACC 480
ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540
ATGTCTCAAT CCATAGAGGT CTGAGCAGG CCGACCCAGA GAGACTTGCA GTACGTGGAG 600
20 AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT 660
AAGCAACACC TGGCCAGGCA GTTTAAGGGC TAACTTAAAA GAGTTTTTTC AATGCTGCAG 720
TGACTGAAGA AGCAGTCCAC TCCCATGTAA CCATGAAAGA GAGCCAGAGA GCTTTTGTGA 780
CCATGCATT TTAATATTAT TTTCCAATAC TTAGCACCAT TTCCTAAGG AACCTTGAAT 840
ACAACACAGA TCCTCCTTTG CATGCGACTG TAGCTGCATT TCATGAATAG TTTGAACCCCT 900
25 TGTCAATGCA TTTTGTGAAA AAGAAAGAAA AAAAAAAGCTT CGTGTATGTG ACTCAAGACA 960
TGTAACCTTA AGATGTGCA TTCTAAACTG ACAATAAGA CCTTTCCTCC

Seq ID NO: B38 Protein sequence
Protein Accession #: NP_006325.1

1 11 21 31 41 51
| | | | | |
30 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQVLPTNPPE SWQVYSSAQD SEGRCTCTVV 60
APQQTMCPSD ARTQQLRQLL EKVNQMSQSI EVLDRRTQRD LQYVEKMEHQ MKGLESKFKQ 120
35 VEESHKQHLA RQPKG

Seq ID NO: B39 DNA sequence
Nucleic Acid Accession #: NM_058199.1
Coding sequence: 286..795

1 11 21 31 41 51
| | | | | |
40 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
CCTGCCCCAGC CCTGCCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
45 CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG 180
GGGACACGAG CCAGGCGCGC CGCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
TCCGCGTCCA CGCAGCGCCG GCGCGGCCAG CACCCAGGGC CCTGCATGCC AGGTCGTTGG 300
AGGTGGCAGC GAGACATGCA CCGGGCCCGG AAGCTCCTCA GCCTCCTCTT CCTCATCTTG 360
50 ATGGGCACTG AACTCACTCA AAATAAAGA GAAACAAAG CAGAGAAGAT GGGAGGGCCA 420
GAGAGCGAGA GGAAGACCAC AGGAGAGAAG AACTGAACG AGCTTCCCTT GTTTTGCCTG 480
GAAAGCCACG CTGGCTCCCT GGCTCTGCC AGGATGTGCA GTCCAAATCC CAATCCAGCA 540
GTGGGGTTAT GTGGTCCCGC TTACCTCAG AGCCCTCTCT CTGGTCTGTC CCAGACGATC 600
AGCCAGTCCC TCCAGGAGAG GTTCTGCATG GCCTCTAGGA GAGAAGTTT CTGGCCCCA 660
55 GGAAGGCGCT GTGGAGGGTG GTGGTTGTGC ACTGTGTCTG GACAGATGCA TTCATTCTAT 720
TGACACACAC CACACACACA TGACACACA GGGGAGCAGA TACCTGCAGA GAAGAGCCAA 780
CCAGTCTCTG ATTAGTGGCA AGCTGCCCA CAAAGGGCTA TGCTGTGTG TTTATTGAGAC 840
ACCTTGGCAA AGAGATGGCT GATTCTGGGT GGTCTCTGAC ATGGCCGCAC CCAAGGGCCC 900
60 TCAAAGCCTT AATGGCACC TGAAGCCTCC ATGCCAGGC CAAAGATGC TTTCTCTCCC 960
TAAAAA AAAAAA

Seq ID NO: B40 Protein sequence
Protein Accession #: NP_478106.1

1 11 21 31 41 51
| | | | | |
65 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TONKRENKAE KMGFPESERK TTGEKTLNEL 60
PLFCLEAHAG SLALPRMCSF NPNPAVGLCR PAYPQSPSPG AAQTISQSL ERFCMASRRE 120
VFLAPGRPG GWLCTVAGQ MHSFMCETH THARTGBQIP AEKSQPGPD

Seq ID NO: B41 DNA sequence
Nucleic Acid Accession #: AY038071.1
Coding sequence: 1..1686

1 11 21 31 41 51
| | | | | |
75 ATGAGCAATC AGTACCAGGA GGAGGGCTGC TCCGAGAGGC COGAGTGCAA AAGTAAATCT 60
CCAACCTTTC TCTCCTCCTA CTGCATCGAC AGCATCTCGG GCGGAGGAG CCGTGCATAA 120
ATGCGTTTGC TGGGAGCGCG GCAGAGCTTG CCTGCTCCCG TGACCAGCCG CGCCGACCCG 180
80 GAAAAGGCCG TGCAAGGCTC CCCTAAGAGC AGCAGCGCCC CGTTGAGGCG CGAGCTGCAC 240
CTGCGGCCCA AGCTGCGCGC CCTGTACGGC CCGGCGGGGG GCGGCTCCTT TCAGGTTGG 300
GCAGCGCGCG CGGCGCGCGC GCGGCGGGCG GCGGAGCGCG CGGCAAGGCG CACGGCGGGT 360
CCACGCGGGG AGGCCCTTCC GCCGCCACCG CCAACCGCGC GCGCGGGGGA ACGGCGGGAC 420
GGCGCAGGGG CGGCGCGCGC AGCGCGGGCC GCGGCGGGCG CGGCTGGGGA CAGGCTCAAG 480
ATCAGCCAGG CGCGCGAGGT GAGCATCAGC CGCAGCAAGT CGTACCGCGA GAAAGGGGCG 540

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CCCTTGTC  CGCGCCGCC  CGCGCTGGAC  GAGCTGGGCG  GCCCGGGGG  CGTCACGAC  600
CCGGAGGAGC  GCCTCGCGGT  GGCGGCGGCC  CGGGGAGCG  CCGCGGCTGC  GGTGTTGGC  660
ACCGGCACCG  AGGACGACGA  GGAGGAGCTG  CTGGAGGACG  AAGAAGATGA  GGACGAGGAA  720
GAGGAAGTGC  TGGAGGACGA  CGAGGAGGAG  CTGCTGGAGG  ACGACGCGCG  CGCGCTGCTC  780
AAGGAGCCCC  GGCGCTGTCC  TGTGGCCGCC  ACTGGCGCGC  TGGCGCGCAG  AGCTGCGGCT  840
GCAGTGGCCA  CAGAGGGCGG  GGAGCTGTCA  CCAAGGAGG  AGCTGCTGCT  GCACCGGAA  900
GACGCTGAGG  GCAAGGACGG  CGAGGACAGC  GTGTGCTCT  CTGCGGGCAG  CGACTCGGAG  960
GAGGGGCTCG  TGAACGCAA  ACAGAGGCGC  TACCGCACA  CGTTCACCAG  CTACGAGCTG  1020
GAGGAAGTGG  AGCGGGCCTT  CCAGAAGACG  CACTACCGG  ACGTCTTAC  CAGGGAGGAA  1080
CTGGCGATGA  GGCTGGACTT  GACCGAGGCG  CGAGTCCAGG  TCTGTTTCCA  GAACCGTCGG  1140
GCCAAGTGGC  GCAAGCGGGA  GAAGGACAGC  GCGCAGACCC  ACCCCCTGG  GCTGCCCTTC  1200
CGGGGGCGCG  TCTCGGCCAC  CACCGCGCTC  AGCCCTACC  TGAAGCCAG  CCGCTTCCT  1260
CGCACCACC  CGCGCTCGA  CTCCGCTTGG  ACTGCGCTG  CCGCGCGCG  CGCGCGCGC  1320
TTCCCGAGCC  TACCTCGGCC  TCCGGGCTCG  GCCAGCTGCG  CGCCAGCGG  GGCGCGCTG  1380
GGCTGAGCA  CTTCCTCGG  AGCGGCACTG  TTCGACACC  CAGCTTTCAT  CAGCCGCGCA  1440
TTGGGAGCG  TCTTTTCCAC  AATGGCCCCC  CTGACCAAGC  CGTGCAGCG  GGCGCGCTC  1500
CTGAGACAG  CCAACCGCG  CGTGGAGGCG  GCAGTGGCAT  CGGGCGCCT  GGCGAGCCG  1560
GCCACGCGG  CGCAGACAG  ACGCGCTCT  AGCATAGCG  CGCTGAGGCT  CAAGGCCAAG  1620
GAGCACGCG  CGCAGCTCAC  GCAGCTCAAC  ATCTGCGCG  GCACGAGCAC  GGGCAAGGAG  1680
GTGTGC
  
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Seq ID NO: B42 Protein sequence
 Protein Accession #: AAK93901.1

25
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 35

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1 11 21 31 41 51
MSNQYQEGEC SERPECKSKS PTLSSYCID SILRRSPCK MRLGAAQSL PAPTSTRADP 60
EKAVQGGSPKS SSAPPEABSLH LPPKLRLRYG PGGRLLQGA AAAAAAATAA AAAAAATATAG 120
PRGEAPPFPF PTARPGERPD GAGAAAAAAA AAAAAMDTLK ISQAPQVIS RSKSYRENGA 180
PFVPPFPALD ELGGPGGVTH PEERLGVAGG PGSAPAAAGG TGTEDEEEL LEDEDEDEE 240
EBLLEDEDEE LLEDDARALL KEPRRCFVAA TGAVAAAAAA AVATEGGEELS PKEELLHPE 300
DAEGKDGEDS VCLSAAGDSE EGLLKRKQRR YRTTFTSYQL EELERAFQKT HYPDVFTREE 360
LAMRLDLTEA RVQVWFQNRK AKWRKREKAG AQTHPPGLPF PGPLSATHPL SPYLDASFPF 420
PHPALDSAW TAAAAAATAA FPLPFPFPGS ASLPPSGAPL GLSTFLGAAV FRHPAFISPA 480
FGRLESTMAP LTSASTAAL LRQPTAVEG AVASGALADP ATAAADRRAS SIAALRLKAK 540
EHAALQLQLN ILPGTSTGKE VC
  
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Seq ID NO: B43 DNA sequence
 Nucleic Acid Accession #: CAT cluster

40
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1 11 21 31 41 51
CGCGTCCCCC CCGCTTGCTT CTCTCTCTTC CTTCTGCTCT GCGTGTCTCG CGTCTTTGG 60
TTCCCGCGGT TCCGTGCGCC CTCTCTGCGC TTCGCGCTCA CCTCCGCTCT GGCTGTGCTC 120
CTGCTCTCCT CCGCTCTCAT GCCCCTTTCA GCTCCTACTC TGGTGTGCTC CCGCTCCCTC 180
GCTCGTTTCT CTGTTCTCTC TCCTTCGCGG TCGTGTCTCT GCTTCTCTGT GTTCCCTCTC 240
GTCTGTGTTT GTGGGTGCTC CTCTGCGTCC TGCCCTCTTC TCTTGCCTTT CGCGCGGCTT 300
CCTGTTTGGG TCCCCCTGGT TCTCGCGCGG TCTGTGTGTC GCGGGCGCGC CGGTCTCTTC 360
TTGGTGTCTT GCTCTGCTC TCTGTCTGGT GTTCTCCGCC GTCTGTGTCT TTCTCTTTT 420
ATCTCTCTGT TTCTCTTTT CTGTTTCTTT CTGTTTCTT TTGTCTTTG TTTTCTCTTA 480
GCTGAGGTTG GGGAGAGATA ACGCTGTAAA CTTTATTTT TCAGGAATC TGGAAACCTA 540
CAGTCTCCAT GCTCTCTCAG CCAAGAAAGG GCTCACTGTG GGCACAGAG ACAGGGAACC 600
AATGTGGAGA CTTGTGAGCC TGTGTCCGCG CCGTGAATCT CAAGCACAGG CGAGGCTTCC 660
TGAGCATTTG AGAGAAATAT TGGGAGAAC AACAAGAAAC TGAAGAATA TGCAAGGTGT 720
CTTCTCTTGA TGTATTTCCT TAGATAGTAG TAGGGGCGAG AGTGAGAGAG GCTGACTAGG 780
TCTGGACATG GAGCTAGGAA GAGTCAGGCT GTGATTCGGA GAGGCGCATG AGAAGGAAGG 840
TGGATTTTAA GGCTGGAAT CTGAGGGTCA GTGTCCAAAG TCACTCAGAG ACAGATCAC 900
AGCATAGCCC TTGCTGATGG CAA
  
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Seq ID NO: B44 DNA sequence
 Nucleic Acid Accession #: NM_014421.1
 Coding sequence: 718..1497

65
 70
 75
 80

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1 11 21 31 41 51
CCACGCGTCC GCGGGGAGCC CGCGGCGAGC GTAGCGCAAG TCGCTCCCT AGGCATGCT 60
GCGCTGGCAG CGATTGCTG TCTCTTGTGA GTCAGGGGAC AAGCTCTCGG GGCACATGTG 120
AGTGCGCGTG TGGGGGACCT CGATTCTCTT CAGATCTCGA GGATTGCTG CCGGGACGTC 180
TCCTGATCCC CTAATAAGC GCCTGCTAAC TTTGAAAAGG AGCACTGTGT CCTGCAAGT 240
TTGACACATA AAGGATAGGA AAAGAGAGGA GAGAAAAGCA ACTGAGTTGA AGGAGAGGAA 300
GCTGATCGCG GCTCTCTGAT CAATTAAGAG GAGAGTTAAA CGCCGAGAT CCGCGCGGGA 360
CCAAGGAGGT GCGGGGCAAG AAGGAACGGA AGCGGTGCGA TCCACAGGGC TGGGTTTCT 420
TGCACCTTGG GTACGCGCTC CTGCGCGAGA AAGCGCTCG CATTTGATTG CTTCCAGTTA 480
TTGCAGAACT TCCTGTCTG GTGGAGAAGC GGGTCTCGCT TGGTTCCGCG TAATTTCTGT 540
CCTGAGGCGT GAGACTGAGT TCATAGGGTC CTGGTCCCG GAACACAGGA GGGTTGAGGG 600
AACACAACTC GCAGGCCCCC GCGACCCAAG TGAGGGGCGC GTGTTGGGG TCCTCCCTCC 660
CTTTGCAATC CCACCCCTCC GGCCTTTGCG TCTTCTGCG GACCCCTCG CCGGGAGATG 720
GCGCGGTGTA TGGCGAGCAA GGATTGCTCC TGCTGCTGCG TCCTACTGCG CGCGGTGCTG 780
ATGGTGGAGA GCTCACAGAT CGGCAGTTCG CGGGCCAAAC TCAACTCCAT CAAGTCTCT 840
CTGGGCGGGG AGACGCTCTG TCAGGCGCGC AATCGATCTG CGGCGATGTA CCAAGGACTG 900
GCATTGCGCG GCAGTAAGAA GGGCAAAAC CTGCGGCGAG CTAACCTTGT TAGCAGTGAT 960
AAGGAGTGTG AAGTTGGGAG GTATTGCCAC AGTCCCAACC AAGGATCATC GGCCTGCATG 1020
GTGTGTGCGA GAAAAAAGAA GCGCTGCCAC CGAGATGGCA TGTGCTGCCC CAGTACCGCG 1080
TGCAATAATG GCATCTGTAT CCGAGTTACT GAAAGCATCT TAACCCCTCA CATCCCGCT 1140
  
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CTGGATGGTA CTGGGCACAG AGATCGAAAC CACGGTCATT ACTCAAACCA TGACTTGGGA 1200
 TGGCAGAAATC TAGGAAGACC ACACACTAAG ATGTACACATA TAAAGGGCCA TGAAGGAGAC 1260
 CCTGCTCTAC GATCATCAGA CTGCATTGAA GGGTTTTGCT GTGCTCGTCA TTCTGGAGCC 1320
 5 AAAATCTGCA AACCACTGCT CCATCAGGGG GAAGTCTGTA CCAACAAACG CAAGAAGGGT 1380
 TCTCATGGGC TGGAAATTTT CCAGOGTTGC GACTGTGCGA AGGGCCTGTC TTGCAAGTA 1440
 TGGAAAGATG CCACCTACTC CTCCAAAGCC AGACTCCATG TGTGTACAGAA AATTGTATCA 1500
 CCATTGAGGA ACATCATCAA TTGCAGACTG TGAAGTTGTG TATTTAATGC ATTATAGCAT 1560
 GGTGGAAAT AAGGTTTACA TGCAGAAAGAA TGGCTAAAT AAGAAACGTG ATAAGAATAT 1620
 10 AGATGATCAC AAAAAGGGAG AAAGAAAACA TGAAGTGAAT AGATTAGAAT GGGTGACAAA 1680
 TGCAGTGCAG CCAGTGTTC CATTATGCAA CTGTCTATG TAAATAATGT ACACATTGT 1740
 GGAATAATGT ATATTAAAGA GAACAAGCAC ACAGTGGAAA TTACTGATGA GTAGCATGTG 1800
 ACTTTCCAAG AGTTTAGGTT GTGCTGGAGG AGAGGTTTCC TTCAGATTGC TGATTGCTTA 1860
 TACAAATAAC CTACATGCCA GATTCTTATT CAACGTTAGA GTTTAACAAA ATACTCTTAG 1920
 15 AATAACTTGT TATACATAG GTTCTAAAAA TAAATTTGCT AAACAAGAAA TGAACACATG 1980
 GAGCATCTGA ATTTACAAAC AGAAAAATTAC CTTTGTATT GTAAACACTAC TTCTGTCTGT 2040
 CAATCAAGAG TCTTGGTAGA TAAAGAAAAA ATCAGTCAAT ATTTCCAAAT AATTGCAAAA 2100
 TAATGGCCAG TTGTTTAGGA AGGCCTTTAG GAAGACAAAT AAATAACAAA CAACACGCCA 2160
 CAAATACTTT TTTTCAAAA TTTTAGTTTT ACCGTGAATT AATAAGAACT GATACAAGAC 2220
 20 AAAAACAGTT CCTTCAGATT CTACGGAAATG ACAGTATATC TCTCTTTATC CTATGTGATT 2280
 CCTGCTCTGA ATGCAATTAT TTTTCCAAAG TATAOCCATA AATTGTGACT AGTAAAAATC 2340
 TTACACAGAG CAGAAATTTT ACAGATGGCA AAAAAATTTA AAGATGTCCA ATATATGTGG 2400
 GAAAAGAGCT AACAGAGAGA TCATTATTTT TTAAGATTG GCCATAACCT GTATTTTGAT 2460
 AGAATTAGAT TGGTAAATAC ATGTATTCTAT ACATACTCTG TGTAAATAGA GACTTGAGCT 2520
 25 GGATCTGTAC TGCACCTGGG TAAGCAAGAA AATTGGGAAA ACTTTTTCGT TTGTTTCAGGT 2580
 TTTGGCACA ATATACATCA ATGTCTGAGG CACAAGTTGG CTGTTCATCT TTGAAACCGA 2640
 GGGATGCACA GTCTAAATGA ATATCTGCAT GGGATTGTCT ATCATAAATN TTCTATGCTN 2700
 GNTGAATTCN GTGTGAGGTC CTGTGTCOGT CCTATCCTCA AATTATTTAT TTTATAGTGC 2760
 TGAGATCTCT AAATAATCTC AATTTCCGAG GTTTCACAAA ATGGACTCCT GAAGTAGACA 2820
 GAGTAGTGAG GTTTCATGCT CCTCTATAAG CTCTGACTA GCCAATGGCA TCATCCAATT 2880
 30 TACTTCCCAA ACCTCTGCAG CATCTGCTTT ATTGCCAAAG GGCTAGTTTC GGTTTTCTGC 2940
 CAGCCATTGC GGTAAAAAAA TATAAGTAGG ATAAGTGTGA AAACCTGCAT ATTGCTAATC 3000
 TATAGACACC ACAGTTTCTA AATTCTTTGA AACCACTTTA CTACTTTTTT TAAACTTAAC 3060
 TCAGTTCTAA ATACTTTGTC TGGAGCACAA AACAATAAAA GGTATCTTTA TAGTTGTGAC 3120
 35 TTTAACTTTT TGTAGACCAA AATTCACTTT TTAGTTTTCT TTTACTTAAA TCCCATCTGC 3180
 AGTCTCAAT TTAAGTTCTC CCAGTAGAGA TTGAGTTTGA GCCTGTATAT CTATTAAAAA 3240
 TTTCACTTC CCACATATAT TTAAGTAGG GATTAGACT TACATTTTCT GCACAGGTCT 3300
 GCAAAAACAA AATTTATAAA CTAGTCCATC CAAGAACCAA AGTTGTGATA AACAGGTTGC 3360
 TATAAGCTG GTGAAATGAA AATGGAACAT TTCAATCAAA CATTTCCTAT ATAACAATTA 3420
 40 TTATATTATC AATTTGGTTT CTGCAATATT TTTCTTATGT CCACCTTTT AAAAATTATT 3480
 ATTTGAAGTA ATTTATTATC AGGAAATGTT AATGAGATGT ATTTCTTAT AGAGATATT 3540
 CTTACAGAAA GCTTTGTAGC AGAATATATT TGCAGCTATT GACTTTGTAA TTTAGGAAAA 3600
 ATGTATAATA AGATAAAATC TATTAAATTT TTTCTCTCTA AAAACTGAAA AAAAAAATAA 3660
 AAAAAAATAA A

45 Seq ID NO: B45 Protein sequence
 Protein Accession #: NP_055236.1

50 1 11 21 31 41 51
 | | | | |
 MAALMRKDS SCCLLLLAIV LMVSSQIGS SRALNSIKS SLGGETPGQA ANRSAGMYQG 60
 LAFGSGKKGK NLQAYPCSS DKECEVGRYC HSPHQSSAC MVRRRKKRC HRDMCCPST 120
 RCNGLICIPV TESILTPHIP ALDGTNRHRR NHGHYSNHD L GWQNLGRPHY KMSHIKSHG 180
 DPCLRSSDCI EGFCCARHFW TKICKPVLHQ BEVCTKQRKK GSHGLEIPQR CDCAGLSCK 240
 VWKDATYSSK ARLHVQCKI

55 Seq ID NO: 46 DNA sequence
 Nucleic Acid Accession #: NM_019885.1
 Coding sequence: 1..1539

60 1 11 21 31 41 51
 | | | | |
 ATGCTCTTTG AGGGCTTGA TCTGGTGTG GGGCTGGCCA CCTGCGCGC GTGCTGGTG 60
 TCCGTGACGC TCGTGTGCGC CGTGTGCGAG CAGCTGTGGC AGCTGCGCTG GGCGGCACT 120
 CGCGACAAGA GCTGCAAGCT GCCCATCCCC AAGGGATCCA TGGGCTTCCC GCTCATCGGA 180
 65 GAGACCGGCC ACTGGCTGCT GCAGGGTTCT GGGCTCCAGT CGTCCGGGAG GAGAAAGTAT 240
 GGCACAGTGT TCAAGACGCA TTTGTTGGGG CGGCCGCTGA TACGCGTGAC CGGCGCGGAG 300
 AACGTGCGCA AGATCTCTAT GGGCGAGCAC CACCTGTGA GCACCGAGTG GCCTCGCAGC 360
 ACCCGCATGT TGTCTGGGCC CAACACGGTG TCCAATTCCA TTGGCGACAT CCACCGCAAC 420
 70 AAGCGCAAGG TCTTCTCCAA GATCTTCAGC CAAGAGGCC TGGAGAGTTA CCTGCCCAAG 480
 ATCCAGCTGG TGAATCCAGG CACACTGCGC GCCTGGAGCA GCCACCCCGA GGCCATCAAC 540
 GTGTACAGG AGGCGCAGAA GCTGACCTTC CGCATGGCCA TCCGGGTGCT GCTGGGCTTC 600
 AGCATCCCTG AGGAGGACCT TGGGACCTC TTTGAGTCT ACCAGCAGTT TGTGGACAAT 660
 GTCTTCTCCC TGCCGTGCGA CCTGCCCTTC AGTGCTTACC GGCGGGGCT TCAGGCTCGG 720
 75 CAGATCTCTG AGAAGGGGCT GGAGAGGCC ATCCGGGAGA AGCTGCAGTG CACACAGGGC 780
 AAGGACTACT TGGACGCCCT GGACCTCTC ATTGAGAGCA GCAAGGAGCA CGGGAAGGAG 840
 ATGACCATGC AGGAGCTGAA GGAAGGGACC CTGGAGCTGA TCTTTGGGCT CTATGCCACC 900
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 AAGCTGCGGG ATGAGCTGCG GGCTCATGGC ATCTGTCACA GTGGCGGCTG CCCTGCGAG 1020
 80 GGCACATGCG GCTCTGACAG GCTCAGTGGG CTGCGCTACC TGGACTGCGT CATCAAGGAG 1080
 GTCATGCGCC TGTTCACGCC CATTTCCGGC GGCTACCGCA CTGTGCTGCA GACCTTCGAG 1140
 CTTGATGTTT TCCAGATCCC CAAAGGCTGG AGTGTCTAT ATAGCATCCG GGACACCCAT 1200
 GACACAGCGC CGGTGTTCAA AGACGTGAAC GTGTTGAGC CCGATGCTT CAGCCAGGCG 1260
 CGGAGCGAGG ACAAGGATGG CCGCTTCCAT TACCTCCGT TCGGTGGGCG GTGTCGGAGC 1320
 TGCCCTGGCA AGCACTGGC CAAGCTGTTT CTGAAGGTGC TGGCGGTGGA GCTGGCTAGC 1380

5 ACCAGCCGCT TTGAGCTGGC TACAOGGACC TTCCCCCGCA TCACCTTGGT CCCCCTCCTG 1440
 CACCCCGTGG ATGGCCTCAG CGTCAAGTTC TTTGGCCTGG ACTCCAACCA GAACGAGATC 1500
 CTGCGCGAGA CGGAGGCCAT GCTGAGCGCC ACAGTCTAAC CCAAGACCCA CCGCCTCAG 1560
 CCCAGCCAGG GCAGCGGGGT GGTGGTGTG GGAGGTAGAA ACCTGTGTGT GGGAGGGGGC 1620
 CGSAACGGGG AGGGCGAGTG GCCCCATAC TTGCCCTCCC TTGCTCCCCC TCCTGGCAA 1680
 ACCCTAGCCA AAGCCAGTGG GCCCATTCCT TAGGGCTGGG CTCCCCCTCT GGCTCCAGCT 1740
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 TCTGCATGCC CGTGACAGTG TTAGGTGTCA GCGGTGCTA CAGTGTTTT GTGATGTTCT 1860
 GAACGTCTCC CTTCCTCCG TTCTTTCCG ACCCTTTTAG CTGGGGTTGG GGGACGGGAA 1920
 10 GAGCCGTGCC CCTTGGGGG CACTCTTCAG CGTCTCTCC TCCTGCGCCC CCACTGCGTC 1980
 TGCCCGAGAA CAGCATCTG GGTAGCAGAA CAGGAGTCAA CCTTGGCGGG GCGGGGGCTG 2040
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 GACAAATTGA AATTACCTAT TGCTGCTACT TGTCTGTCC TCTGACCTG GGGCAAGGA 2160
 15 GCCCCAGGCT CTGTCTCCCC AGCATCTCTC CTGGTGGCCC TGGGCAGGTG CACTGACACC 2220
 CCCACCTTCC CAGTCCCTG TGAACCAAGC CCTGTTACAC ACAGCGCCTT AAGGCCCGCG 2280
 GCTCATGTGC TGCCCGCCCC CATATTATT CACTGATAGA GAATCTTGGG GATGCTGGGG 2340
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 ACTTCTGTGA GTGAAGAGGA AGGGGTCTCT GGTCAAACCC AGCCCCCAGG GCCTAGGGTT 2460
 20 GAAAGCCTTC CCGGCTCCG GGCATTATT GGGTTAATC TOGGAGCCTC ACTCCTGGAC 2520
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 25 TCOCGCCGTA AAAAGGTGTC CTGAAGTCC CTTCACCTC TATGCCACTG TCTGCTTAGC 2820
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 CCTCGGAGCT GATTGCAGGG CCTGTGTGG TCTCCGACA GCTCGGGGAA GGCTGCCGCA 2940
 GCTGAAGCTG AAGAGCGGGC TACGTGCGGT TTGTACGGG GATTGGGTTG AAAACTGGCC 3000
 AGTCGGGATG ACTGGGTGAA AGAGGAGTAG CTCTGCCAC TGGCGTTTTG AGTGTGGCA 3060
 30 ATTTGGGATG CCTCCTGGGG AAGGTTTCCG GCGCTTTGGT GAGTCTCTAG ATTTTCTCTT 3120
 GCTTCTCTG TTTATTGGTT TTTGATGTTG TAAAAGCAAT GAATCCCTT TACAAGAAAA 3180
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 TGCTCCCTC AGACAGATC CCGTAGGCAG CCCCACAGAC CGACCTGAC CCCACTACA 3300
 35 GCCACCTCAG AGATAGACTA TAGGAACGGG CCATACAC ACAGACTGCT CTCCAATCCC 3360
 TGAGTCTCAG ATGTTTCATT TATTCTCTAC TTTTCCACTA CTAAGAAACA GTGTGGAATA 3420
 GACATATTGT GCAAAATTGC TCATCCCTAA TCCTGAAAAA CAGGCCAGAA TGGGTAAGA 3480
 CTTGTCAAAG CTTGCAACAT AGTACATGG TGCACCCGGA CTGTACCCC CTCGCCCAA 3540
 CACAAACCA GTGCTGGGA GGTTCATTTT CCTTTAACT GATCCAGCTG GCCCTGAACC 3600
 40 AATTGTTTTT GACTGAGTAT CTAGGAGAGC AGTAAGTGA ACTTCAGACA AGCCCACTGG 3660
 GTCTGTCCA GGTGAGGGGC AGGGGGCATG GGGCTGGGAG GTCTCAGGGG CCTTCCCTGG 3720
 GGGTGGCCAG CCTGTAGGG GGCAGAGAAG GAAAGCTGA GGGGGTCCC TGTGAGGGAG 3780
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 CTCGTGGCTG CTGACAGGAT CCCTGTGTTG TAATTGGTCC CTCCTTCAG CTCTCTAGTG 3900
 45 AGATGCCCGT GTCTGTGCGT GTGCGTGTGT GTTTCATACA GCTAGCATTG GATGGGTGAT 3960
 GTTCTTACTT TATCATCCCT AACTATTGCA ACTTGACCTT AAAAGACAA AACCCACAA 4020
 AACTCTTCTT GCCACGGGCT TGCAGATTGA AGCACTTTCG ATGTTGGGCG CTGGCGTTTG 4080
 TGTCTGGGCG ACCACCGTGA CCCTGCCAGC ATGGCTATAA TATTATTTTA TACACAAACC 4140
 TTTTTTTCA TAAATGTTAT AATTTGTGT CTGTCTTTAT AAATATTAT AAGTACTATT 4200
 50 TTTGTTATAA TCAAAATAG ATATTAGTA TAAAGTTTT GCTGTTAAAT ATTTGTTATT 4260
 TAGTAAATA TGAATTTTGC TCTATTGTAA ACATGGTTCA AAATATTAT ATGTTTTTAT 4320
 CACAGTCGTT TTAATATTGA AAAAGCACTT GTGTGTTTTG TTTTGATATG AAACGTGTAC 4380
 CGTGTGAGTG TTTTGTCTGT CGTGGTTTTA ATCTGTATAT AATATTCCAT GTTGATATT 4440
 AAAAA

Seq ID NO: B47 Protein sequence
 Protein Accession #: NP_063938.1

1 11 21 31 41 51
 60 MLFEGLDLVS ALATLAACLIV SVTLILLAVSQ QLWQLRWAAT RDKSCKLPIK KSGMGFPLIG 60
 ETGHWLQGS GFQSSRRREKY GNVFKTHLLG RPLIRVTGAE NVKRLIMGEH HLVSTENPRS 120
 TRMLLGNPTV SNSIGDIHRN KRKVPSKIFS HEALESYLPK IQLVIQDTRL AWSHPRAIN 180
 VYQEAQKLT RMAIRVLGFP SIPEEDLGLH FEVYQQFVDN VPSLPVDLPF SGYRRGIQAR 240
 QILQKLEKA TREKLQCTQG KDYLDALELL IESSKEHGKE MTMQELKDTG LELIFAAVAT 300
 65 TASASTSLIM QLLKHPTVLE KLRDELRAHG ILHSGGCPCE GTLRDLTSLG LRYLDCVIKE 360
 VMRLFTPISG GYRTVLQTFE LDGFQIPKGV SVMYSIRDTH DTAPVFKDVN VFPDRFSA 420
 RSEDKDGRFH YLPFGGVRRT CLGKHLAKLP LKVLAVELAS TSFELATRT FPRITLVPVL 480
 HPVDGLSVKF FGLDSNQNEI LPETBAMLSA TV

Seq ID NO: B48 DNA sequence
 Nucleic Acid Accession #: AB040527.1; AL136582.1
 Coding sequence: 94..2319

1 11 21 31 41 51
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 TGAGGGAGGC TTCAGCGTGC AATCGGAAG CTACAGTGTT GAAGACATGG ATGAGGGTAG 120
 CGACGAAGTC GGGGAGGAAG AGATGGTTGA AGGCAAGAC TATGAAGAAT TCGGTGCGTT 180
 TGGTGGCTAT GGCACCTCA CCAGCTTTGA CATCCATATC CTCAGAGCCT TCGGAAGCTT 240
 80 GGGTCCAGGC CTTCGCATCT TATCGAATGA GCCCTGGGAA CTGGAAGAAC CTGTGCTGGC 300
 CCAGACCTG GTGGAGGATG TGCAGCTGGA TCCGGAACA CTTCGAATG AGACGGCCGC 360
 CGTGTGCGC AACGTAGCCC GCGCGCCGC CTCACACGT GCGCTCGGG CCGCTGCCGC 420
 CGCTGCCCGT ACCGCCCTCA GTCAGGTGGT GCTAGCCAC CGGTGGGCA CGCCGAGGT 480
 CTCAGGAGAG GATACCCAGC CCACGACCTA GCGCGCGAG GCTCAGGGG CACCCCTGA 540
 GCCACCCCTT GCTTCTCCGC AGACCTCCCA GATGTTAGTC ACCAGTAAGA TGGCTGCCCC 600

CGAGGCTCCG GCAACCTCCG CACAGTCCCA GACAGGCTCC CCGGCCACGG AGGCTGCTAC 660
 TGAGGGCCCT AGTAGCGCCT GTGCTTTCTC TCAGGCTCCG TGTGCCAGGG AGGTGGACGC 720
 CAACCGGGCC AGCAGAGCCT TCCTGGGCCA GAATGATGTC TTGATTTTCA CTCAGCGCGC 780
 AGGTGTCTAGT GGCATGGCCT TCCCGGCGCC CAAGAGACCT GCCCCAGCCC AAGAGGCTGC 840
 CACAGAGGGC CCAAGTGTCT CCTCTGGTGT GCCCCAGACG GGACCTGGCA GGGAGGTGGC 900
 AGCCACCCGG CCAAGAGCCA CCAAGTCGGG GAAGGCGCTG GCCAAGACTC GGTGGGTGGA 960
 GCCTCAGAAT GTTGTGGCAG CAGCTGTCTG CAAGGCCAAG ATGGCCACGA GCATCCCTGA 1020
 GCCGAGGGGT GCAGCTGTCT CCACTGTCTA GCACAGTGCT GAGCCCTGGG CCAGGATGGG 1080
 AGGCAAGAGG ACCAAGAGT CCAAGCACCT GGATGATGAG TATGAGAGCA GCGAGGAGGA 1140
 GAGAGAGACT CCGCGGTGCC CACCCACCTG GAGAGCATCA CAGCCCTCAT TGACGGTGGG 1200
 GGCCTCAGTTG GCCCTCGGGC CCGCGATGGC CCGGAGGTCC CAGATACCTT CAAGGCACGT 1260
 ACTGTGCAAG CCCCCCGCA ACGTGACCTT TCTGCAGGAG AGGGCAATA AGTTGGTGAA 1320
 ATACCTGATG ATTAAGGACT ACAAGAGAT CCCCATCAAG CGCGCAGACA TGCTGAAGGA 1380
 TGTCTATCGA GAATATGATG AACATTTCCC TGAGATCATT GAACGAGCAA CGTACACCTT 1440
 GGAAGAAGAG TTTGGGATCC ACCTGAAGGA GATGACAAG GAAGAACACC TGTATATTCT 1500
 TGTCTGCACA CCGGACTCCT CAGCTCGCCT CCTTGGAAAA ACCAAGGACA CTCCAGGCT 1560
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 TGTCTCTCTG GAGGCACTAC GCAAGATGGG ACTGCGCCTT GGGGTGAGGC ACCCATCTCT 1680
 CGGCGATCTG AGGAAGCTCA TCACAGATGA CTTTGTGAAG CAGAAGTACC TGAATACAA 1740
 GAAGATCCCC AACAGCAACC CACCTGAGTA TGAATTCCTC TGGGCGCTGC GAGCCCGCCA 1800
 TGAGACCCAG AAGATGAGGG TCCTGAGATT CATCGCCAG AATCAGAAC GAGACCCCG 1860
 GGAATGGAAG GCTCATTTCT TGGAGGCTGT GGATGATGCT TTCAAGCAA TGGATGTGGA 1920
 TATGGCCGAG GAACATGCCA GGGCCAGAT GAGGCGCCAG ATGAATATCG GGGATGAAGC 1980
 GCTGATTGGA CGTGGAGCT GGGATGACAT ACAAGTGGAG CTCTGACCT GGGATGAGGA 2040
 CGGAGATTTT GCGGATGCCCT GGGCCAGGAT CCCCCTTGCT TTCTGGGCCA GATACCATCA 2100
 GTACATTTCT AATAGCAACG GTGCCAAGAG GAGGCGCCAG TGGAGAGCTG GCGTCAGCAG 2160
 TGGCACAAT GAGGGGGCCA GCACCAAGCT CTTAGATGGC CCCAGCACA GCTCAACCAT 2220
 CCGGACCAGA AATGCTGCCA GAGCTGGCGC CAGCTTCTTC TCCTGGATCC AGCACCGTTG 2280
 ACGAATGCA GCGATCTTAC TGGCCAAGCC AGAGCGCCTC CTCTCAGATT CTTTCTCGAC 2340
 ACAGACCCCT AGGCGGCTTC TTCTGTCTAG TCGAGGTGG CATGCAAGAT GAAGCTCTCT 2400
 TTGCTCTCC TGCTTTCATT TTGTGCTTTT CCTTGTGTTT TCATGTTTG GGTATCAGTG 2460
 TTACATTAAA GTTGCAAAAT TAAA

Seq ID NO: B49 Protein sequence
 Protein Accession #: BAB33378.1; CAB66517.1

1 11 21 31 41 51
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 MAEGSPFSVQS ESYSEVEDMDE GSDEVGEEM VEGNDYEEFG AFGGYGTLS FDIHILRAFG 60
 SLGPGLRILS NEPWLENPV LAQTLVEALQ LDFETLANET AARAANVARA AASNRAARAA 120
 AAAARTAFSQ VVASHRVATP QVSGEDTQPT TYAAEAQGPT PEPPLASPT SQMLVTSKMA 180
 APEAPATSAF SQTGSPAQEA ATEGPSSACA FSQAPCAREV DANRPSTAFI QNDVFDPTQ 240
 PAGVSGMAFP RPKRPAPAQE AATEGPSAAS GVPQTGPGRV VAATRPKTKK SGKALAKTRW 300
 VEPQNVVAAA AAKAKMATSI PEPGEGAAAT AQHSAEPWAR MGGKRTKKSK HLDDEYESS 360
 EERETPAVPP TWRAQPSLT VRAQLAPRPP MAPRSQIPSR HVLCLPRNV TLLQERANKL 420
 VKYLMIKDYK KIPKIRADML KDVIREDYEH FPBIIRATY TLEKKGPIHL KSIDKBEHLY 480
 ILVCTRSSA RLGLKTKDTP RLGLLLVILG VIFMNGNRAS EAVLWEALRK MGLRPGVRHP 540
 FLGLRLKLT DDFVKQKYLE YKKIPNSNPP EYEFWGLRA RHETSKMRLV RFTAQNRD 600
 PREWKAHFE AYDDAFKIMD VDMABEHARA QMRAQMNIGD BALIGRWSWD DIQVELLTWD 660
 EDGDFGDAWA RPPFAFWARY HQYILNSNRA NRRATWRAGV SSGTNGAST SVLDGPSTSS 720
 TIRTRNARA GASPFWSIQH R

Seq ID NO: B50 DNA sequence
 Nucleic Acid Accession #: XM_084965.1
 Coding sequence: 356..2014

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 TTGTGTTTTT TAGAGGCATT TCGTGATCCA TGGTTGCGCT CCGGTGAAGA GCGAGCTAG 240
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 GACGAGCCGG AGCCGCGGCG GCGGCGGGGC TGTCAGCGAG CGCGGCGGAG CTGGCGCGTC 420
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 CATGGAACCT CATTGTGACT GTGCCGCGGA AACGCGCGCC GCGGAGCCGC CTTGCGGGAA 540
 GATTATATAA GCTGCCCTTCA AATTATTCAA GAAGAGGAAA TCGGTGGCA CCATGCCAG 600
 CATTTTTGGG GTCAAAAACA AAGGGGACGG GAAAAGCTCG GGTCCGACGG GGTGCTGAG 660
 GAGCAGGACC CACGACGGAC TTGCGGAGGT GCTGGTGTCT GAGAGCGGCA GGAAGGAGGA 720
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 CAGAGCGCGA GGGCGCGGCG GGGGCTCCCT CGCCAGCAGC TGGTGGGCA AGTCGACAG 840
 CTTCTTCTCG CTGCTGAAGA AGAACGCGCG CTGGGAAAC GGCAAGGAG AGCCTGTGGA 900
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 TCCTAAGGAG GAGCCCAAGC ACCCGAGGAA GGAGCAGCAG GAAGGCGTCC CCAACAGCGA 1560

CGAGGGCTAC TGGGACTCCA CCACGCCAGG CCCAGAGGAA GACAGCTCGA GCAGCGGGAA 1620
 GAAGGCGGGC ATCCCCCGGG ATAGCTACAG CCGGGAAGCG CTCTATGATC TCTATGCTGA 1680
 CCGGAGCGGA AGTCCAGCAA CCCTTCCTGG AGGGAAGGAC AACGAGGAGA CGTCTCCCT 1740
 GTCCCGGTTA AAGCCCGTAT CTCAGGCAC CATCACTGT CCACTGCGAA CACCAGGCAG 1800
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 ACGTTTCCTT CCTTCCCTTC TTTCTCTTT CTTTCCAGT T

Seq ID NO: B51 Protein sequence
 Protein Accession #: XP_084965.1

1 11 21 31 41 51
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 EEPFGGDSG GGGGGRPNPG PPRAAGPGGG SLASSSVAKS HSFFSLKKK GRSENGKGE 180
 VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAAAEGRAP GGLILPGSL TASLECVKEE 240
 TPRAAREPEE PSQDAPRDP A GCDIADQE EEAGPSCDKH VPGPGKPLS KKNPGVVAYQ 300
 GGGEEAMSPD EVDDTYLQEF WDMLSQTEQ GPEPQEGAAK VAAALETKV PETPKDTRCV 360
 EAAKDASSVK RRRLNRIPIE PPKKEPKPH EKEQQEGVPN SDEGYWDSST PGPEEDSSSS 420
 GKAGIPRDS YSGDALYDLY ADPDGSPATL PGKEDNEETS SLRLKVPSP GTITCPLRTP 480
 GSLKDSKIP ISIKHLTNLP SSRPVVHQPP SRSEMPRTKI FVSKVLVRRV SNRGLAGTTI 540
 RATACHDSAK KL

Seq ID NO: B52 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..2016

1 11 21 31 41 51
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 GCGTCCGTGG GGGTCTGCAG GAGGAAGGCG GAGGCGCGGG CCGGACCGCG GACCTCGCG 120
 GCAGACATGG ACTTGCATTG TGACTGTGCC GCGGAACGCG CGGCCGCGGA GCGCCGTGCG 180
 GGAAGATTGA ATAAAGCTGC CTTCAAAATTA TTCAAGAAGA GGAATCCGGG TGGCACCATG 240
 CCGAGCATTT TTGGGGTCAA AAACAAAGGG GACGGGAAAA GCTCGGGTCC GACGGGGCTG 300
 GTGAGGAGCA GGACCCACGA CGGACTTGCC GAGGTGTCTG TGTCTGAGAG CGGCAGGAAG 360
 GAGGAGCGCG CGGCGGGGGG CGACAGCGGC GGGGCGGGCG GGGGCGGGCC GAACCCGGGG 420
 CCCCCAGAG CCGCAGGGCC CGGCGGGGGC TCCTTCGCGA GCAGCTCGGT GGCCAAAGTCG 480
 CACAGCTTCT TCTCGCTGCT GAAGAAGAAC GGGCGCTCGG AAAACGGCAA GGGAGAGCCT 540
 GTGACGCGGA GCAAGCGCGG CGGCAACAA AAGCGGGGCG TGCGGGGGCT GTTCAGCGGC 600
 ATGCGCTGGC ACAGGAAGA CAAGCGGGCC AAGCGGAGG CCGCGGAGG GCGCGCGCCC 660
 GGGGCGGGCT TGATCTTACC CGGCTGCTC ACCGCCAGCC TGGAGTGCCT CAAGGAGGAG 720
 AGGCCAGAG CCGCGCGCGA GCGGAGGAG CCCAGCCAGG ACGCCCGCGG AGACCCAGCA 780
 GGTGAGCCCG CAGGGGGAGA GGAGGTGCCG GCGCCCGCGG ACGCGCGCCC AGCGCGGAGC 840
 TGCCGAGAGG CAGAGGGCTT CGCGCACCCC GCGCACACCG GCGCCCGGGG AGAGGACGCC 900
 GCGGGGCATC GCGCGGCCGA GCGCGGGCCC GGGGAGGTCC GCAAGGAGG GACGCTTCC 960
 AGGACGGGGG CGGTTCCTGT AAAGACGCTC CCCTTGTGCT ACTCGAAGG CGGCAGCGGC 1020
 CGGGCGCCCG CCGCCCGAGA CCCTGCTCTT GTGATCCAC CCTCAGACCC GTCCGCGAGT 1080
 CGTATTGTGT TGATGTTTTT TGACGTGACT TCACTGAAAA GCTTTGACTC TCTTACAGGC 1140
 TGTGGAGATA TTATTGCAGA CCAAGAGGAA GAGGCAGGTC CCAGCTGTGA CAAGCATGTC 1200
 CCGGGCCAGG GCAAGCCGCG TCTGTCTAAA AAGAACCCTG GGTGGTGGC CTACCAAGGA 1260
 GCGGGGAAG AGATGGCCAG CCGGAGCAG GTGGACGACA CCTATCTACA GGAGTTCTGG 1320
 GACATGCTCT CCGACAGCGA GGAGCAGGGA CCGGAGCCCC AGGAGGGCGC GGCTAAGGTG 1380
 GCAGCTGCGC TGGAAACCAA GGTGGTGCCC GAGACCCCCA AAGACACCAG GTGTGTGGAA 1440
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 CATCTAAGG AGGAGCCCAA GCACCCGAGG AAGGAGCAGC AGGAGGCGT CCCCACAGC 1560
 GACGAGGGCT ACTGGGACTC CACCAAGCCA GCGCCAGAGG AAGACAGCTC GAGCAGCGGG 1620
 AAGAAGGCGG GCATCCCGCG GGATAGCTAC AGCGGGGAGC CGCTCTATGA TCTCTATGCT 1680
 GACCGGAGG GAAGTCCAGC AACCTTCTCT GGAGGGAAGG ACAACGAGGA GACGCTCTCC 1740
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 AGCTTGCTGA AGGACTCTAA GATCCCTATT AGCATCAAGC ACCTGACCAA CCTTCCATCT 1860
 AGCCATCCCG TGGTGACCA GCAACCTTCC AGGAGTGAGA TGCCACAGAA AAAAATCCCG 1920
 GTTTCCAAAG TGCTGTGTCG CAGAGTCAGC AACCGGGGCT TGGCTGGGAC CACCATCAGA 1980
 GCAACGGCCT GCCACGACAG TGCCAAAAAG TTGTGA

Seq ID NO: B53 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
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 EEPFGGDSG GGGGGRPNPG PPRAAGPGGG SLASSSVAKS HSFFSLKKK GRSENGKGE 180
 VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAAAEGRAP GGLILPGSL TASLECVKEE 240
 TPRAAREPEE PSQDAPRDP A GEPAGGEEVP APADRAPARS CREAEGLAHP GDTGARGEDA 300

5 AGHRRASPGP GEVRTAEDAS RTGAVPVKTV PLVDSEGGSG RAPAAPDPAS VDPFSDPSAD 360
 RICLMFSDVT SLKSPDSLTV CGDIIADQEE EAGPSCDKHV PGPKRPALSK KNPGVVAYQG 420
 GGEEMASPDE VDDTYLQEFW DMLSQTEBQG PEPQEGAAKV AAALETKVVP ETPKDTRCVC 480
 AAKDASSVKR RRLNRIPIEP HPKEEPKHPE KEQOEGVPNS DEGYWDSTTP GPEDSSSSSG 540
 KKAGIPRDSY SGDAILYDLYA DPDGSPATLP GGDNEETSS LSRLKPVSPG TITCPLRTPG 600
 SLLKDSKIPI SKHLTNLPS SHPVVHQPS RSEMPRTKIP VSKVLVRRVS NRGLAGTTIR 660
 ATACHDSAKK L

10 Seq ID NO: B54 DNA sequence
 Nucleic Acid Accession #: NM_014138.1
 Coding sequence: 60..854

15 1 11 21 31 41 51
 CTGCAGAGAC TTCCAGGAA GGTCCAGCGC CCTCTCAGCC TTCGTACTCA GAACAGCCGA 60
 TGATGGGCTT CAGTAACCTG AGCCCCGGTC CTGGCCCCAG CCAGGCCGTG CCTCTCCAG 120
 AGGGCTGTCT CGCCACGCGG TACAGAGAGG AGAAGACCTT GGAAGAGCGG CGGTGGGAGA 180
 GGCTGGAGTT CCTTCAGAGG AAGAAAGCAT TCCTGCGGCA TGTGAGGAGG AGACACCGCG 240
 ATCAGATGGC CCCCTATGCT GTTGGGAGGG AAGCCAGAAT CTCCCCATTA GGTGACAGAA 300
 20 TCAGAAATCG ATTCCGATGT GAATGTCGAT ACTGCCAGAG CCACAGGCGG AATCTTTCTG 360
 GGATCCCTGG GGAGAGTAAC AGGGCCCCAC ATCCCTCCTC CTGGGAGACG CTGGTGACGG 420
 GCCTCAGTGG CTTGACTCTC AGCCTAGGCA CCAACCAACC CGGGCCTCTG CCTGAAGCGG 480
 CACTCCAGCC ACAGGAGACA GAGGAGAAGC GCCAGCGAGA GAGGCAGCAG GAGAGCAAAA 540
 TAATGTTTCA GAGGCTGCTC AAGCAGTGGT TAGAGGAAAA CTGAGACGTG CACCCCATAT 600
 25 GGATGGAGAC CCGAAGGGAC TCAGACGGAG CGCCCGTGTG GGCAGCGCCT GGGTGTGGGC 660
 CCATTTTGGG GACCAACAG CAGCTGTGG TCGATGAGT GCCAGGACCT GTGTACCGGG 720
 ACACGTGGGA GTCTCTCCAG CATGATGCTT GACTGACCCG AGGAAGGTCC TCATGTTTCG 780
 TGCTCTCAT TCTCGGATGG CTGTGAGGCA TTCCTTGGCA AGGGACGCTG CGTACCAGCG 840
 GCTCTCACCG CATCTCACAT GGCTCCTGTG ATGCATGTTG TCGCTTTCCC ACCCGGGATC 900
 30 TCCATCTCTC TTCCTTCCTT GCTGTGAGTA AGAGATCACA TGTCTGTGTA GTGTGAATCG 960
 CTGTGCTGTG TCTGTGCTT TTGCACCATT GAGTTGACTG CCTCTGAGAA GCAGCACTAG 1020
 GCCTGTGTA AATGCAATGTG CTGCCCTGAG ATCCAGTTTC AAGAATGGGC AGTAAAGCG 1080
 AGTGTGGGAA AGGAATGTGG AATGAGAACT TGGTGGTTCA CGCTGTACT ATTTGTGTAA 1140
 ATGTTTACGT ATGTGATAAG CTACATGTAT GTAAATGTTG CAATACCCCT AACAGTCGAG 1200
 35 TAGTAGTCTC CCTTACAGGA ATTTTGTACG GGGTTCCTCA TCATCAATAC CAAATAAATA 1260
 TATGTAGGAA TGGAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1320
 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1380
 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAA

40 Seq ID NO: B55 Protein sequence
 Protein Accession #: NP_054857.1

45 1 11 21 31 41 51
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 DHMAPYAVGR EARIISPLGDR SQNRFRBCBR YCQSHRPNLS GIPGESNRAP HPSSWSWTLVQ 120
 GLSGLTLSLG TNQPGPLEPA ALQPQETEEK RQRERQESK IMPQRLKQW LEEN

50 Seq ID NO: B56 DNA sequence
 Nucleic Acid Accession #: NM_000025.1
 Coding sequence: 198..1424

55 1 11 21 31 41 51
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 GTCCCCCTCC CTGAGCCAGG TGATTTGGGA GACCCCTCC TTCCTTCTTT CCCTACCGCC 180
 CCAAGCGGGA CCGGGGATG GCTCCGTGGC CTCACAGAAA CAGCTCTCTT GCCCCATGGC 240
 CGGACCTCCC CACCTGGCG CCCAATACC CCAACACAG TGGCTGCCA GGGGTTCGT 300
 60 GGGAGCGCG CCTAGCCGG GCCCTGTGG CGCTGGGGGT GCTGGCCACC GTGGGAGGCA 360
 ACCGTCTGT CATCGTGGC ATCGCCTGGA CTCGAGACT CCAGACCATG ACCAACGTGT 420
 TCGTGAATTC GCTGGCCGA GCGGACCTGG TGATGGGACT CTGGTGGTG CCGCGCGGG 480
 CCACCTTGGC GCTGACTGG CACTGGCCGT TGGGCGCCAC TGGCTGGAG CTGTGGACCT 540
 CGGTGGACGT GGTGTGTGT ACCGCCAGCA TCGAAACCTT GTGCGCCCTG GCGCTGGACC 600
 65 GCTACCTGGC TGTGACCAAC CGCTGTGCTT ACGGCGCACT GGTACCAAG CGCTGCGCCC 660
 GGACAGCTGT GGTCTGTGT TGGGTCTGT CGGCGCGGT GTCGTTTGG CCCATCATGA 720
 GCCAGTGTG GCGGTAGGG GCGGACCGG AGGCGCAGG CTGCCACTCC AACCGCGCT 780
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 70 TGCGCTTGT GCGCGGGGAG CTGGGCCGCT TTCGCGCGGA GGAGTCTCG CCGGCGCGT 960
 CGCGCTCTT GCGCCCGGCC CCGGTGGGGA CGTGCGCTCC GCGCGAAGGG GTGCGCGCT 1020
 GCGGCGCGG GCGCGCGGC CTCCTGCTTC TCGGGAACA CCGGCGCTG TGCACTTGG 1080
 GTCTCATCAT GGGCACCTTC ACTCTCTGCT GGTGCGCTT CTTCTGGCC AACGTGCTGC 1140
 GCGCCTTGG GGGCCCTCT CTAGTCCGG GCGCGCTTT CTTGCGCTG AACTGGCTAG 1200
 75 GTTATGCCAA TTCTGCTCTT AACCGCTCA TCTACTGCG CAGCGCGGAC TTTCGCGAG 1260
 CCTTCGCGG TCTCTGTGC CGCTGCGGCC GTGCGCTGCC TCGGAGGCC TGGCGCGCG 1320
 CCGCGCGGC CTTCTTCCC TCGGGGCTT CTGGGCGCG GAGCAGCCA GCGCAGCCA 1380
 GCGCTTGGCA ACGGCTCGAG GGGGCTTCTT GGGGAGTTT TTAGGCTGA AGGACAAGAA 1440
 80 GCAACACTC TGTGTATCAG AACCTGTGA AACCTGTGG CCTGTGTTCA GAATGAGTCC 1500
 CATGGGATC CCGGCTGTG CACTCTACC CTCAGAACG TGACGACTGG GCCATGTGAC 1560
 CCAAGGAGG ATCTTACCA AGTGGGTTT CACCATCCT TTGCTCTCTG TCTGAGAGAT 1620
 GTTTTCTAAA CCCCAGCTT GAACCTCACT CCTCCCTCAG TGGTAGTGT CAGGTGCGGT 1680
 GGAGCAGCAG GCTGGCTTG GTAGGGGAC CCATCACCG GCTTGCTGTG GCAGTCAGT 1740
 AGTGCTTAGG GCAAGAGAG CTCCTTGGT TCCTTCTCT CTGCCACCA AACCTGATG 1800

5
10
15

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AGACCTTAGT GTTCTCCAGG CTCTGTGGCC CAGGCTGAGA GCAGCAGGGT AGAAAAGACC 1860
AAGATTGGGG GTTTTATCTC TGGTTCCCTT ATTACTGCTC TCAAGCAGTG GCCTCTCTCA 1920
CTTTAGCCAT GGAATGGCTC CGATCTACCT CACAGCAGTG TCAGAAAGAC TTCGCCAGGG 1980
TTTTGGAGAG TCAGAGGTTT ATAAGAAGGT GAACCAITAG AACAGATCCC TTCTTTTCTT 2040
TTTGCAATCA GATAAATAAA TATCACTGAA TGCAGTTCAT CTOGGGCCCA CTTCCTCTCC 2100
GTTTGTTTTC TTTTCATAAT CCACCTACTC CCTTCCCTTC TACTCTGCGC TGGCTTTTGA 2160
CAGAGGCAGT AAATTAGGCC TAATCCTCAC TCTTTTCTTC CTAATCTTCA TCAACAAAAA 2220
AATGAAAACT CTGTCTGGAC GAAGGGGAGT GAGCTTGAGC CTTTGATATC TTGCTCCCCC 2280
ACCTTCTCTG AAATCTTTGA AATCCAGITG CCATTGAGTA GCAAAGCCAC GCTCCCCACA 2340
GGACTTGGAC AGAGGGGCCA CAGGGGGATG GGCTGGCTGT GGGCAGGTTT AGGGCAGGGG 2400
GCATTGTGCC CCTCCATGCT ATAATCCAGT GGTGCTTAC ATGGTGTGTG TGTGTGTGTG 2460
TGCCTGTGTG TGTGTGTGTG TGTGTCTGGA GGCACAGGCA CAAAGCATTG CTGGGTTGG 2520
TCAATGTCTT TGTGTCTATA ATATATTCTG ATGTTTCCCA GCCTTCCAC AACCTCTACC 2580
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TTAC

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Seq ID NO: B57 Protein sequence
Protein Accession #: NP_000016.1

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1      11      21      31      41      51
MAPWPHENSS LAPWFDLPTL APNTANTSGL PGVPWEAALA GALLALAVLA TVGNNLLVIV 60
AIAMTPLLQT MTNVEVTSIA AADLVMLGLV VPPAATLALT GHWPLGATGC ELWTSVDVLC 120
VTASIELTCA LAVDRYLAVT NPLRYGALVT KRCARTAVVL VVVVSAAVSF APIMSQWREV 180
GADAEARQCH SNPRCCAFAS NMPYVLLSSS VSFYLPALLVM LPVYARVFFV ATRQLRLLRG 240
ELGRFPPEES PPAPSRSLAP APVGTCAPEE GVPACGRRFA RLLPLREHRA LCTLGLIMGT 300
FTLCWLPPFL ANVLRLGSGP SLVPGFAPLA LNNLGYANSA FNPLIYCRSP DFRSAFRRL 360
CRCGRRLPPE PCAAARPALF PSGVPAARSS PAQPRLCQRL DGASWGV

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Seq ID NO: B58 DNA sequence
Nucleic Acid Accession #: NM_032553.1
Coding sequence: 37..1038

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ATTCTTGTGC CAGGCTCAT AGGGAATATA TTAGCCCTGT GGGTATTCTA TGGTTATATG 180
AAAGAACCAA AACGAGCTGT GATATTATG ATAACTTAG CCATTGCTGA CTTACTACAA 240
GTCTTTTCTT TGCCACTGAG GATCTTCTAC TACTTGAATC ATGACTGGCC ATTTGGGCCT 300
GGTCTCTGCA TGTTCGTGTT CTACCTGAAG TATGTCAACA TGTATGCAAG CATCTACTTC 360
TTGGTCTGCA TCAGTGTGCG ACGATTTTGG TTTCTCATGT ACCCCTTTCC CTTCCATGAC 420
TGCAACAGCA AATATGACCT GTACATCAGC ATTGCTGGCT GGCTGATCAT CTGCCCTGGC 480
TGTGTAATCT TTCCACTCCT CAGAACCAGT GATGATACCT CTGGCAATAG GACCAAAATG 540
TTTGTGGATC TTCCCTACAG GAATGTCAAC CTGGCCAGT CCGTTGTAT GATGACCATT 600
GGCGAGTTGA TTGGGTTTGT AACTCCGCTT CTGATTGTCC TATATTGTAC CTGGAAGACG 660
GTTTATCAC TGCAAGATAA ATATCCCATG GCCCAAGATC TTGGAGAGAA ACAGAAAGCC 720
TTGAAGATGA TTCTAACCTG TGCAAGGGTA TTCTAATTT GCTTTGCACC TTATCATTTC 780
AGTTTCTCTT TAGATTCTCT GGTGAAGTCC AATGAAATTA AAAGCTGCTT AGCCAGAAGG 840
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CCAGTCATAT ACTACTTTTC CACTAATGAG TTCCGAAGAC GGCTTTCAG ACNAGATTTC 960
CATGACAGCA TCCAATCCCA TGCAAAATCC TTTGTGAGTA ACCATACAGC TTCCACCATG 1020
ACACCTGAAT TAGCTTAAAA CAAAAACCA AACTGAATGT GACCTGAAT GCAAGTACAT 1080
CAGAACATAT CTGCAATACC CAAGCCACAG GGAAGAACTT GCAAAACCA ACAGCTTTTC 1140
AGTTCGTCTC TATCTTACTG CTATGGGGAA TTCATCTCTT CAAAGCAGGA CCTATTGGA 1200
GCATTACGAT CCACGATTAT TGATGTTGAC ATGTCCATGT AGTAATTTT CTTCAGAT

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Seq ID NO: B59 Protein sequence
Protein Accession #: NP_115942.1

60
65
70

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1      11      21      31      41      51
MPANYTCTRP DGDNTDFRYP IYAVITYTVIL VPGLIGNILA LWFVGYMKE TKRAVIFMIN 60
LAIADLLQVL SLPLRIFFYL NHDWPFPGPL CMFCPYLYKV NMYASIFYLV CISVRFWFL 120
MYPRFHDCK QKYDLYISIA GWLIICLACV LPFLLRTSD TSGNRKCFV DLPTRNVLNA 180
QSVMMTIGB LIGFVTPLLI VLYCTWKTVL SLQDKYPMAQ DLGEKQKALK MILTCAGVFL 240
ICFAPYHFSF PLDFLVKSNE IKSCLARRVI LIHFSVALCL ASLNSCLDFV IYFSTNEFR 300
RRLSRQDLHD SIQLHAKSFV SNHTASTMTP ELC

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Seq ID NO: B60 DNA sequence
Nucleic Acid Accession #: CAT cluster

75
80

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1      11      21      31      41      51
GATTCGGATT TTAATCCGAC TCACTATAGG GAATTTTGGC CCTCGAGGCC AAGAATTCCG 60
CCCGAGGGTT AGACATTAA CTGAGTCTT TTCAATACAC GGTATGCTTT TATTTTACC 120
TCATATATAA TTAATTTTCA TCTGGGCATA TATTTCCAGA TTAGAAATCA TTTCTTTTCA 180
TACATTTTAA GGAATTTATA CATTTGCATC TGAAATTTGA TTCATTATCT TCTAGAAACC 240
AAGAGTGGAC TTGGTATCCG TCTGATTATA TTTTCTTTGT TGGTAAAGAG CCTCTTTTTT 300
CCTTTTTTAT TTTCACTCTC TCTTCTCTA GTGTTTATAA TCTTATTTTT ATGAATGTAG 360
TCTAATATT TAGAACCTG TCTCGAGTA TGTGTTTATT TGGGTTTGTG TTTTGAACAT 420
TGCTCCAGG TGCGAGTTTA TGTGTGTTTA TGTTCCTAT TTGAGGTTGG ACCTTAGAA 480
AATTTTCTCA ATTCGAAAC TATTTTCTT CAGCACTCAG AAATTTTAT CAAAGATTAT 540
TTCCAGGATT ATTTCTCTG CTGGGTTTT OGRGTTCTTA ACCTAGAATT CAATTGTTA 600

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	ATGTTAGACC	TTACACATCT	TCAATGTATC	ATATATATTT	CACATCATAT	ATTTATTGTC	660
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	AAACTHCAT	TTTCAAATTT	AATACACACA	AAATGTGCAT	ACCCACACAC	ATATACCACA	780
5	GATATATTCA	TTTTCAGSAT	TTCTTTAAGT	GTTATTTTAA	AAATAATCAT	ATTCATTATT	840
	TGTGAACGTG	GGGATTTCCT	GAAACTTTTT	GAAACTCTC	ATTAGTCTGT	GTTTGTGTGG	900
	TTCTTTTAAA	TTATCTCTTC	CTTCAGAAAT	ACTTTTGTGT	TTTGAATTTG	AGTCTTTGCC	960
	ATTCATAAGG	CGGGCTTTCC	TTGAATACCA	GATAACTCTG	AGTTCTCTGT	TCATATTTTA	1020
	GAATAAATAA	CCTAATTGGA	AAAAAAAAAA	AAAAA			
10	Seq ID NO: B61 DNA sequence Nucleic Acid Accession #: NM_014522.1 Coding sequence: 846..3911						
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	ATATTAATAG	CTATTCTTGT	TTTTCTTATC	CAAAGAAAAA	TCCCTCTAATC	CCCTTTTCAC	180
	ATGATAGTTG	TTACCATGTT	TAGGCATTAG	TCACATCAAC	CCCTCTCCTC	TCCCAAACTT	240
20	CTCTCTTCA	AATCAAACTT	TATTAGTCCC	TCCTTTTATA	TGATTCCTTG	CCTCGTTTTA	300
	TCCAGATCAA	TTTTTTTTCA	CTTTGATGCC	CAGAGCTGAA	GAAATGGACT	ACTGTATAAA	360
	TTATTCATTG	CCAAGAGAA	AATTGCATTT	TAAACCCATA	TTATAACAAA	GAATAATGAT	420
	TATATTTTGT	GATTGTAAAC	AAATACCCCT	TATTTTCCCT	TAACATTGGA	ATTAAATATT	480
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25	TATCAATGGT	GGACACTTTT	ATAGGTACTC	TGTGTCAATT	TTGATACTGT	AGGTATCTTA	600
	TTTCATTAT	CTTTATTCCT	AATGTACGAA	TTCAATATAT	TTGATTGAGA	ACAAATTTAT	660
	CACATATTAA	CAGAGTGTCA	ATTATGCTAA	CATCTCAATT	ACTGATTTTA	ATTAAAAACA	720
	GTTTTTGTGA	ACATGCAATG	TTAGGGTTGG	CTTCTTAAATA	ATTTCTTCTT	CCTCTTCTCT	780
	CTCTCCTCTT	CTTTTGTGTA	GTGTTGTGGG	GGTTAATACA	ACAAACTGTA	ACAAGTGTAC	840
30	CTGATATGGA	CTTGTGTGCC	GGGACGTACA	TTTTGCGGGT	CCTGCTAGCA	TGCGTGGTGT	900
	TCCACTCTGG	CGCCAGGAG	AAAACTACA	CCATCCGAGA	AGAAATGCCA	GAAAAAGTCC	960
	TGATAGGCGA	CTTGTGAAA	GACCTTAACT	TGTCGCTGAT	TCCAAACAAG	TCCTTGACAA	1020
	CTGCTATGCA	GTTCAGCTA	GTGTACAGA	CCGAGATGT	GCCACTGATT	CGAATTGAAG	1080
	AGGATACTGG	TGAGATCTTC	ACTACTGGGG	CTCGCATTTA	TGCTGAGAAA	TTATGTGCTG	1140
35	GTATCCCAAG	GGATGAGCAT	TGCTTTTATG	AAGTGGAGGT	TGCCATTTTG	CCGGATGAAA	1200
	TATTTAGACT	GGTTAAGATA	CGTTTTCTGA	TAGAAGATAT	AAATGATAAT	GCACCATTTG	1260
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	TTAAGAGTCA	AAACATTTTT	GGCCTCGATG	TCATTGAAAC	ACCAGAAGGA	GACAAGATGC	1440
40	CACAACTGAT	TGTTCAAAG	GAGTTAGATA	GGGAAGAGAA	GGATACCTAC	GTGATGAAAG	1500
	TAAAGGTTGA	AGATGGTGGC	TTTCTCTCAA	GATCCAGTAC	TGCTATTTTG	CAAGTGAGTG	1560
	TACTGTATAC	AAATGACAA	CACCCAGTCT	TTAAGGAGAC	AGAGATTGAA	GTCAGTATAC	1620
	CAGAAATGCG	GCTCTGAGG	ACTTCAGTGA	CACAGCTCCA	TGCCACAGAT	GCTGACATAG	1680
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	AAATTGCTCT	CATACTGTG	ACGGATAAGG	ATGCGGACCA	TAAATGGCAG	GTGACATGCT	2040
50	TCACAGATCA	TGAATCCCTT	TTCAGATTAA	GGCCAGTATT	CAGTAATCAG	TTCTCTCTGG	2100
	AGACTGCGAG	ATATCTTGAC	TATGAGTCCA	CAAAAGAATA	TGCCATTAAA	TTACTGGCTG	2160
	CGATGTCTGG	CAAACTCTCT	TTGAATCAGT	CAGCAATGCT	CTTCATCAAA	GTGAAAGATG	2220
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	CAGGATGCTG	GACTGTAGTG	AAGAACTAG	ATAGAGAAAA	AGAGGATAAA	TATTTATTCA	2460
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	GTGATGTTAC	AGACCTTGGT	TTACACAGAG	TGTTGGTCAA	AGCTAATGAC	TTAGGACAGC	3120
	CTGATTCTCT	CTTCAGTGT	GTAATTGTCA	ATCTGTTGCT	GAATGAGTGG	GTGACCAATG	3180
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70	AGTAGTCTGA	TGTATCTCTA	CCAACTAGTG	ACTATGTCAA	GATCCTGTTT	GCAGCTGTTG	3300
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	CACCACACCT	TAAAGCTGCT	CAGAAAACA	AGCAGAAATC	TGAATGGGCT	ACCCCAAAAC	3420
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	AGAACTTGCT	GCTTAAATTTT	GTCACTATTG	AAGAACTAA	GGCAGATGAT	GTGACAGTGG	3540
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	ACAATTGGGT	AACCTACACT	ACTACTTTCA	AGCCGACAG	CCCTGATTGG	GCCCGACACT	3660
	ACAAATCTGC	CTCTCCACAG	CCTGCTTCC	AAATTCAGCC	TGAACTCTCC	CTGAATTGCA	3720
	AGCAACCAT	CATCCAGAA	CTGCTCTCG	ATAACACCTT	TGTCGCTGCT	GACTCTATCT	3780
	CCAAAGTGTG	CTCAAGCAGT	TCAGATCCCT	ACAGGTTTC	TGACTGTGGC	TATCCAGTGA	3840
	CGAUCTTGA	GGTACCTGTG	TCCGTACACA	CCAGACCGGT	AGGTATCCAA	GTTTCTAACA	3900
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5 CTAGAGAATA TATTGAAAAA AACTTCAACA CAAAGGGTTG TAGCACTGTC CTCAGTACCA 4200
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 GCATATTAT GCAAGGTATT TTGAGCCCTT CAGAAGACAT TCT

10 Seq ID NO: B62 Protein sequence
 Protein Accession #: NP_055337.1

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 MQFKLVYKYG DVPLIRIEED TGEIPTTGAR IDREKLCAGI PRDEHCFYEV EVAILPDEIF 120
 RLVKIRFLIE DINDNAPLFP ATVINISIEP NSAINSKYTL PAAVDPDFGI NGVQNYELIK 180
 SQNIFGLDVI ETPGDKMPQ LIVQKELDRE EKDTYVMKVK VEDGGFPQRS STAILQVSVT 240
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 20 HLNATTLGIT IKESPLDREEST PNHKLVLAS DGLMPARAM VLVNVTDVND NVPSIDIRYI 360
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 AAYLDYESTK EYAIKLLAAD AGKPLNQSA MLFIKVKDEN DNAPVFTQSF VTSIPENNLS 480
 PGIQLTQVSA MDADSGBNAK INYLLGPDAP PEFSLDCRTG MLTVVKLLDR EKEDKYLFTI 540
 25 LAKDNGVPPL TSNVTVFVSI IDQNDNSPVF THNEYNFYVP ENLPRHGTVG LITVTDPDYG 600
 DNSAVTLLSL DENDDPTIDS QTGVIRPNIS FDREKQESYT FYVKAEDGGR VSRSSSAKVT 660
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 RDLFAIDQET NITILMERKD VTDLGLHRLV VKANDLQPD SLFSVVIVNL FVNESVTNAT 780
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 HLKRAQKNKQ NSEWATPMPE NRQMIMMKKK KKKKQHSPPN LLLNFVTIEE TKADDVDSG 900
 NRVTLDLPID LEEQTMGKYN WVTTPTFKP DSPDLARHYK SASPQAPQI QPETPLNSNT 960
 HIIQELPLDN TIVACDSISK CSSSSSDPYS VSDCGYFVIT FEVFSVHTR PVGIQVSNNT 1020
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35 Seq ID NO: B63 DNA sequence
 Nucleic Acid Accession #: XM_059180.2
 Coding sequence: 276..3740

40 1 11 21 31 41 51
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 GCGCGCTAGC GAGCCTGCGG GTGCGACCCA GCGAGCGCAG CGACGGGGGG CTGCGCTGGCC 180
 CAGGCGGCACA CGGAAGTGCG CTCTCTGTA GAGCTTTGG AAGTAGAGA AGAAAATCCA 240
 45 GTTGTCTCTC TGGAGAACAC TGGACAGCTG AATAAATGCA GTATCTAAAT ATAAAGAGG 300
 ACTGCAATGC CATGGCTTTC TGTGCTAAAA TGAGGAGCTC CAAGAAGACT GAGGTGAACC 360
 TGGAGGCCCC TGAGCCAGGG GTGGAAGTGA TCTTCTATCT GTCGACAGG GAGCCCCCTC 420
 GGCTGGGCGG TGGAGAGTAC ACAGCAGAGG AACTGTGCAT CAGGGCTGCA CAGGCATGCC 480
 GTATCTCTCC TCTTTGTGCA AACCTCTTTG CCTGTATGA CGAGAACACC AAGCTCTGGT 540
 50 ATGCTCCAAA TCGCACCATC ACCGTTGATG ACAAGATGTC CCTCCGGCTC CACTACCGGA 600
 TGAGGTTCTA TTTCACCAAT TGGCATGGAA CCAACGACAA TGAGCAGTCA GTGTGGCGTC 660
 ATTCTCCAAA GAAGCAGAAA AATGGCTACG AGAAAAAATA GATTCCAGAT GCAACCCCTC 720
 TCCTTGATGC CAGCTCAGTG GAGTATCTGT TTGCTCAGG ACAGTATGAT TTGGTGAAAT 780
 GCCTGGCTCC TATTGAGAGC CCCAAGACCG AGCAGGATGG ACATGATATT GAGAACGAGT 840
 55 GTCTAGGGAT GGCCTGCTCG GCCATCTCAC ACTATGCCAT GATGAAGAAG ATGCAAGTTC 900
 CAGAACTGCC CRAAGCATC AGCTACAGC GATATATTCC AGAAACATTG AATAAGTCCA 960
 TCAGACAGAG GAACCTTCTC ACCAGGATGC GGATAAATAA TGTTTTCAAG GATTCTCTAA 1020
 AGGAATTTAA CAACAAGACC ATTTGTGACA GCACGGTGTC CACGCATGAC CTGAAGGTGA 1080
 60 AATATCTTGC TACTTGGAAA ACTTTGACAA AACATTACGG TGCTGAATAA TTGAGACTT 1140
 CCATGTTACT GATTTCATCA GAAAATGAGA TGAATTGGTT TCATTGGAAT GACGGTGGAA 1200
 ACGTTCCTTA CTACGAGTG ATGGTGACTG GGAATCTTGG AATCCAGTGG AGGCATAAAC 1260
 CRAATGTTGT TTCTGTTGAA AAGGAAAAAA ATAAACTGAA GCGGAAAAAA CTGGAAAAATA 1320
 AACACAGAAA GGATGAGGAG AAAAAACAAGA TCGGGGAAGA GTGGAACAAT TTTTCTTACT 1380
 TCCTGGAAT CACTCACATT GTAATAAAGG AGTCTGTGGT CAGCATTAA CAGCAGGACA 1440
 65 ACAAGAAAAT GGAACGAAAG CTCTCTTCCC ACAGGAGGCG CTGTCTCTTT GTGTCCCTGG 1500
 TAGATGGCTA CTTCGGGCTC ACAGCAGATG CCCATCATT CTTCTGCACC GACGTGGGCC 1560
 CCCGTTGAT CGTCCACAAC ATACAGAATG GCTGTCTATG TOCAATCTGT ACAGAATAAG 1620
 CCATCAATAA ATTGCGGCAA GAAGGAAGCG AGGAGGGGAT GTACGTGCTG AGGTGGAGCT 1680
 GCACGACATT TGACAACATC CTCATGACCG TCACCTGCTT TGAGAAGTCT GAGCAGGTGC 1740
 70 AGGGTGCCCA GAAGCAGTTC AAGAACTTTC AGATCGAGGT GCAGAGGGCG CGCTACAGTC 1800
 TGCAOAGTTC GGAACGCGAG TTCCCCAGCT TGGGAGACCT CATGAGCCAC CTCAGAAGC 1860
 AGATCTCTGG CAGCGATAAC ATCAGCTTCA TGCTAAAAAG CTGCTGCCAG CCCAAGCCCC 1920
 GAGAAATCTC CAACCTGCTG GTGGCTACTA AGAAAGCCCA GGAGTGGCAG CCGCTCTACC 1980
 CCATGAGCCA GCTGAGTTTC GATCGGATCC TCAAGAAGGA TCTGTGTCAG GCGAGCACC 2040
 75 TTGGGAGAGG CACGAGAACCA CACATCTATT CTGGGACCCCT GATGGATTAC AAGGATGACG 2100
 AAGGAACCTT TGAAGAGAAG AAGATAAAG TGATCTCTCA AGTCTTAGAC CCCAGCCACA 2160
 GGGATATTTC CTGCGCTTC TCGAGGCAG CAGCATGAT GAGACAGGTC TCCACAAAC 2220
 ACATCGTGTG CCTCTATGGC GTCTGTGTCC GCGACGTGGA GAATATCATG GTGGAAGAGT 2280
 TTGTGGAAGG GGGTCTCTCT GATCTCTTCA TGCAACGGAA AAGCGATGTC CTTACCACAC 2340
 80 CATGGAATTT CAAAGTTGCC AAACAGCTGG CCAAGTCCCT GAGCTACTTG GAGGATAAAG 2400
 ACCTGGTCCA TGGAAATGTG TGTACTAAAA ACCTCTCTCT GGGCCGTGAG GGCACTGACA 2460
 GTGAGTGTGG CCGATTCATC AAGCTCAGTG ACCCGGCAT CCCCATTACG GTGCTGTCTA 2520
 GGCAGAAATG CATTGAACGA ATCCCATGGA TTGCTCTGTA GTGTGTTGAG GACTCCAAGA 2580
 ACCTGAGTGT GGCTGCTGAC AAGTGGAGCT TTGGAACACC GCTCTGGGAA ATCTGCTACA 2640
 ATGGGAGAGT CCCCTTGAAA GACAAGACGC TGAATTGAGAA AGAGAGATTCT TATGAAAGCC 2700

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GGTGAGGCC AGTGACACCA TCATGTAAGG AGCTGGCTGA CCTCATGACC CGCTGCATGA 2760
ACTATGACCC CAATCAGAGG CCTTCTCTCC GAGCCATCAT GAGAGACATT AATAAGCTTG 2820
AAGAGCAGAA TCAGATATAT GTTTCAGAAA AAAAACCAGC AACTGAAAGT GACCCACAC 2880
ATTTGAAAA GCGCTTCTCA AAGAGGATCC GTGACTTGGG AGAGGGCCAC TTTGGGAAGG 2940
TTGAGCTCTG CAGGTATGAC CCCGAAGGGG ACAATACAGG GGAGCAGGTG GCTGTTAAAT 3000
CTCTGAAGCC TGAGAGTGGG GGTAAACCACA TAGCTGATCT GAAAAAGGAA ATCGAGATCT 3060
TAAGGAACCT CTATCATGAG AACATTGTGA AGTACAAAGG AATCTGCACA GAAGACGGAG 3120
GAAATGGTAT TAAGCTCATC ATGGAATTTT TGCCTTGGGG AAGCCTTAAG GAATATCTTC 3180
CAAGAATAAA GAACAAAATA AACCTCAAAC AGCAGCTAAA ATATGCCGTT CAGATTTGTA 3240
AGGGGATGGA CTATTGGGGT TCTCGGCAAT ACGTTCACCG GGACTTGGCA GCNAGAAATG 3300
TCCTTGTGTA GAGTGAACAC CAAGTGAATA TTGGAGACTT CGGTTTAACC AAAGCAATTG 3360
AAACCGATAA GGAGTATTAC ACCGTCAAGG ATGACCGGGA CAGCCCTGTG TTTTGGTATG 3420
CTCCAGATAG TTTAATGCAA TCTAAATTTT ATATTGCCCT TGACGTCTGG TCTTTTGGAG 3480
TCACTCTGCA TGAGCTGCTG ACTTACTGTG ATTCAATTTC TAGTCCCATG GCTTTGTGCC 3540
TGAAATGAT AGGCCCAACC CATGGCCAGA TGACAGTCAC AAGACTTGTG AATACGTTAA 3600
AAGAAGGAAA ACGCCTGCCG TGCCCCACTA ACTGTCCAGA TGAGGTTTAT CAACTTATGA 3660
GGAAATGCTT GGAATTCCAA CCATCCAATC GGACAAGCTT TCAGAACCTT ATTGAAGGAT 3720
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TTCTGTCCAA AAAGTCACTG AACTCATACT TCAGTACATA TACATGTATA AGGCACACTG 3900
TAGTGCTTAA TATGTGTAAG GACTTCCTCT TTAATTTTGG TACCAAGTAA TTAGTGACAC 3960
ATAATGACAA CAAAATATT TGAAAGCACT TAAGCACTCC TCCTTGTGGA AAGAATATAC 4020
CACCATTTC TCTGGCTAGT TCACCATCAC AACTGCATTA CCAAAAGGGG ATTTTGTAAA 4080
ACGAGGAGTT GACCAAAATA ATATCTGAAG ATGATTGCTT TTCCCTGCTG CCAGCTGATC 4140
TGAAATGTTT TGCTGGGCACA TTAATCATAG ATAAAGAAAG ATTGATGGAC TTAGCCCTCA 4200
AATTTGAGTA TCTATACAGT ACTAGACCAT GCATTCTTAA AATATTAGAT ACCAGGTAGT 4260
ATATATTGTT TCTGTACAAA AATGACTGTA TTCTCTCACC AGTAGGACTT AAACTTTGTG 4320
TCTCCAGTGG CTTAGCTCCT GTTCTCTTGG GTGATCACTA GCACCCATT TTAGAGAAAGC 4380
TGGTTCTACA TGGGGGGGATA GCTGTGGAAT AGATAATTG CTGCATGTTA ATTCTCAAGA 4440
ACTAAGCCTG TGCCAGTGCT TTCCTAAGCA GTATACCTTT AATCAGAACT CATTCCCGA 4500
ACCTGGATGC TATTACACAT GCTTTTAAAG AACGTCAATG TATATCCTTT TATAACTCTA 4560
CCACTTTGGG GCAAGCTATT CCAGCACTGG TTTTGAATGC TGTATGCAAC CAGTCTGAAT 4620
ACCACATACG CTGCACTGTT CTTAGAGGGT TTCCATACCT ACCACCGATC TACAAGGGTT 4680
GATCCCTGTT TTTACCATCA ATCATCACCC TGTGGTGCAA CACTTGAAG ACCCGGCTAG 4740
AGGCATATG GACTTTCAGG TCCACTAGAC AGTTTTCAGT TTGCTTGGAG GTAGCTGGGT 4800
AATCAAAAT GTTTAGTCAT TGATTCAATG TGAAGGATTA CGGTCTTAT GACCAAGAGT 4860
CTGAAAATCT TTTTGTATG CTGTTAGTA TTGCTTGTG ATTGTTACTT TTCACCTGTT 4920
GAGCCCAAT TACAGATTGG TTCAGTGGCA GCAATGAAGT TGCCATTTAA ATTTGTTTAT 4980
AGCCTACATC ACCAAGGTCT CTGTGTCAA CCTGTGGCCA CTCTATATGC ACTTTGTTTA 5040
CTCTTTATAC AAATAAATAT ACTAAAGACT TT

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Seq ID NO: B64 Protein sequence
Protein Accession #: A39577

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1 11 21 31 41 51
| | | | |
MQYLNKEDC NAMAPCAKMR SSKKTEVNLE APEPGVEVIF YLSDREPLRL GSGEYTAEEEL 60
CIRAAQACRI SPLCNLFAL YDENTKLWYA PNRTITVDDK MSLRLHYRMR FYPTNWHGTN 120
DNEQSVWRHS PKQKNGYEK KKIIPDAPLL DASSLEYLFA GGQYDLVKCL APIRDPKTEQ 180
DGHDIENECI GMAVLAISHY AMMKMQLPE LPKDISYKRY IPETLNSIR QRNLLTMRI 240
NNVFKDFLKE FNNKTI CDSS VSTEDLKVKY LATLETLLKH YGAEIPETSM LLISSENEMN 300
WFHSDGNGV LYEYVMVTGN LGIQWREKFN VVSVBKERNK LKRLKLENKD KDDEKKNKIR 360
EWNWNSFSEF EETHIVIKES VVSINKQDNK KMLKLSSEH EALSFSVLVD GYFRLTADAH 420
HYLCTDVAPP LIVHNIQNGC HGPICTEYAI NKLKRBGSEE GMYVLRWSTC DFDNILMTVT 480
CFEKSQVQGG AQKQFKNFQI EVQKGYSILH GSDRSFPLSG DLSHLKQKI LRTDNISFML 540
KRCCQPKPRE ISNLLVATKK AQEWQPVYPM SQLSFDRILK KDLVQGEHLG RGTRTHIYSG 600
TLMYKDDDEG TSEEKKIKVI LKVLDPSHRD ISLAPPEAAS MMRQVSHKHI VYLYGVCVRD 660
VENIMVEEFV EGGPILDFMH RKSDVLTTPW KFKVAKQLAS ALSYLEDKDL VHGNVCTKNL 720
LLAREGIDSE CGPFIKLSDF GIPITVLSRQ ECIERIPWIA PECVEDSKNL SVAADKNSFG 780
TTLWEICYNQ EIPLKDKTLI EKERFYESRC RPTVPSCKEL ADLMTROMNY DPNQRPPFRA 840
IMRDINKLEE QNPDI VSRKK NQPTVDPTH FEKRLKRLR DLGEGHFGKV ELCRYDPEDN 900
TGEQVAVKSL KPESGGNHIA DLKKEIEILR NLYHENIVRY KGICTEDGGN GIKLIMEFPL 960
SGSLKEYLEP NKNKINLKQQ LKYAVQICKG MDYLGSRQYV HRDLAARNVL VESEHQVKIG 1020
DFGLTKAIET DKEYYTVKDD RDSVPFWYAP ECLMQSKFYI ASDVMSFGVT LHELLTYCDS 1080
DSSPMALFLK MIGPTHGQMT VTRLVNTLKE GKRLPCCPNC PDEVYQLMRK CNEFPQSNRT 1140
SPQNLIIEGFE ALLK

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Seq ID NO: B65 DNA sequence
Nucleic Acid Accession #: NM_004867.1
Coding sequence: 140..931

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1 11 21 31 41 51
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GATCCAGAGC CTCGGCTTGC AGTAGTGTGA GACTGAAGAT AAAGTAAGTG CTGTTTGGGC 60
TAACAGGATC TCCTCTTGCA GTCTGCAGCC CAGGAAGCTG ATTCCAGCAG CGCCTTACCG 120
CGCAGCCGGA AGATTCACTA TGGTGAAAAA CGCCTTCAAT ACCCTACCG CGGTGCAAAA 180
GGAGGAGGGG CGGCAAGAGG TGGAGGCCCT CTGAGCCGCG ACGGTGAGAA CTCAGATACT 240
GACCGGCAAG GAGCTCCGAG TTGCCACCCA GGAAGAAAGG GGCTCCTCTG GGAGATGTAT 300
GCTTACTCTC TTAGGCCTTT CATTATCTT GGCAGGACTT ATTGTTGGTG GAGCCTGCAT 360
TTACAAGTAC TTCAATGCCA AGAGCACCAT TTACCGTGGG GAGATGTGCT TTTTGTATTC 420
TGAGGATCTC GGAATATCCC TTGTTGGAGG AGAGCCTAAC TTCTGCGCTG TGACTGAGGA 480
GGCTGACATT CGTGAGGATG ACACATTGCG AATCATGTAT GTGCTGTGCC CCAAGTTCTC 540
TGATAGTGAC CCTGCAGCAA TTATTATGTA CTTTGAAGAG GGAATGACTG TTACTCTGGA 600
CTGTGTGCTG GGGAACTGCT ATCTGATGCC CCTCAATACT TCTATTGTGA TCCTCCAAA 660

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AAATCTGGTA GAGCTCTTTG GCAAACTGGC GAGTGGCAGA TATCTGCCTC AAACCTATGT 720
 GGTTCCGAGAA GACCTAGTTG CTGTGGAGGA AATTCGTGAT GTTAGTAACC TTGGCATCTT 780
 TATTTACCAA CTTTGCATAA ACAGAAAGTC CTTCGCGCTT CGTCGAGAG ACCTCTTGCT 840
 GGGTTTCAAC AAACGTGCCA TTGATAAATG CTGGAAGATT AGACACTTCC CCAAGGAATT 900
 TATTTGTGAG ACCAAGATCT GTCAGAGTA AGAGGCAACA GATAGAGTGT CCTTGGTAAT 960
 AAGAAGTCAG AGATTTACAA TATGACTTTA ACATTAAGGT TTATGGGATA CTCAGATAT 1020
 TTACTCATGC ATTTACTCTA TTGCTTATGC CGTAAAAAAA AAAAAA AAAA 1080
 AA

Seq ID NO: B66 Protein sequence
 Protein Accession #: NP_004858.1

1 11 21 31 41 51
 MVKIAFNPT AVQKEEARQD VEALLSRTVR TQILTGKELR VATQKEKGSS GRCLMTLLGL 60
 SFILAGLIVG GACIYKYFMP KSTIYRGEMC PFDSEDPANS LRGGEPNPLP VTEEADIRE 120
 DNIAIIDVPV PSFSDSDPAA IHDPEKGMT AYLDLLLGNC YLMLPLNTSIV MPPKNLVELF 180
 GKLAGSRYLP QTVVREDLV AVEEIRDVS N LGIFYQLCN NRKSFRLRRR DLLLGFNKRA 240
 IDKCWKIRHF PNEFIVETKI COE

Seq ID NO: B67 DNA sequence
 Nucleic Acid Accession #: XM_083862.1
 Coding sequence: 121..813

1 11 21 31 41 51
 ACGCGGGAGG TCTGAGTGT GGGCTGAGGC AGCGCAGCCG CTGCGCCAGG GTGCGCGATG 60
 CCTTGAACCT GGGAACTAT GTGAAGCAAC ACTCTGGATT TTGAAAGACA TCITTTTCATC 120
 ATGGGACAGC AAATTTCCGA TCAGACACAG TTGGTTATTA ACAAGTACAC AGAAAAAGTA 180
 GCAAAACATG TTACGTTGGT TCGAGAGAGT GGCTCCTTAA CTTATGAAGA ATTTCTCGGG 240
 AGAGTAGCTG AGCTTAATGA TGTACGGCT AAAGTGGCTT CTGGCCAGGA AAAACATCTT 300
 CTCCTTGAGG TACAACCTGG GTCTGATTCC TCTGCTTTT GGAAAGTGGT TGTACGGGTG 360
 GTCTGTACCA AGATTAAACA AAGCAGTGGC ATTGTGGAGG CATCACGGAT CATGAATTTA 420
 TACCAGTTTA TTCAACTTTA TAAAGATATC ACAAGTCAAG CAGCAGGAGT ATCGGCACAG 480
 AGCTCCACCT CTGAAGAACC TGATGAAAC TCATCCTCTG TAACATCTTG TCAGGCTAGT 540
 CTTTGGATGG GAAGGGTGAA GCAGCTGACC GATGAGGAGG AGTGTGTAT CTGTATGGAT 600
 GGGCGGGCTG ACCTCATCTT GCCTTGTGCT CACAGCTTTT GTCAGAAGTG TATTGATAAA 660
 TGGAGTGATC GACACAGGAA TTGCCCTATT TGTGCGCTAC AGATGACTGG AGCAAAATGA 720
 TCTTGGGTGG TATCAGATGC ACCCACTGAA GATGATATGG CTAACATAT TCTTAACATG 780
 GCTGATGAGG CAGGCCAGCC CCACAGGCCA TGACCTTGAA GTGAAAGTCT TCTGTGCTA 840
 TTGTGGGCTC AAATATTGG TCAATGGGGA AGAATGTAGG GTTGTGGCAC TGGCACAGAC 900
 ACAGGAAAT ACTTTTCCC CACTCTTTA TTTTGTCTAT TCTGATCAT TGTCCCCCTT 960
 TTAATAATAA CATTCCCATG TCTTCAAAA AAAAAA AAAA

Seq ID NO: B68 Protein sequence
 Protein Accession #: XP_083862.1

1 11 21 31 41 51
 MQQISDQTO LVINKLPEKV AKHVTIVRES GSLTYEEFLG RVALNDVTA KVASQEKHL 60
 LFEVQPGSDS SAFWKVVVRV VCTKINKSSG IVEASRIMNL YQFIQLYKDI TSQAAGVLAQ 120
 SSTSEEPDEN SSVVTSQAS LWMGRVKQLT DEBECCICMD GRADLILPCA HSPCKKCIDK 180
 WSDRHRNCPI CRLQMTGANE SWVVSADPTE DDMANYILNM ADEAGQPHRP

Seq ID NO: B69 DNA sequence
 Nucleic Acid Accession #: NM_002975.1
 Coding sequence: 180..1151

1 11 21 31 41 51
 CGACCAACGG ACCGGACAGA GACGAGGAGA GGAACAGGAA GAGAGAAGCT GGGAGAATCG 60
 GGAACCTGGG GGCTAGTGAC CTGCACACAG GGCAGGGGCA CTGCGCAGTT CCCAGAGGCC 120
 ACCCTCCCA CCCAGACAT CCAGACATCT GGAACCTTGG GTGCCAAGAG TCCAGCTTAA 180
 TGCAGGCAGC CTGGCTTTTG GGGCTTTTGG TGGTCCCCCA GCTCTTGGGC TTTGGCCATG 240
 GGGCTCGGGG AGCAGAGAGG GAGTGGGAGG GAGGCTGGGG AGGTGCCAG GAGGAGGAGC 300
 GGGAGAGGGA GGCCCTGATG CTGAAGCATC TGCAGGAAGC CCTAGGACTG CCTGCTGGGA 360
 GGGGGGATGA GAATCCTGCC GGAACCTTGG AGGGAAGAAG GGAAGTGGAG ATGAGGAGG 420
 ACCAGGGGGA GGAAGAGGAG GAGGAAGCAA CGCCAAACCC ATCCTCCGGC CCCAGCCCTC 480
 CTCCCAACCC TGAGGACATC GTCACTTACA TCCTGGGCGG CCTGGCCGGC CTGGACGCAG 540
 GCCTGCACCA GCTGCACTG CGTCTGCACG CGTTGGACAC CCGGTGAGTC GAGCTGACCC 600
 AGGGGCTGGG GACGCTGGG AACGGGGCAG GCGACACCGG CGATGCGGTG CAAGCCCTGC 660
 AGGAGGGGCA GGGTCGGGCC GAGCGCGAGC ACGCGCGCTT GGAGGGCTGC CTGAAGGGGC 720
 TGGCGCTGGG CCACAAGTGC TTCTGTCTCT CGCGCGACTT CGAAGCTCAG GGGCGGGCGC 780
 AGGCGCGGTG CACGGCGCGG GCGGGGAGCC TGGCGCAGCC GGCAGACCGC CAGCAGATGG 840
 AGGCGCTCAC TCGGTACCTG CGCGCGGGCG TCGCTCCCTA CAACTGGCCC GTGTGGCTGG 900
 GCGTGCACGA TCGCGCGGCC GAGGGCTCT ACCTCTTGA AAACGGCCAG CGCGTGTCT 960
 TCTTGCCTG GCATCGCTCA CCGCGCCCGG AGCTCGGCGC CAGCGCCAGC GCCTGGCGGC 1020
 ATCCGCTCAG CCGGACAGG CCCAACGGTG GCACGCTCGA GAACTGCGTG GGCAGGCGCT 1080
 CTGACGACGG CTCCTGTGTG GACCAAGACT GCGAGGGGCG TCTTACTAC GTCTGCGAGT 1140
 TCCCTTCTTA CGGGGGCGGG TACCCGCGCT CCTTGGCCAT CCCACCAACC GGCTTTTCCC 1200
 TCGCGCGTGC CACCCCTCT COGGAATGSC CTTTCCCTTC CTGGCCACGA ATGGCAGCGT 1260
 CCTCCCGGAC CCCCAGTCTG GCGGCTTCTG GAGGGGCTCT TCGGCTGCGC GCACTCTCTC 1320
 TTGTTAGTGT CTTTCTTGA AGGGGCGGGC ACCAGGCTAG GTCGCTGGCC AATAAATCCT 1380
 TGTGGAATCT GAAAAA AAAA

Seq ID NO: B70 Protein sequence
Protein Accession #: NP_002966.1

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5      1      11      21      31      41      51
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MQAANLLGAL VVPQLLGFH GARGAEREWE GWMGGAQEEREREREALMLKH LQEAALGLPAG 60
RGDENPAGTV EGKEDWEMEE DQGEHEEEEA TPTPSSGSPSPTPEDIVTY ILGRLAGLDA 120
GLHQLHVRHL ALDTRVVELT QGLRQLRNAA GDTRDAVQAL QEAQGRAERE HGRLEGCLKG 180
10    LRLGHKCPFL SRDFEAQAAA QARCTARGGS LAQPADRQOM EALTRYLRAA LAPYNWVWL 240
GVHDERAEGE YLFENGQRVS FFAWHRSPRF ELGAQPSASE HPLSPDQPNG GTLENCVAQA 300
SDDGSWWHDH CQRRLYVCE FPF

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Seq ID NO: B71 DNA sequence
Nucleic Acid Accession #: BC000839.1

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15      1      11      21      31      41      51
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CTGGCCAGGG CGACTGCGCG ATAAGGCTCT GTGCGTGGCC TCGAGGCTTA AAAGTAGCAG 60
20    TGGGGCTTTG TGAAAGGACAA AATGGCGATG GCGGGCCGTG TAGGTCCCCC TTCCTATGAT 120
GAGGACCTTT TCACAGACCT GTACTGAGCT CCGTGAGGAT AAGTAACTCT GAGGAGATGG 180
GCCCTGCAAG CCTCTTCTTT AGCCGCTCTGT TCAGAAAATA GCGTTTTCGA AATGCCCTGA 240
GTTGACCTAA TGCTCTATTG GGCTCCTGTC TGCAGGATTT ACGCGCACGT TGGAAACGAA 300
GAGAGCTCTG TTGTTGCAAT GTTCAGCCCA CAAGAGCTTA CTGCTGAAGG AATGGGACAA 360
GACCCATCTT TATGCAAAGC CAGCGTTACA GTAATGTTCC AGCATCTCAT AATCTATCCT 420
GGGGAATTCG GCTGCCCTCC AGGGTGAATA CAGGTATTCC TGATGACAGT CTGCCCTCTAT 480
CTTACAGAGC AGCTTGTTGC TATATACCAT TGAAAAGCCT TCAGAGCTGA GAGGTACTAC 540
TAACCAATAA CCTGCTTGGC TCAAAAGGCC AGCACCTTCT CTCTAAAGCC CAAGAGGAGT 600
TTCAGGAAAA CTAGGTGTCT GTGTTCACCT CAGGCTGAAG TTACAGGTCT GAGCAATAAA 660
GGTGTATATA AATAGGAATC TGTCTTGGAG GACATCAGAA GGTGAATTTT CCAAGTTCTT 720
GGACAACCTA GCTGTTGAAA AGCTTTCTGG GTTTGGGGGG TATTTCAGAT GTACCTTAAA 780
GTGTTAGCAG ATACAGATTA AGACACTGGG AGCCAATGAA ACAGCAGTTG AGGGTTTGCT 840
GTGTATCACA TTTCTGTATT TTATCACCCT CTTCCTGCAA CATTATTTAT CTGGAATCTA 900
CCTGCCCTTT TGTTTTTTAG ATACAAGGGC TTGGTTTTGT TACCCAGGCT GGTTCAGAG 960
CCATAGCTTT AAGAGACCTT CTCACCAAGG ATTTCCAAAG TGCTGGGATT GCAGGTGTGA 1020
TTCATGCGAC CCAGACTTTG CTGCCCTTCT TACATGATCC AGGCCACGAA CCCAAACTCA 1080
GGCACTGTAT AGATGACCAC TTTCGTAAAC TACTGACCTA GCTTGTGGCC AATGTGTGAT 1140
TGAACITCCC ATAACCTCCAC TTGCTGTCTG TTCTCTGTGA TACAGCCACC TTCTGTTCCTC 1200
GTCTAGAGCC TTAGGCTCTC CATTGTGCATA TTGCAAAATC TATGTTCCAT GTAGGTAGCT 1260
40    CATTCAGGCC CTGCTCTCTC ACTTCAAAAA AGGTTCCCTT GAGGACTGGC TGTCAATTTG 1320
TGTGCTGTGT TTGTTGTTG ATGAAATAA TAAATGATT GATTACATAA AAAAAAATAA 1380
AAAAAA

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Seq ID NO: B72 DNA sequence
Nucleic Acid Accession #: CAT cluster

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45      1      11      21      31      41      51
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TGCTAGTAGG GCCTGGGTTA ATCGGCCGAG GGTGGCTTGG TGGTCTTTAT AGCTGTTACT 60
50    CTTGTACTT GTCTTTTCT TTTATTTCT TTTGAGCGAT TGTGCGAACA TAGCATAGCA 120
CGCACTATGG CACGAGGCTC GTGCTGCTCG GCCAGGGCGA CTGGCGGATA AGGCTCTGTG 180
CGTGCCCTCG AGGCTTAAAA GTAGCAGTGG GGCCTTTTGA AGGACAAAAT GCGGATGGCG 240
GGCGGTGTAG GTCCGCCCTC CTATGATGAG GACCTTTTCA CAGACCTGTA CTGAGCTCCG 300
TGAGGATAAA TAACTCTGAG GAGATGGGCC CTGCAAGCCT CTGCTTAGC CGTCTGTCTA 360
55    GAAAATAGCG TTTTCGAAAT GCCCTGAGTT GACCTAATGT CTTATTGGGC TCCTGTCTGC 420
AGGATTTACG CGCACGTTGG AACCGAAGAG AGCTCTGTGG TTGCAATGTT CAGCCCAACA 480
GAGCTTACTG GTGAAGGAAT GGGACAAGAC CCATCTTTAT GCAAGGCCAG CGTTACAGTA 540
ATGTTCCAGC ATCTCATAAT CTATCTGGG GAATTGAGCT GCCTCCGAGG GTGAATACAG 600
GTATTCTCGA TGACAGTCTG CCTCTATCTT ACAGAGCAGC TTGTTGCTAT ATACCATTTA 660
60    AAAGCCTTCA GAGCTGAGAG GTACTACTAA CCAATAACCT GCTTGGCTCA AAGGGCCAGC 720
ACCTTCTCTC TAAAGCCCAA GAGGAGTTTG AGGAAAACTA GGTGTCGTG TTCACTCCAG 780
GCTGAAGTTA CAGGCTCTGAG CAAATAAGGT GTATAAAAAA TGGAACTCTG CTGAGGAGAC 840
ATCAGAAGGT GAATTTTCCA AGTTCTTGA CAACTAGCT GTTGAAGAGC TTTCTGGGTT 900
TGGGGGGTAT TTCAAGTATA CCTTAAAGTG TTAGCAGACA CAGATTAGA CACTGGGAGC 960
65    CAATGAAACA GCAGTTGAGG GTTTGCTGTG TATCACATTT CTGTATTTTA TCACCCCCTT 1020
CCTGCAACAT TATTTATCTG GAATCTACCT GCCCTTTTGT TTTTATAGATA CAAGGGCTTG 1080
GTTTGTGTTAC CCAGGCTGTG TTCAAGGCCA TAGCTTTAAG AGATCCTCTC ACCACAGATT 1140
TCCAAGTGC TGGGATTGCA GGTGTGATTC ATGGCACCCT GACITTTGCTG CCTTCTTAC 1200
70    ATGATCCAGG CCCAGAACCC AAACCTCAGG ACTGTATAGA TGACCACTTT CGTAAACTAC 1260
TGACCTAGCT TGTGTCGAAT TGTGATTGA ACTTCCATA ACTCCACTTC GTGCTGTGTC 1320
CTCTGTATAC AGGCACCTTC TGTCCCGTC ATGAGCCTTT AGGTCTCCAT TTGCATATTG 1380
CAATACTACT GTTCCATGTA GGTAGCTCAT TCAGGGCCTT GCTCTTCACT TCAAAAAAGG 1440
TTCCCTTGAG GACTGGCTGT CAATTGTGT TGTGTGTGTG GTTGTGTATG AAAAAATAA 1500
75    AATGATTGAT TACATAAAAA AAAAAAATAA AAAAAAATAA AAAAAAATAA CAAAAAAT 1560
GCGCGGCTT TTTCCCGGGC GCACAAAGTT ATAAACGCC GTCCATC

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Seq ID NO: B73 sequence
Nucleic Acid Accession #: NM_000222.1
Coding sequence: 22..2952

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80      1      11      21      31      41      51
|      |      |      |      |      |
GATCCCATCG CAGCTACCGC GATGAGAGGC GCTCGCGCGC CCTGGGATTT TCTCTGCGTT 60
CTGCTCTCTAC TGCTTCGCGT CCAGACAGGC TCTTCTCAAC CATCTGTGAG TCCAGGGGAA 120

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	CCGTCTCCAC	CATCCATCCA	TCCAGGAAAA	TCAGACTTAA	TAGTCCGCGT	GGGCGACGAG	180
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	ACGAATGAGA	ATAAGCAGAA	TGAATGGATC	ACGGAAAAGG	CAGAAGCCAC	CAACACCGGC	300
5	AAATACACGT	GCACCAACAA	ACAOGGCTTA	AGCAATTCCA	TTTATGTGTT	TGTTAGAGAT	360
	CCTGCCAAGC	TTTTCCCTGT	TGACCGCTCC	TTGTATGGGA	AAGAAGACAA	CGACACGCTG	420
	GTCCGCTGTC	CTCTCAGAGA	CCCAGAAGTG	ACCAATTATT	CCCTCAAGGG	GTGCCAGGGG	480
	AAGCCTCTTC	CCAAGGACTT	GAGGTTTATT	CCTGACCCCA	AGGCGGGCAT	CATGATCAAA	540
	AGTGTGAAAC	GGCGCTACCA	TCGGCTCTGT	CTGCATTGTT	CTGTGGACCA	GGAGGGCAAG	600
10	TCAGTGTCTG	GGGAAAATTT	CATCCTGAAA	GTGAGGCCAG	CCTTCAAAGC	TGTGCTGTTT	660
	GTGTCTGTGT	CCAAGCAAG	CTATCTTCTT	AGGGAAGGGG	AAGAATTCAC	AGTGACGTGC	720
	ACAATAAAAG	ATGTGTCTAG	TTCTGTGTAC	TCAACGTGGA	AAAGAGAAAA	CAGTCAGACT	780
	AAACTACAGG	AGAAATATAA	TAGCTGGCAT	CACGGTGACT	TCAATTATGA	ACGTCAGGCA	840
	ACGTTGACTA	TCAGTTCAGC	GAGAGTTAAT	GATTCTGGAG	TGTTTCATGTG	TTATGCCAAT	900
15	AATACTTTTG	GATCAGCAAA	TGTCACRACA	ACCTTGGAA	TAGTAGATAA	AGGATTCATT	960
	AATATCTTCC	CCATGATAAA	CACCTACAGTA	TTTGTAAACG	ATGGAGAAAA	TGTAGATTGG	1020
	ATTGTTGAAT	ATGAAGCAAT	CCCCAARCTT	GAACACCAAG	AGTGGATCTA	TATGAACAGA	1080
	ACCTTCACTG	ATAAATGGGA	AGATTATCCC	AAGTCTGAGA	ATGAAAAGTAA	TATCAGATAC	1140
	GTAAAGTAAT	TTATCTTAAC	GAGATTAAAA	GGCACCGAAG	GAGGCCACTTA	CACATTCCTA	1200
	GTGTCCAAAT	TGTACGCTCA	TGCTGCCATA	GCATTAAATG	TTTATGTGAA	TACAAAACCA	1260
20	GAAATCCTGA	CTTACGACAG	GCTCGTGAAT	GGCATGCTCC	AATGTGTGGC	AGCAGGATTG	1320
	CCAGAGCCCA	CAATAGATTG	GTATTTTTGT	CCAGGAACCTG	AGCAGAGATG	CTCTGCTTCT	1380
	GTACTGCCAG	TGGATGTGCA	GACACTAAAC	TCATCTGGGC	CACCGTTTGG	AAAGCTAGTG	1440
	GTTCAGAGTT	CTATAGATTG	TAGTGCAATC	AAGCACAATG	GCACGGTTGA	ATGTAAGGCT	1500
25	TACAACGATG	TGGGCAAGAC	TTCTGCCTAT	TTTAACTTTG	CATTTAAAGG	TAACAACAAA	1560
	GAGCAAAATC	ATCCCCACAC	CCTGTTCACT	CCTTTGCTGA	TTGGTTTCGT	AATCGTAGCT	1620
	GGCATGATGT	GCATTATTGT	GATGATTCTG	ACCTACAAAT	ATTACAGAAA	ACCCATGTAT	1680
	GAAATACAGT	TGAAGGTGGA	TGAGGAGATA	AATGGAAAACA	ATTATGTTTA	CATAGACCCA	1740
	ACACAACCTC	CTTATGATCA	CAAATGGGAG	TTTCCCAGAA	ACAGGCTGAG	TTTTGGGAAA	1800
30	ACCTCGGGTG	CTGGAGCTTT	CGGGAAGGTT	GTGAGGCCAA	CTGCTTATGG	CTTAATTAAAG	1860
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	TGCTATGGTG	ATCTTTTGAA	TTTTTTTGAGA	AGAAAACGTG	ATTCAATTAT	TTGTTCAAAG	2100
35	CAGGAAGATC	ATGCGAAGAG	TGCACCTTAT	AAGAACTCTC	TGCATTCAAA	GGAGTCTTCC	2160
	TGCAGCGATA	GTACTAATGA	GTACATGGAC	ATGAAACCTG	GAGTTTCTTA	TGTTGTCCCA	2220
	ACCAAGGCCG	ACAAAAGGAG	ATCTGTGAGA	ATAGGCTCAT	ACATAGAAAG	AGATGTGACT	2280
	CCCGCCATCA	TGGAGGATGA	CGAGTTGGCC	CTAGACTTAG	AAGACTTGCT	GAGCTTTTCT	2340
	TACCAGGTGG	CAAAGGGCAT	GGCTTTCTCT	GCCTCCAAGA	ATTGTATTCA	CAGAGACTTG	2400
40	CGAGCCAGAA	ATATCCTCCT	TACTCATGGT	CGGATCACAA	AGATTGTGTA	TTTTGGTCTA	2460
	GCCAGAGATA	TCAAGCAATGA	TTCTAATTAT	GTGGTTAAAG	GAACCGCTCG	ACTACCTGTG	2520
	AAGTGGATGG	CACCTGAAAG	CATTTTCAAC	TGRTATACA	CGTTTGAAAG	TGACGTCTGG	2580
	TCCTATGGGA	TTTTTCTTTG	GGAGCTGTTC	TCITTAGGAA	CGAGCCCCTA	TCCTGGAATG	2640
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45	CACGCACCTG	CTGAAATGTA	TGACATAATG	AAGACTTGCT	GGGATGCAGA	TCCCTTAAAA	2760
	AGACCAACAT	TCAAGCAAT	TGTTCACTGA	ATTGAGAAGC	AGATTTCAGA	GAGCACCAAT	2820
	CATATTTACT	CCAACCTTAG	AAACTGCAGC	CCCAACCGAC	AGAAGCCCGT	GGTAGACCAT	2880
	TCTGTGCGGA	TCAATTCTGT	CGGCAGCACC	GCTTCTCTCT	CCCAGCCTCT	GCTTGTGCAC	2940
	GAGCATGTCT	GAGCAGAAATC	AGTGTTTGGG	TCACCCCTCC	AGGAATGATC	TCITCTTTTG	3000
50	GCCTCCATGA	TGGTTATTTT	CTTTCTTTTC	AACTTGCTATC	CAACTCCAGG	ATAGTGGGCA	3060
	CCCCATGCA	ATCCGTCTTT	TCAGAGCACA	CTTTAGTGGC	CGATGATTTT	TGTCATCAGC	3120
	CACCATCTTA	TTGCAAGGTT	TCCAACGTGA	TATATTCCCA	ATAGCAACGT	AGCTTCTACC	3180
	ATGAACAGAA	AAACATTCTGA	TTTGGAAGAA	GAGAGGGAGG	TATGGACTGG	GGGCCAGAGT	3240
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55	GGTAGTAATC	ACAGTTGGCC	TTCAGAACCA	TCCATAGTAG	TATGATGATA	CAAGATTAGA	3360
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	ATGAACACCT	GGGCTTAAGA	AATCTAGTAT	TTCTATGCTG	GAATGAGACA	TAGGCCATGA	3480
	AAAAAATGAT	CCCCAAGTGT	GAACAAAAGA	TGCTCTTCTG	TGGACCACTG	CATGAGCTTT	3540
	TATACTACCG	ACCTGCTTTT	TAAATAGAGT	TTGCTATTAG	AGCAATTGAAT	TGGAGAGAAG	3600
60	GCCTCCCTAG	CCAGCACTTG	TATATACGCA	TCTATAAATT	GTCCGTGTTC	ATACATTGTA	3660
	GGGGAAGAAC	CCATAAGGTT	TCGTTTCTGT	ATACAACCTT	GGCATTATGT	CCACTGTGTA	3720
	TAGAAGTAGA	TTAAGAGCCA	TATAAGTTTG	AAGGAACAG	TTAATACCAT	TTTTTAAGGA	3780
	AACAATATAA	CCACAAAGCA	CAGTTTGAAC	AAAATCTCCT	CTTTTAGCTG	ATGAACCTAT	3840
	TCGTAGATT	CTGTGGAACA	AGCCTATCAG	CTTCAGAAATG	GCATGTACT	CAATGGATTT	3900
65	GATGCTGTTT	GACAAAGTTA	CTGATTCACT	GCATGGCTCC	CACAGGAGTG	GGAAAACACT	3960
	GCCATCTTAG	TTTGGATTCT	TATGTAGCAG	GAATAAAGT	ATAGGTTTAG	CCTCCTTCGC	4020
	AGGCATGTCC	TGGACACCGG	GCCAGTATCT	ATATATGTGT	ATGTACGTTT	GTATGTGTGT	4080
	AGACAAATAT	TTGGAGGGGT	ATTTTGGCCC	TGAGTCCAAG	AGGGTCTTTT	AGTACCTGAA	4140
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70	TAGCTTACCA	GAAGCTTCCA	TAGTGGTGCA	GAGGAAGTGG	AAGGCATCAG	TCCCTATGTA	4260
	TTTGCACTTC	ACCTGCACCT	AAGGCACCTT	GTTATTTAGA	CTCATCTTAC	TGTACCTGTT	4320
	CCTTAGACCT	TCCATAATGC	TACTGTCTCA	CTGAAACATT	TAAATTTTAC	CCTTTAGACT	4380
	GTAGCCTGGA	TATTTATCTT	GTAGTTTACC	TCTTTAAAAA	CAAAACAAAA	CAAAACAAAA	4440
	AACCTCCCTT	CCTCAGTCCC	CAATATAAAA	GGCAAAATGTG	TACATGGCAG	AGTTTGTGTG	4500
75	TTGTCTTGAA	AGATTTCAGG	ATGTTGCCTT	TATGGTTTCC	CCCTTCTACA	TTTCTTAGAC	4560
	TACATTTAGA	GAACCTGTGG	CGTTATCTGG	AAGTAACCAT	TTGCACTGGA	GTCTTATGCT	4620
	CTCGACCTTG	TGTAAGTTTA	ACAGATTTTG	GGGTTGTGTT	GTCAACCAAG	AGATTGTTGT	4680
	TTGCCATACT	TTGTCTGAAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4740
	AAGTGGTTGT	TAGTTATAGA	TGTTCTAGGA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTGC	4800
80	TTGCCATACT	TTGTCTGAAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4860
	AAGTGGTTGT	TAGTTATAGA	TGTTCTAGGA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTGC	4920
	AATGCTTTT	GAAATTTCCC	AAGCCCATGA	GTCCCTGAAA	ATATTTTTTA	TATATACAGT	4980
	AACCTTATGT	GTAATATACAT	AAGCGGCGTA	AGTTTAAAGG	ATGTTGGTGT	TCCACGTGTT	5040
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Seq ID NO: B74 protein sequence
Protein Accession #: NP_000213.1

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DRSLYGKEDN DTLVRCPLTD PEVTNYSLKG CQKPLPKDL RFIPDPKAGI MIKSVKRAYH 180
RLCLHCSVDQ EGKSVLSEKF ILKVRPAFKA VPVSVSKAS YLLREGEFT VTCTIKDVSS 240
10 SVYSTNWKREN SQTQLQEKYN SWHHGDFNYE RQATLTISSA RVNDSGVFMC YANNTFGSAN 300
VTTTLEVVOK GFINIFPMIN TTVFVNDGEN VDLIVEYBAF PKPEHQWMIY MNRTFTDKWE 360
DYPKSENESEN IRYVSELHLT RLKGTGGTY TFLVNSDVN AAIANVYVN TKPEILTYDR 420
LVNGMLQCVA AGFPEPTIDW YFCPGTEQRC SASVLEVDVQ TLNSSGPFPG KLVVQSSIDS 480
SAFKHNGTVE CKAYNDVGKT SAYFNFAFKG NNKEQIHPT LFTPLLIGFV IVAGMMCIIIV 540
15 MILTYKYLQK PMYEVQWKVV EEINGNNYVY IDPTQLPYDH KWEFPPNRRLS FGKTLGAGAP 600
GKVVEATAYG LKSDAAMTV AVKMLKPSAH LTEREALMSE LKVLVSLGNH MNIVNLLGAC 660
TIGGTTAVIT EYCCYGDLLN FLRRKRDSFI CSKQEDHAEA ALYKNLLHSK ESSCSDSTNE 720
YMDMKPGVSY VVPTKADRRR SVRIGSYIER DVTFAIMEDD ELALDLEDLL SFSYQVAKGM 780
AFLASKNCIH RDLAARNILL THGRITKICD FGLARDIKND SNYVVKGNAR LPVKWMAPEP 840
IFNCVYTFES DVNSYGFILW ELFSLGSSPY PGMVDSKFPY KMIKEGFRML SPEHAPAEY 900
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GSTASSQPL LVHDDV

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Seq ID NO: B75 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58..2298

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GGCCAGACTG GGAAGAAATC TGAGAAGGGA CCAGTTTGTT GGCGGAAGCG TGTAATAATCA 120
GAGTACATGC GACTGAGACA GCTCAAGAGG TTCAGACGAG CTGATGAAGT AAAGAGTATG 180
TTTAGTTCCA ATCGTCAGAA AATTTTGGAA AGAACGGAAA TCTTAAACCA AGAATGGAAA 240
35 CAGCGAAGGA TACAGCCTGT GCACATCCTG ACTTCTGTGA GCTCATTGCG CGGGACTAGG 300
GAGTGTTCGG TGACCAAGTA CTGTGATTTT CCAACACAAG TCATCCCATT AAAGACTCTG 360
AATGCAGTTG CTTCACTACC CATAATGTAT TCTTGTGCTC CCCTACAGCA GAATTTTATG 420
GTGGAAGATG AAATGTTTTT ACATAACATT CCTTATATGG GAGATGAAGT TTTAGATCAG 480
GATGTGACTT TCATTGAAGA ACTAATAAAA AATTATGATG GGAAGTACA CGGGATAGA 540
GAATGTGGGT TTATAAATGA TGAATTTTTT GTGGAGTTGG TGAATGCCCT TGGTCAATAT 600
40 AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAAGAGAAGA AAAGCAGAAA 660
GATCTGGAGG ATCACCAGAG TGATAAAGAA AGCCGCCAC CTCCGAAATT TCCTCTGAT 720
AAAATTTTGG AGGCCATTTT CTCAATGTTT CCAGATAAGG GCACAGCAGA AGAATCAAG 780
GAAAAATATA AAGAACTCAC CGAACAGCAG CTCACAGGCG CACTTCCTCC TGAATGTACC 840
CCCAACATAG ATGGACCAAA TGCTAAATCT GTTCAGAGAG AGCAAGGCTT ACACCTCTTT 900
45 CATACGCTTT TCTGTAGGCG ATGTTTTAAA TATGACTGCT TCCTACATCC TTTTCATGCA 960
ACACCCAACA CTTATAAGCG GAAGAACACA GAAACAGCTC TAGACAACAA ACCTTGTGGA 1020
CCACAGTGTG ACCAGCATTT GGAGGGAGCA AAGGAGTTTG CTGCTGCTCT CACCGCTGAG 1080
CGGATAAAGA CCCACCAAAA ACGTCCAGGA GCGCGCAGAA GAGGACGGCT TCCTCAATAAC 1140
50 AGTAGCAGGC CCGACACCCC CACCATTAAAT GTGCTGGAAT CAAAGGATAC AGACAGTGAT 1200
AGGGAAGCAG GGAAGTAAAC GGGGGGAGAG AACATGATA AAGAAGAAGA AGAGAAGAAA 1260
GATGAAACTT CGAGCTCCTC TGAAGCAAAT TCTCGGTGTC AAACACCAAT AAAGATGAAG 1320
CCAAATATTG AACTCTCTGA GAATGTGGAG TGGAGTGGTG CTGAAGCCTC AATGTTTAGA 1380
GTCTCATTTG GACTCTACTA TGACAATTTC TGTGCCATTG CTAGGTAAAT TGGGACCAAA 1440
55 ACATGTAGAC AGGTGTATGA GTTTAGAGTC AAAGAATCTA GCATCATAGC TCCAGCTCCC 1500
GCTGAGGATG TGGATACTCC TCCAAGGAAA AAGAAGAGGA AACACCGGTT GTGGGCTGCA 1560
CACTGCAGAA AGATACAGCT GAAAAAGGAC GGCTCCTCTA ACCATGTTTA CCAATATCAA 1620
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60 CCTGACCTCT GTCTTACTTG TGGAGCCGCT GACCATTGGG AAGTAAAAA TGTGTCTGTC 1860
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GCAGGCTGGG GGATTTTAT CAAAGATCCT GTGCAGAAA ATGAATTCAT CTCAGAATAC 1980
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65 ATGTGCAGCT TTCTGTTCAA CTTGAACAA GATTTTGTGG TGGATGCAAC CCGCAAGGGT 2100
AACAAAATTC GTTTTGCAAA TCATTCCGTA AATCCAACT GCTATGCAAA AGTTATGATG 2160
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CTGTTTGTGG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCGG CATCGAAAGA 2280
GAAATGTGAA TCCCTTGACA TCTGTACTCT CTTCCCTCTC CTCTGAAACA GCTGCCTTAG 2340
70 TCTCAGGAAC CTCAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAATTTCTG 2400
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Seq ID NO: B76 Protein sequence
Protein Accession #: NP_004447

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MVEDSTVLBN IPYMGDEVLD QDGTFLIELI KNYDGKVBHD RECGFINDEI FVELVNALGG 180
YNDDDDDDDG DDPEERBEKQ KDLEDRDDDK BSRPPRKFPF DKILEAISSM PFDKGTAEEL 240
KEKYKELTEQ QLPALPPEC TPNIDGPNK SVQREQSLHS FHTLFCRRCP KYDCFLHPFH 300
ATPNTYKRKN TETALDNKFC GPQCYQHLEG AKFAAALTA ERIKTPPKRP GRRRRGLFPN 360

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5
 NSSRPSTPTI NVLESKDSTD DREAGTSTGG ENNDKEEBEK KDETSSSSEA NSRCQTFIKM 420
 KPNIEPPENV EWSGAEASMF RVLIGTYIDN FCAIARLIGT KTCRQVVEPR VKESSIIAPA 480
 PAEDVDTPPR KKRKRHLWA AHCRKIQLKK DGSSNHVYNY QPCDHPRPQC DSSPCVIAQ 540
 NFCEKFQCS SEQNRFPGC RCKAQCNTRQ CPCYLAVREC DFDLCLTCGA ADHWDKNVS 600
 CKNCSTQGRS KKHLLAPSD VAGWGFIFKD PVOKNEFISE YGBIISQDE ADRRGKVYDK 660
 YMCSTFLNIN NDFVVDATRK GNKIRFANHNS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720
 ELFVDYRYSQ ADALKYVGIE REMEIP

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 Seq ID NO: B77 DNA sequence
 Nucleic Acid Accession #: NM_007015
 Coding sequence: 1..1005

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 GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240
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 ATGCCAGTCA AATATGAAGA AATTCCTCT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540
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 CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGAAGAA GAGAAGTGGT AAGAAAAATT 660
 GTTCCAACCT CCACAAAAGG ACCACACAGT GGACCAACGA GCAACCCAGG CGCTGGAAGA 720
 CTGAATTAAT AAACCAAGCC CAGTGTTCAC GAGGACTCAC AAGCCTTCAA TCCTGATAAT 780
 CCTTATCATC ASCAGGAAGG GGAAGCATG ACATTGACCC CTAGACTGGA TCACGAAGGA 840
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40
 Seq ID NO: B78 Protein sequence
 Protein Accession #: NP_008946

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 TGIRFAGGEK CYIKAQVKAR IPEVGAUTKQ SISKLEKGI MPVKYEENSL IWVAVDQPVK 180
 DNSFLSKVL ELQGLPIFW LRPTYKPIEQ RERREVRKI VPTTTKRPHS GPRSNPAGR 240
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Seq ID NO: B79 DNA sequence
 Nucleic Acid Accession #: NM_012449.1
 Coding sequence: 66..1085

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 AAAGACCTGT GCTTTTGCAT TTGCACCAAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240
 CAGAACTTCA GCACACACAG GAATCTTTT CACAGTGGCA CTTGCCAATT AAAATAGCTG 300
 CTATTATAGC ATCTCTGACT TTTCTTTACA CTCTTCTGAG GGAAGTAATT CACCCCTTAG 360
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 CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACTA TATTCAGAGC AAGCTAGGAA 840
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 TGTGTTGCTC GATATTAAAG AGCATACTAT TOCTGCCATG CTTGAGGAAG AAGATACTGA 1020
 AGATTAGACA TGGTTGGGAA GACGTCACCA AAATTAACAA AACTGAGATA TGTTCACAGT 1080
 TGTAGAATTA CTGTTTACAC ACATTTTGT TCAATATTGA TATATTTTAT CACCAACATT 1140
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80
 Seq ID NO: B80 Protein sequence
 Protein Accession #: NP_036581.1

1 11 21 31 41 51
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 LQHTQELFPQ WHLPKIAAI IASLTPLYTL LREVIHPLAT SHQQYFYKIP ILVINKVLEPM 120

VSITLLALVY LPGVIAAIQV LHNGTKYKPF PHWLDKMLT RKQFGLLSFF FAVLEAIYSL 180
 SYPMRRSYRY KLINWAYQVQ QONKEDAWIE HDVVRMEIYV SLGIVGLAIL ALLAVTSIPS 240
 VSDSLTWREF HYIQSKLIV SLLGLTIHAL IPANWKWIDI KQFVWYTPPT FMAVFLPIV 300
 VLIFKSILFL PCLRKKILKI RHGWEDVTKI NRTBICSQL

5

Seq ID NO: B81 DNA sequence
 Nucleic Acid Accession #: NM_000684
 Coding sequence: 87..1520

10 1 11 21 31 41 51
 TGCTACCCGC GCCCGGGCTT CTGGGGTGT CCCCACACAC GGCAGAGCCC TGCCACACCC 60
 CCGCCCCCG GCCTCCGAG CTCGGCATGG GCGGGGGGT GCTCGTCTG GCGGCTCCG 120
 AGCCCGGTAA CCTGTCTGT GCGGCACCG TCCCGACGG CCGGCCACC GCGGCGGGC 180
 15 TGCTGTGTGC CCGTCTGTG CCGGCTCGT TGCTGCCTCC CGCCAGCGAA AGCCCGGAGC 240
 CGCTGTCTCA GCAGTGGACA GCGGGCATGG GTCTGTCTAT GCGCTCATC GTGCTGTCTA 300
 TCGTGTGGGG CAATGTGCTG GTGATCGTGG CCATCGCCAA GACGCGCGG CTGCAGACGC 360
 TCACCAACCT CTTTCATCATG TCCCTGGCCA GCGCGACCT GGTCTATGGG CTGCTGTGTG 420
 TGCGGTTCGG GGCACCATC GTGGTGTGG GCGCTGGGA GTACGGCTCC TTCTTCTGCG 480
 20 AGCTGTGGAC CTCAGTGGAC GTGCTGTGCG TGACGGCCAG CATCGAGACC CTGTGTGTCA 540
 TTGCCCTGGA CCGCTACCT GCCATCACCT CCGCTTCCG CTACAGAGC CTGTGTGTCA 600
 GCGGCGGGG GCGGGGCTC GTGTGCACCG TGTGGCCAT CTCGCGCTG GTGTCTTCC 660
 TGCCCATCCT CATGCACTGG TGGCGGGCG AGAGCGACGA GCGCGCGCG TGCTACACCG 720
 ACCCAAGTG CTGCGACTTC GTCACCAACC GGGCTTACG CATCGCTCG TCCGTAGTCT 780
 25 CCTTCTACGT GCCCTGTGC ATCATGGCT TCGTGTACT GCGGGTGTTC CGGAGGGCC 840
 AGAAGCAGT GAAGAAGAT GACAGCTGG AGCGCGCTT CCTCGCGCG CAGCGCGCG 900
 CGCGCTCGC CTCGCGCTG CCGTCCCG CCGCGCGCG GCGCGCGGA CCGCGCGCG 960
 CCGCGCGCG CCGCGCGCG GCGCGCGCG CCAACGGCG TCGGGTAA GCGCGCGCT 1020
 CGCGCTCGT GCGCTACG GAGCAGAAG CGCTCAAGAC GCTGGGCATC ATCATGGCG 1080
 30 TCTTCTACGT CTGCTGTGCT CCGTCTTCC TGGCCAAGT GGTGAAGCC TTCCACCGG 1140
 AGCTGTGTGC CGACCGCTC TTGCTTCTT TCACTGGCT GGGCTACGC AACTCGGCT 1200
 TCAACCCAT CATCTACTG CGCAGCGCG ACTTCGCAA GCGCTTCCG GACTGTCT 1260
 GCTGCGCGG CAGGGCTGCC CCGCGCGCG ACGGACCCA CGGAGACCG CCGCGCGCT 1320
 CGGCTGTCT GCGCGCGCG GAGCGCGCG CATCGCGCG GCGCGCTCG GAGCAGCG 1380
 35 ACGACGATG GTGCGGGCG ACGCGCGCG CCGCGCTGCT GGAGCGCTG CCGCGCTGCA 1440
 ACGCGCGCG GCGCGCGCG AGCGACTCG GCCTGACGA GCGTGGCGC CCGCGCTCG 1500
 CCTCGGAATC CAAGGTGTAG GCGCGCGCG GCGCGCGCG CTCGCGCGC GCGTTCGAG 1560
 GCGAAGAGG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAACCTGA AGCCCAAT 1620
 40 CCTGTCTGA ATCATCGAG GCAAGAGAA AAGCCACGA CCGTTCGCA AAAAGGAA 1680
 TTTGGGAGG GATGGAGAG TGGCTGTCT ATGTTCTTG TTG

Seq ID NO: B82 Protein sequence
 Protein Accession #: NP_000675.1

45 1 11 21 31 41 51
 MGAGVLVLA SEPGNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASEP EPLSQQWTAG 60
 MGLLMALIVL LIVAGNVLVI VAIKTPRLQ TLNLFIMSL ASADLVMLGL VVPFGATIVV 120
 WGRWEYGSFF CELWTSVDVL CVTASITLC VIALDRYLAI TSPFRYQSL TRARARGLVC 180
 50 TWHAISALVS FLFILMHWRR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCIM 240
 AFVYLRVREF AQKQVKIDS CERRFLGGA RPPSPSPSPV PAPAPPGP RPAAAAATAP 300
 LANGRAGRR PSRLVALREQ KALKTLGIIM GVFTLCNLP FLANVVKAFH RELVPDRLFV 360
 FPNWLYGANS AFNPIIYCRS PDKRAEQGL LCARRAARR RHATHGDRPR ASGCLARPGP 420
 PPSGAAASD DDDVVGATP PARLLEPWAG CNGGAAASD SLDPECRPG FASESKV

55

Seq ID NO: B83 DNA sequence
 Nucleic Acid Accession #: NM_000729.2
 Coding sequence: 2..421

60 1 11 21 31 41 51
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 AGCCATGAAC AGCGGCTGT GCCTGTGCGT GCTGATGGG GACTGCGCG CTGGCGCCT 120
 GACGACGCG GTGCTCCCG CAGATCCCG GGGCTCCGG CTGACGCGG CAGAGGAGGC 180
 65 GCGCGTAGG CAGCTGAGG TATCGCAGG AACGATGGC GAGTCCCGG CGCACTGGG 240
 CGCCCTGCTG GCAAGATACA TCCAGCAGG CCGGAAAGCT CCTCTGGAC GAATGTCCAT 300
 CGTTAAGAAC CTGCAAGAAC TGGACCCAG CCACAGGATA AGTGACGGG ACTACATGG 360
 CTGGATGGAT TTTGGCGTC GCAGTGGGA GGAGTATGAG TACCCCTCT AGAGGACCCA 420
 70 GCGCCATCA GCGCAACGA AGCAACCTCC CAACCCAGG GAGGAGAAAT AAGACAACAA 480
 TCACACTCAT AACTCATTGT CTGTGGAGT TGACATTGAA TGTATCTATT TATTAGTTC 540
 TCAATGTGAA AATTGTGTCT GTAAGATTGT CCAGTGCAAC CACACACGT CACGAGAAT 600
 TGTGAAACT GAAGACAAA CTGTTTCTT CATCTGTGAC TCCTGTCTG AAAATGTTG 660
 TATGCTATTA AAGTGATTTC ATTCTGCC

75

Seq ID NO: B84 Protein sequence
 Protein Accession #: NP_000720.1

80 1 11 21 31 41 51
 MNSGVCLCVL MAVLAAGALT QVPPADPAG SGLQRAEAP RRQLRVSRQ DGESEHLAGA 60
 LLARYIQAR KAPSGRMSIV KNLQNLDPH RISDRDYMGW MDPGRSAEB YEYPS

TABLE 74 Gene Sequences Up- or Down-Regulated in Cancer

Angiogenesis

5	A1 DNA SEQUENCE	
	Gene name:	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Unigene number:	Hs.154210
	Probeset Accession #:	M31210
10	Nucleic Acid Accession #:	M31210
	Coding sequence:	251-1396
15	TCTAAAGGTC GGGGGCAGCA GCAAGATGCG AAGCGAGCCG TACAGATCCC GGGCTCTCCG 60 AAGGCAACTT GGCCTGCTT GAGGAGGCT GGGTTTCCG AGGCCCTCTC CAGCCAAGGA 120 AAAGCTACAC AAAAAGCCTG GATCACTCAT CGAACCAACC CTGAAGCCAG TGAAGGCTCT 180 CTCGCTCGC CCTCTAGCGT TCGTCTGGAG TAGCGCCACC CCGGCTCTCT GGGGACACAG 240 GGTTGGCACC ATGGGGCCCA CCAGCGTCCC GCTGGTCAAG GCCCACCSCA GCTCGGTCTC 300 TGACTACGTC AACTATGATA TCATCGTCCG GCATTACAAC TACACGGGAA AGCTGAATAT 360 CAGCGCGGAC AAGGAGAACA GCATTAAACT GACCTCGGTG GTGTTCAATC TCATCTGCTG 420 CTTTATCATC CTGGAGAACA TCTTTGTCTT GCTGACCATT TGGAAAACCA AGAAATTCCA 480 CCGACCATG TACTATTTTA TTGGCAATCT GGCCTCTCA GACCTGTTGG CAGGAGTAGC 540 CTACACAGCT AACCTGCTCT TGTCTGGGGC CACCACCTAC AAGCTCACTC CCGCCAGTG 600 GTTTCTGCGG GAAGGGAGTA TGTTTGTGGC CCGTCAAGCC TCCGTTTCA GTCTCTCGC 660 CATCGCCATT GAGCGCTATA TCACAATGCT GAAATGAAA CTCACAACG GGAGCAATAA 720 CTTCGGCTCT TTCCTGCTAA TCAGCGCTCG CTGGGTCTAT TCCCTCATCC TGGGTGGCCT 780 GCCTATCATG GGCTGGAAGT GCATCAGTGC GCTGTCCAGC TGCTCCACCG TGCTGCGGCT 840 CTACCAACAG CACTATATCC TCTTCTGCAC CACGCTCTTC ACTCTGCTTC TGCTCTCCAT 900 CGTCAATCTG TACTGAGATA TCTACTCCTT GGTCAAGACT CGAGCGCGC GCCTGACGTT 960 CCGCAAGAAC ATTTCCAAGG CCAGCGCGAG CTCGAGAAT GTGGCGCTGC TCAAGACGCT 1020 AATTATGCTC CTGAGCGTCT TCATCGCCTG CTGGGCACCG CTCCTCATCC TGCTCCTGCT 1080 GGATGTGGGC TGCAAGGTGA AGACCTGTGA CATCCTCTTC AGAGCGGAGT ACTTCTGTGT 1140 GTTAGCTGTG CTCAACTCCG GCACCAACCC CATCATTTAC ACTCTGACCA ACAAGGAGAT 1200 GGCTCGGGCC TTCTCGGGA TCATGTCTCG CTGCAAGTGC CCGAGCGGAG ACTCTGCTGG 1260 CAAAATTCAG CGACCCATCA TCGCGGCGAT GGAATTCAGC CGCAGCAAT CGGACAAATC 1320 CTCCCAACCC CAGAAAGACG AAGGGGACAA CCCAGAGACC ATTATGTCTT CTGGAACGCT 1380 CAACTCTTCT TCCTAGAACT GGAAGCTGTC CACCCACCGG AAGCGCTCTT TACTTGGTGC 1440 CTGGCCACCC CAGTGTGTTG AAAAAAATCT CTGGGCTTCG ACTGCTGCCA GGGAGGAGCT 1500 GCTGCAAGCC AGAGGGAGGA AGGGGGAGAA TACGAACAGC CTGGTGGTGT CGGTGTGTTG 1560 TGGGTAGAGT TAGTTCCTGT GAACAATGCA CTGGGAAGGG TGGAGATCAG GTCCCGGCTC 1620 GGAAATATATA TTCTACCCCC CTGAGCTTTT GATTTTGCAC TGAGCCAAAG GTCTAGCATT 1680 GTCAAGCTCC TCCTAGAACT ATTTGGCCCC TCCTCAAGA CATATGTCCC CATGTGAAAG 1740 CGTCTCTTTG TCTGAGCTT TGAGGAGATG TTTTCTCTCA CTTTAGTTTC AAACCCAAAT 1800 GAGTGTGTGC ACTTCTGCTT CTTTAGGGAT GCCCTGTACA TCCACACCC CACCCCTCCT 1860 TCCTTTCATA CCCCTCCTCA ACGTTCCTTT ACTTTTACT TTAACCTACCT GAGAGTTATC 1920 AGAGCTGGGG TTGTGGAATG ATCGATCATC TATAGCAAT AGGCTATGTT GAGTACGTAG 1980 GCTGTGGGAA GATGAAGATG GTTTGGAGGT GTAAACAAT GTCCTTCGCT GAGGCCAAAG 2040 TTTCCATGTA AGCGGATCC GTTTTGTGGA ATTTGGTTGA AGTCACTTTC ATTTCTTTAA 2100 AAAAATCTT TTCAATGAAA TGTGTTACCA TTTTCATATC ATTGAAGCCG AAATCTGCAT 2160 AAGGAGCCCC ACTTTATCTA AATGATATTA GCCAGGATCC TTGGTGTCTT AGGAGAAACA 2220 GACAGCAAAA ACAAAGTGAA AACCGAATGG ATTAACCTTT GCAAAACCAAG GGAGATTCTT 2280 TAGCAAAATGA GTCCTAACAA TATGACATCC GTCCTTCCCA CTTTGTGTTA TGTTTATTTC 2340 AGAAATCTGT GTGATTCATT TCAAGCAACA ACATGTGTGA TTTTGTGTG TTAAGATAC 2400 TTTTCTTGAT TTTTGAATGT ATTTGTTTCA GGAAGAGTGC ATTTTATGGA TTTTCTAAC 2460 CCGTGTTAAT TTTTCTAGAA TCCACCTCTT TGTGCCCTTA AGCATTACTT TAACGTGTAG 2520 GGAAACGCCAG AACTTTTAAG TCCAGCTATT CATTAGATAG TAATGAGA TAATGATAAA 2580 TATTACAAAG AATAAAAATA TATTACTGTC TCTTTAGTAT GGTTTTCAGT GCAATTAAAC 2640 CGAGAGATGT CTTGTTTTTT TAAAAAAGAT AGTATTTAAT AGGTTTCTGA CTTTGTGGA 2700 TCATTTTGCA CATAGCTTTA TCAACTTTTA AACATTAATA AACTGATTTT TTTAAAG	
60	A2 Protein sequence:	
	Gene name:	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Unigene number:	Hs.154210
	Probeset Accession #:	M31210
65	Protein Accession #:	AA52336
	Signal sequence:	none found
	Transmembrane domains:	50-71, 92-110, 122-140, 160-177, 202-222, 251-269, 283-301
	Cellular Localization:	plasma membrane
70	1 11 21 31 41 51 MGPTSVPLVK AHRSSVSDYV NYDIIVRHYN YTGKLNISAD KENSIKLTSTV VFILICCFII 60 LENIPVLLTI WTKTKFHERPM YFIGNLALS DLLAGVAYTA NLLSGATTY KLTFAQWFLR 120 EGSMFVALSA SVFSLAIAI ERYITMLKKK LHNGSNPNRL PLLISACWVI SLILGGLPIM 180 GWNCSIALSS CSTVLPVLYK HYILFCTTVF TLLLLSIVIL YCRIYSLVET RSRRLTFREN 240 ISKASRSSEN VALLKTVIIV LSVFIACWAP LFILLLLDVG CKVKTCDILF RAEYFLVLAV 300 LNSGTNPPIY TLTNKMERRA FIRIMSCCKC PSGDSAGKFK RPIIAGMEFS RSKSDNSSHP 360 QKDEGDNFET IMSSGNVNSS S	
80	A3 DNA SEQUENCE	
	Gene name:	G protein-coupled receptor 51
	Unigene number:	Hs.198612
	Probeset Accession #:	AA452928
	Nucleic Acid Accession #:	NM_004624.1

5	1	11	21	31	41	51	
	ATGGCTTCCC	CGCGGAGGTC	CGGGCAGCCA	GGGCGGGCGC	CGCGCGCGCC	ACGCGCGCCC	60
	GC CGCCTG C	TACTGCTACT	GCTGCTGCCG	CTGCTGCTGC	CTCTGGCGCC	GGGGGCTGG	120
	GGCTGGGCGC	GGGGCGCCCC	CGGGCGCGCG	CCGAGCAGCC	CGCGCTCTCT	CATCATGGGC	180
10	CTCATGGCGC	TCACCAAGGA	GGTGCCCAAG	GGCAGCATCG	GGCGGGTGTG	GCTCCCCGCC	240
	GTGGAACGTG	CCATCGAGCA	GATCGGCRAAC	GAGTCACTCC	TGCGCCCCCTA	CTTCTCTGAC	300
	CTGCGGCTCT	ATGCACA CGA	GTGCGACGAA	CGAAAAGGGT	TGAAGACCTT	TACAGATGCA	360
	TAAATAATCG	GGCGGAACCA	CTTGATGGTG	TTTGGAGGCG	TCTGTCCATC	CGTCACATCC	420
	ATCATTTGAG	AGTCCCTCCA	CGAGGTGAAAT	CTGTTGTCAGC	TTTCTTTTGG	TGCAAAACGAG	480
15	CTGTTCTTAG	CGATAAGAA	AAAATACCTC	TATTTCTTTC	GGACCGCTCC	ATCAGACAAT	540
	GCGGTGAATC	CAGCCATTCT	GAAGTTGTCT	AAGCACTAOC	AGTGGAAAGC	CGTGGGACAG	600
	CTGACGCAAG	ACGTTCTCAG	GTTTCTCTGAG	GTGCGGAATG	ACCTGACTGG	AGTTCTGTAT	660
	GGCGAGGACA	TTGAGATTTC	AGACACCGAG	AGCTTCTCCA	ACGATCCCTG	TACCAATGTC	720
	AAAAGAGTGA	AGGGGAATGA	TGTGCGGATG	ATCCTTGCCC	AGTTTGACCA	GAATATGGCA	780
20	CGAAAAGTGT	TCGTGTTATC	ATACGAGGAG	AACATGTATG	GTAGTAACCA	TCAAGTGATC	840
	ATTCCGGGCT	GGTACGAGCC	TTCTTGGTGG	GAGCAGGTGC	ACACGGAAGC	CAATCTCATG	900
	CGCTGCTTCC	GGAGAATGCT	CTTGCTTGCC	ATGAGAGGGT	ACATTGGCGT	GGATTTCCAG	960
	CCCGTAGGCT	CCAGAGCAGAT	CAGGACCATC	TCAGGAAGA	CTCCACAGA	GATGAGAGA	1020
	GAGTACAACA	ACAAGCGGTG	AGGCGTGGGG	CCGACAGAT	TCCAACGGTA	CGCCTACGAT	1080
25	GGCATCTGGG	TCAATCGCCAA	GACACTGCGA	GGGGCCATGG	AGACATGTCA	TGCCAGCAGC	1140
	CGGCACCGAG	GGATCCAGCA	CTTCAACTAC	ACGGACCCAC	CGCTGGGCG	GATCATCTCT	1200
	AATGGCCATG	ACGAGACCAA	CTTCTCTCGG	GTCCAGGGTC	AAGTTNGATT	CGGGAATGGG	1260
	GAGAGAAATG	GGACCACTAA	TTTACTCTAA	TTTCAAGACA	CAGGGGAGT	GAAGTGGGGA	1320
	GAGTACAACG	CTGTGGCCGA	CACACTGAGG	ATCATCAATG	ACACCATCAT	GTTCACAGGA	1380
30	CTCGAARCC	CAAAAGACAA	GACCATCATC	CTGGAGCAGC	TGCGGAAGAT	CTCCCTACCT	1440
	TCCACAGCA	TCCCTCTGCG	CTCAACATC	CTCGGATGTA	TCTAGGCCAG	TGCTTTTCTC	1500
	TTTCTCAACA	TCAGAAGAAC	GAATCAAGAG	CTCAATAAGA	TGTGAGTGAT	ATACATGAAC	1560
	AACCTTATCA	CTCTTGGAGG	GATGCTCTCC	TATGCTTCCA	TATTTCTCTT	TGGCCTGTAT	1620
	GGATCTTTTG	TCTCTGAAAA	GACCTTTGAA	ACACTTTGCA	CCGTCAAGAC	CTGGATTCTC	1680
35	ACCGTGGGCT	ACAGCGCCGC	TTTGGGGCG	ATGTTTGGAA	AGACCTGGAG	AGTCCAACGC	1740
	ATCTTCAAAA	ATGTGAAAT	GAAAGAGAAG	ATCATCAAGG	ACCAAGAACT	GCTTTGTATC	1800
	GTGCGGGGCA	TGCTGCTGAT	CGAAGCTGTT	ATCTGTATCT	GCTGGCAGGC	TGTGAGATCC	1860
	CTGCGAAGGA	CAGTGGAGAA	GTACAGCATG	GAGCGCGACC	CAGCAGGACG	GGATATCTCC	1920
	ATCCGCGCTC	TCTTGGAGCA	CTGTGAGAAC	ACCCATATGA	CCATCTGGCT	TGGCATCGTC	1980
40	TATGCGTACA	AGGAGATCTT	CATGTTGTTC	GGTGTGTTCT	TAGCTTTGGGA	GACCCGCAAC	2040
	GTGACATCTC	CGGCATCTAA	CGACAGCAGC	TACATCGGGA	TGAGTGTCTA	CTAGTGGGGG	2100
	ATCATGTGCA	TCAATGGGGC	CGCTGTCTCC	TTCTGACCC	GGGACCCAGC	CAATGTGACG	2160
	TTCTGTATCG	TGGCTCTGGT	CATCATCTTC	TGCAGCACCA	TCACCTCTGC	CTCTGTATTTC	2220
	GTGCGGAGCG	TCTACACCTC	GAGAACAAAC	CCAGATGTGAG	CCAGCAGGAA	CAGGCGATTTC	2280
45	CAGGTTCACT	AGAAATCAGAA	GAAAGAGAAT	TCTAAAACGT	CCACCTTGGT	CACAGGTGATG	2340
	AAACAGCGCA	GCACATCCCG	CTCGGAGGGC	CTACAGTCAG	AAACCATCGT	CCTGGGAATG	2400
	AAGATCACAG	AGCTGGATAA	AGACTTGGAA	GAGGTACCA	TGCAGCTGCA	GGACAACCCA	2460
	GAAAGAGCTA	CTCATATTAC	ACAGAAAGCA	TACCCAGAGC	TCAATGACAT	CCTCAACCTG	2520
	AAGAAACTCA	CTGAGAGCAC	AGATGGAGGCA	AAGGCCATTG	TAAAATAATCA	CTCTGATCAA	2580
	AATCCCCAGC	TACAGTGGAA	CACAACAGAG	CCCTCTCGAA	CATGCAAGAA	TCTCTATAGAA	2640
50	GATATAAACT	CTCCAGAACCA	CTCCAGAGCT	CGGCTGTCCC	TCCAGCTCCC	CATCTCCGAC	2700
	CATGCTCTACC	TCCCATCCAT	CGGAGGCGTG	GAGGCCAGCT	GTGTGAGCCC	CTGCGTCAGC	2760
	CCCCCGCCCA	GCCCCCGCCA	CAGACATGTG	CCACCTCTCT	TCCGAGTCAT	GGTCTGGGGC	2820
	CTGTAA						

65	1	11	21	31	41	51	
	MASPRRSQGP	GRPPPPPPPP	ARLLLLLLLL	LLPLPAPGAW	GWARGAPRPP	PSSPPLSIMG	60
	LMPLTKEVAK	GSIGRGVLP	VELAEIQIRN	BSLLRPFPFLD	LRLYDTBCDN	AKGLKAFYDA	120
70	IKYGNHMLMV	PGGVCPSVTS	IIABSLQGWV	LVQLSFAATL	PVLADKKKYP	YFPRTPVSDN	180
	AVNPAILLKAL	KHYQKRWKVF	LTQDPQAFEE	VNRDLTVGLY	GEDIISDSTE	SFSDNICTSV	240
	KKLKGNVDRI	ILGQPDQNMA	AKVFCWAYE	NMYSKKQWVI	IPGWYEPSMW	EQVTEANSS	300
	CLRLKNLTLAA	MBGYIUVDSF	PLSSQKQFTI	SGKTPOQYER	EYNNKRSRGV	PSKFHGYAYD	360
	GIWVIATKLQ	RAMETLHASS	RHQRIQDINT	TDHTGLRIIL	NAMNETNFGV	TVQGVFRNG	420
75	ERMGTIKFTKP	QDSREKXVGF	EYNAVADTLE	LINDTRFQGF	SEPPKDKTII	LEQLRKISLP	480
	ILSLISALTI	LQDINASAFI	FPNIKRNQKZ	LKMSGSPYMN	NIILGLGMS	YASIFLPGLD	540
	GSFVSEKTFE	TLCTVRTWIL	TVGYTIFARG	MPAKICVRVHA	IFKNVNMKKK	LTKDQKLLVI	600
	VGGMLLDILC	LILCQAVDP	LRRITVEKYSM	PEDPAGRDISI	IRFLLEHCEN	THMTIWLGIT	660
	YAYKGLMLML	GCLFAWETRN	VSPALNDSKC	YIGMSVYNVG	IMCIIGAAYS	FLTRDQPMVQ	720
80	FCIVALVIIIF	CSTITLCLVF	VPKLITLRTN	PDAATQNRFR	QPTQNKQKED	SKTSTSVTSV	780
	NQASTSRLEG	LQSENERLRM	KITELDKOLE	EVTMQLQDTP	EKTTYIKQNH	YQELANDLNL	840
	GNFTPSIDGG	KAILKNHLDL	NPQLQWNTTE	PSRTCKDPIE	DNSNPEHIQR	RLSLQLPILH	900
	HAPEBSIYGV	PATSCPVCVS	PASPRHVVH	PPSFRVMVSG	L		

A5 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

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10 1      11      21      31      41      51
   |      |      |      |      |      |
AGCAACGACG CCGGGCAGCG GGAGCGGCGG CGCGCCCATG TGGCTGCTGG GGCCGCTGTG 60
CCTGCTGCTG AGCAGCGCCG CGGAGAGCCA GCTGCTCCCC GGGAAACAACT TCACCAATGA 120
GTGCAACATA CCAGGCACACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCCTGGCA 180
GTGTGACGGG CTGCCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
15 GTGAAATGTG GGCCTCAACCT TCTTCCCTCG TGCCAGCGGC ATCCATTGCA TCATTGGTGG 300
CTTCCGCTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
AAACCCCTCG CTTTGCTCCA CGGCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA 420
GAGCTTCATC TGGATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
AAGTTCCTAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
20 TTACCCGAGC ATCACTCTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
CCTGCTGGCA CTGTCTTGTC ACCACCAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
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CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
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25 TGCGTGGTAT GACCTTCCCTC CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900
CGACCTGCCC CCCTACCGCT CCGGTCCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960
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AACTATCTCT GCATTCCCTT CCTCCCCAG ACTTCAGAGA TGTTTTCTG GGTCTCAGT 1260
TGACATGATC TGTGTGCGT CTTTTCTGTC AGGTCATCTT TCCCTTGGGA CCCGAGATCA 1320
CACCTCATTT TTTCACATTA TTCTGTTTCT GTTGGAGAGA CAGCATATAA AACAGTATTG 1380
AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
35 CGCTGAGACC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTGGGGGA TTTGGGTTAG 1500
ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAATT CCATTGAGC 1560
ATCAAAACCT GCTTTGCACA ATCCTATTGG ATGCCCCAG TTCCAGAGAG TCAGTGGCCA 1620
AAGAAACCTT TGGACGTGAG TAACACCCCT CAGCAGTGGC AACGTTATT TGGTTTGTG 1680
AAGGACTCTG AAACCATCTA CCTGTATAA ATTCGTGGCT TAGAAATTG CCCAAGAAAG 1740
40 CTCTTCTGA GAGCTTCCCT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800
GAGCCCTTCC CATGAGTTTA TCCAAGTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860
TACACCTGCC CTGCTCTAC AGCCACTTAC CTGCTTCTG GACTGTCAAC CTCCAGCTG 1920
ACCTGCCCCT AGCCCAAGGA TGAGGACCTA ACTTGAGTTG GCCCAAGTGC TGACCTGGCT 1980
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45 CTCCAAAGTT CCCTTAACAC TTGCAAAATC CTTTATTACCT GTGCAATTGG ACTTGAGGAC 2100
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GGTCAGGGTG AGGCTCTTCC CAACATCCCA GTAGTTTCTC CTCAGAGACA CATGGGCAAG 2280
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55 TTCTCTGTGT CCAGTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACTGT 2700
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CCACTCCGGG CAGCTGTGAC CCATTGAGAA CTCTCTCCG CAGCTGAAGA AATGTTGAGT 2820
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CTGATTAAAT CAATAAGAA CTTTGTATGA CAGCCAGAAAT GTGTTAGAAT TCTGGCTGAA 3120
GATTCATCT CTGTGAGTC AGAAGGGCTT TATTTCTCCC TTTGATGGGG CCCCTCTCTC 3180
65 TTTCTGTTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240
GAGTTAATCT CACTGCTTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTATAGT 3300
AGATAAGGGA TGCTTACTAA TGCTTTTATA AAACAACAG GGCATTTTTT ATTATAGATT 3360
TGATTTTATT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGC GGCAGGGTTT 3420
TTTTTGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGCG ACATTAGTGG CCAGCAATAT 3480
70 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAATCTA OGCCAACAG 3540
AAAAATAGCT CATCTCTTTT TTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAAT 3600
AGTTACACTT TGATGACTGG OCTATTACCT GACTCAGCTC CCTCTACCTT GAAATGACA 3660
TTTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGAGG CTCAAAGTTA ATGTAAACTG 3720
GAAAGGTTGT GTGTGTTGTC TTTTGTGTTT TTGGTTAGGC TTGGTTTGT TTTTAAATTT 3780
75 TTATACTTTC TAATAAATTT GCAGTTTCAT TCTTTCTGTT TGTGCAAAAG GWMCTAMARM 3840
AAMMAAAAC ANYWTTGGGG GGGCTTGGGC CTGCGAAAAA GTTTTAAACA CCACTTCGGG 3900
TGGGGCGGCG GGGCCCAAGT AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAG 3960
GAAACCTTGG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAAAAAAAA ACGCGCGCGG 4020
GGAAACCGCA GAGTGTGCG TAAACCAAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080
80 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

```

A6 Protein sequence:

Gene name: ESTs

Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 5 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

10 1 11 21 31 41 51
 MWLLGPLCLL LSSAAESQLL PGNFTNECN IPGNFMCSNG RCIPGANQCD GLPDCFDKSD 60
 EKECPKAKSK CGTPFPKAS GIHCIIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
 15 KNLGLCIDKSP ICDGQNNQD NSDEESCESS QEPGSGQVFP TSENQLVYYP SITYAIIGSS 180
 VIFVLVVALL ALVLHHQRRR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240
 YVASQAQNA SEVGSPPSYS EALLDQRPBW YDLPPPPYS DTESLNQADL PPRSRSSGSA 300
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTREV

20 A7 DNA SEQUENCE
 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
 Unigene number: Hs.149609
 Probeset Accession #: X06256
 Nucleic Acid Accession #: NM_002205
 25 Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
 ATGGGGAGCC GGACGCCAGA GTCCCTCTC CACGCGGTGC AGCTGCGCTG GGGCCCCCGG 60
 CGCCGACCCC CGCTSSSTGCC GCTGCTGTG CTGCTSSSTGC CGCCGCCACC CAGGGTCGGG 120
 GGCTTCAACT TAGACGCGGA GCGCCACGCA GTACTCTCGG GCGCCCGGG CTCTTCTTTC 180
 GGATTCTCAG TGGAGTTTAA CCGCCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240
 35 CCCAAGGCTA ATACCAGCCA GCCAGGAGTG CTGCAGGGTG GTGCTGTCTA CCTCTGTCTC 300
 TGGGGTGCCA GCGCCACACA GTGCACCCCC ATTGAATTG ACAGCAAAGG CTCTCGGCTC 360
 CTGAGTCTCT CACTGTCCAG CTCAGAGGGA GAGGAGCCTG TGGAGTACAA GTCTTGCAG 420
 TGGTTCGGGG CAACAGTTGG AGCCCATGGC TCCTCCATCT TGGCATGCGC TCACATGTAC 480
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 40 GATAACTTCA CCGGAATTCT GGAGTATGCA CCTGCGGCT CAGATTTCAG CTGGGACGCA 600
 GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCGGAGTTCA CCAAGACTGG CCGTGTGGTT 660
 TTAGGTGGAC CAGGAAGCTA TTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG 720
 ATTGCAGAA CTATTATACC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780
 CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGTGTGAA 840
 45 TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAAGGGAA CCTCACTTAC 900
 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTGATGCC TCTACAATT CTCAGGGGAA 960
 CAGATGGCCT CACTACTTGG CTATGCAATG GCGCCACAG ACGTCAATGG GAGCGGGCTG 1020
 GATGACTTGC TGGTGGGGGC ACCCTGCTTC ATGGATCGGA CCCCTGAACG GCGGCTCAG 1080
 GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCCAGCGG GCATAGAGCC CACGCCACC 1140
 50 CTTACCTTCA CTGTGGTATA TGAGTTTGGC CGATTGGCA GCTCCTTGAC CCCCTGGGG 1200
 GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGG CTCCCTTGG TGGGGAGACC 1260
 CAGCAGGGAG TAGTGTGTGT ATTTCTTGGG GCGCCAGGAG GGCTGGGCTC TAAGCCTTCC 1320
 CAGGTTCCTG AGCCCTCTGT GGCAGCCAGC CACACCCAG ACTTCTTGG CTCTGCCCTT 1380
 CGAGAGGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCCTTGGT 1440
 55 GTGGACAAGG CTGTGGTATA CAGGGGCGGC CCCATCGTGT CGCTAGTGC CTCCTCACC 1500
 ATCTTCCCG CCATGTTCAA CCCAGAGGAG CGAGCTGCA GCTTAGAGGG GAACCTGTG 1560
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 GGTTCACAG TGGAACTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA 1680
 CTGTTCTGG CCTCCAGGCA GGCAACCTTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
 60 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAAAT TOGAGACAAA 1800
 CTCTCGCCGA TTCATATGCC TCTCACTTC TCCTTGGACC CCCAAGCCCC AGTGACAGC 1860
 CAGGCGCTCA GGCCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920
 ATCTTGCTGG ACTGTGAGA AGACAACATC TGTGTGCTG ACCTGCAGCT GGAAGTGTTC 1980
 GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCC TGAACTCAC TTTCCATGCC 2040
 65 CAGAAATGGG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACCGC CCTCCAGAG 2100
 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCTGAG CTGTGACTAC 2160
 TTTGCCGTGA ACCAGAGCGG CTGTCTGTG TGTGACTGG GCAACCCAT GAAGGCAGGA 2220
 GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCGGGGACAC TAAGAAAACC 2280
 70 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAG CGACGTGGTT 2340
 TCCTTTGGGC TCTCCGTGGA GGCTCAGGCC CAGGTCAACC TGAACGGTGT CTCCAGCCT 2400
 GAGGCAGTGC TATTCCAGT AAGCGACTGG CATCCCGAG ACCAGCTTCA GAAGGAGGAG 2460
 GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT 2520
 AGCCAGGGTG TGCTGGAACT CAGCTGTCCC CAGGCTCTGG AAGGTGAGCA GTCCTATAT 2580
 75 GTGACCAGAG TTAACGGACT CAACTGCACC ACCAATCACC CCATTAACCC AAAGGGCCTG 2640
 GAGTTGGTACT CCGAGGGTTC CCTGCACCC CAGCAAAAAC GGGAACTCC AAGCGCAGC 2700
 TCTGCTTCTC CGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGTTC CAGGCTGGC 2760
 TGTGAGCTCG GCGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAAGTGCA TTTCCAGTTC 2820
 TGGGCCAAGA CTTTCTTGA GCGGAGCAC CAGCCATTTA GCTGCAAGTG TGAGGCTGTG 2880
 80 TACAAGCCC TGAAGATGCC CTACCGAATC CTGCTCGGC AGCTGCCCA AAAAGAGCGT 2940
 CAGGTGGGCA CAGCTGTGCA ATGGAACCA GCAAGAGGCA GCTATGGCGT CCACTGTGG 3000
 ATCATCATCC TAGCCATCCT GTTGGCCTC CTGCTCCTAG GTCTACTCAT CTACATCTC 3060
 TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CCGCATGGA AAAAGCTCAG 3120
 CTCAGGCTC CAGCCACCTC TGATGCTCGA

A8 Protein sequence:

Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
 Unigene number: Hs.149609
 Probeset Accession #: X06256
 Protein Accession #: NP_002196
 Signal sequence: 1-42
 Transmembrane domains: 998-1020
 Integrin alpha domains: 56-115, 268-318, 322-384, 388-444, 452-503, 1022-1036
 Cellular Localization: plasma membrane

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15      1      11      21      31      41      51
      |      |      |      |      |      |
      MGSRTFESFL HAVQLRWGFR RRPPLPLLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60
      GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCP WGASPTQCTP IEFDSKGSRL 120
      LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCTYLS 180
      DNFTRILEYA PCRSDPSWAA GQGYCQGGFS AEPTKTGRVV LGGPGSYFWQ GQILSATQEQ 240
      IAESYYPEYL INLVQGQLQT RQASSIYDDS YLGYSVAVGE PSGDDTEDFV AGVPKGNLTY 300
      GYVTILNGSD IRSLYNFSGE QMASYFCYAV AATDVNGDGL DDLVLVGAPLL MDRTPDGRPQ 360
      EVGRVYVYLQ HPAGIEPTPT LTLTGHEDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420
      QQGVVVFVPG GPGGLGSKPS QVLQPLWAAS HTTPDFGSAL RGGRLDGNNG YPDLIVGSFG 480
      VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNFV ACINLSFCLN ASGKHVADSI 540
      GFTVELQLDW QKQKGGVRRR LFLASRQATL TQTLLIQNGA REDCREMKIY LRNESEFRDR 600
      LSPIHIALNF SLDPQAPVDS HGLRPAHYQ SKSRIEDKAQ ILDDCGEDNI CVPDLQLEVP 660
      GEQNHVYLGD KNALNLTFHA QNVGEGGAYE AELRVTPAPE AEYSGLVREP GNPSLSLSCDY 720
      FAVNQSRLLV CDLGNPMKAG ASLWGLRFT VPHLRDTKKT IQDFDQILSK NLNNSQSDVV 780
      SFRLSVEAQA QVTLNGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
      SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPGSLHSH QQKREAPSR 900
      SASSGPQLLK CPEAECFRLR CELGPLHQQE SQSLQLHFRV WAKTFLOREH QPFSLQCEAV 960
      YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFLGL LLLGLLIYIL 1020
      YKLGFKKRSL PYGTAMEKAQ LKFPATSDA
  
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A9 DNA SEQUENCE

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)
 Unigene number: Hs.287797
 Probeset Accession #: X07979
 Nucleic Acid Accession #: NM_002211.1
 Coding sequence: 1-2397 (underlined sequences correspond to start and stop codons)

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45      1      11      21      31      41      51
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      ATGAATTAC AACCAATTTT CTGGATTGGA CTGATCAGTT CAGTTTGCTG TGTGTTTGCT 60
      CAACACAGATG AAAATAGATG TTTAAAAGCA AATGCCAAAT CATGTGGAGA ATGTATACAA 120
      GCAGGGCCAA ATTGTGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCTACT 180
      TCTGCACGAT GTGATGATTT AGAAGCCTTA AAAAAGAAAG GTTGCCCTCC AGATGACATA 240
      GAAAATCCCA GAGGCTCCAA AGATATAAAG AAAAATAAAA ATGTAAACCA CCGTAGCAAA 300
      GGAACAGCAG AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCA CAAGTTGGTT 360
      TTGCGATTAA GATCAGGGGA GCCACAGACA TTTACATTAA AATTCAAGAG AGCTGAAGAC 420
      TATCCCATTT ACCCTCTACTA CCTTATGGAC CTGCTTACT CAATGAAAGA CGATTGGAG 480
      AATGTAAAAA GTCTTGGAAC AGATCTGATG AATGAAATGA GGAGGATTAC TTCGGACTTC 540
      AGAATTGGAT TGTGGAATTT TGTGGAATTT ACTGTGATGC CTTACATTAG CACAACACCA 600
      GCTAAGCTCA GGAACCCCTG CACAAGTGAA CAGAAGTCCA CCAGCCCAT TAGCTACAAA 660
      AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTTGTGCG AAAACAGGCG 720
      ATATCTGGAA ATTTGGATTC TCCAGAAGGT GGTTCGATG CCATCATGCA AGTTGCAGTT 780
      TGTGGATCAC TGATTGGCTG GAGGAATGTT ACACGGCTGC TGGTGTGTTT CACAGATGCC 840
      GGGTTTCACT TTGCTGGAGA TGGGAAACTT GGTGGCATTG TTTTACCAAA TGATGGACAA 900
      TGTCACTGCG AAAATAATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT 960
      CACCTTGTCC AGAAACTGAG TGAATAATAT ATTACAGCAA TTTTTCAGT TACTGAAGAA 1020
      TTTAGGCTTT TTTACAAGGA GCTGAAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080
      TCTGCAAAAT CTAGCAATGT AATTCAATTT ATCATTGATG CATACAATTC CCTTCTCTCA 1140
      GAAATCATTT TGGAAAAACG CAAATTGTCA GAAGGAGTAA CAATAAGTTA CAAATCTTAC 1200
      TGCAAGAACG GGGTGAATGG AACAGGGGAA AATGGAAGAA AATGTTCCTA TATTTCCATT 1260
      GGAGATGAGG TTCAATTTGA AATTAGCATA ACTTCAATA AGTGTCCTAA AAAGGATTCT 1320
      GACAGCTTTA AAATTAGGCC TCTGGGCTTT AOCGAGGAA TAGAGGTTAT TCTTCAGTAC 1380
      ATCTGTGAAT GTGAATGCCA AAGCGAAGGC ATCCCTGAAA GTCCCAAGTG TCATGAAGGA 1440
      AATGGGACAT TTGAGTGTGG CGCGTGCAGG TGCAATGAAG GCGGTGTGG TAGACATTGT 1500
      GAATGCAGCA CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAC 1560
      AGTTTCAGAA TCTGCAGTAA CAATGGAGAG TGGCTCTGCG GACAGTGTGT TTGTAGGAAG 1620
      AGGATAATA AAGATGAAT TTAATCTGGC AAATCTCTCG AGTGATGATA TTTCAACTGT 1680
      GATAGATCCA ATGGCTTAAT TTGTGGAGGA AATGGTGTGT GCAAGTGTG TGTGTGTGAG 1740
      TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTCTTT TGGATACTAG TACTTGTGAA 1800
      GCCAGCAACG GACAGATCTG CAATGGCCGG GGCATCTGCG AGTGTTGGTGT CTGTAAGTGT 1860
      ACAGATCCGA AGTTTCAAGG GCAAACTGTG GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920
      GCTGAGCATA AAGAATGTGT TCAGTGCAGA GCCTTCAATA AAGGAGAAAA GAAAGACACA 1980
      TGCACACAGG AATGTTCTTA TTTTAACATT ACCAAGGTAG AAAGTCGGGA CAAATTACCC 2040
      CAGCCGGTCC AACCTGATCC TGTGTCCCAT TGTAAAGAGA AGGATGTTGA CGACTGTTGG 2100
      TTCTATTTTA COTATTTCAGT GAATGGGAAC AACGAGGTCA TGGTTTCATG TGTGGAGAA 2160
      CCAGAGTGTG CCACCTGGTC AGACATCATT CCAATTGTAG CTGGTGTGTT TGCTGGAATT 2220
  
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GTTCCTTATTG GCCTTGCACTT ACTGCTGATA TGGAGCTTTT TAATGATAAT TCATGACAGA 2280
 AGGGAGTTTG CTAATTTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAAT 2340
 CCTATTATA AGAGTGCCGT AACAACTGTG GTCATCCGA AGTATGAGG AAAATGA

5 **A10 Protein sequence:**
 Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)
 Unigene number: Hs.287797
 Probeset Accession #: X07979
 Protein Accession #: NP_002202.1
 10 Signal sequence: 1-21
 Transmembrane domains: 732-754
 INB domain: 34-464
 PSI domain: 26-76
 15 Cellular Localization: plasma membrane

20 1 11 21 31 41 51
 | | | | | |
 MNLQPIFWIG LISSVCCVFA QTDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLQEGMPT 60
 SARCDLLEAL KKKGCPDDI ENPRGSKDIK KNKNVTNRSK GTAEKLKPED ITQIQPQQLV 120
 LRLRSGEPQT FTLKPKRAED YPIDLYLMD LSYSMKDDLE NVKSLGTDLM NEMRRITSDF 180
 RIGFGSFVEK TVMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKG VFNELVGKQR 240
 25 ISGNLDSPEG GFDAIMQVAV CGSLIGWRNV TRLLVFTDA GFHPAGDGKL GGIVLPNDGQ 300
 CHLENNMYTM SHYYDPSIA HLQVQLSENN IQTIFAVTBE FQPVYKELKN LIPKSAVGTL 360
 SAMSSNVLIQL IIDAYNSLSS EVILENGKLS EGVTSISKSY CRNGVNGTGE NGRKCSNISI 420
 GDEVQFEISI TSNKCPKQDS DSPKIRPLGF TEEVEVILQY ICECECQSEG IPESPKCHEG 480
 NGTFEGCAGR CNEGRVGRHC ECSTDEVNSE DMDAYCRKEN SSEICSNNGE CVCGQCVCRK 540
 RDNTNBIYSG KFCECNFNC DRSNGLIOGG NGVCKCRVCE CNPNYTGSA CDSLDTSTCE 600
 30 ASNGQICNGR GICECVCCK TDPKFQGTTC EMCQTCLGVC AEHKECVQCR AFNKGKKKDT 660
 CTQECSYFNI TKVESRDKLP QFVQPDFVSH CKEKDVEDCW FYFTYSVNGN NBVMVHVVEN 720
 PECPGPDIPI PIVAGVVAGI VLIGLAILLI WKLLMIHDR REFAPKEKEK MNAKWDGTGEN 780
 PIYKSAVTTV VNPKYEGK

35 **A11 DNA SEQUENCE**
 Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 40 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 | | | | | |
 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGA 60
 GCTGTGCTTT ACAACACCTC CAOGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
 CAGCAAAGGT ACACACACCT GGTTCGAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180
 TCATATTGA GCTATTCAAC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300
 50 GAACCAACA ATAGGCAAAA AGATGAGGAC TGCGTGGAGA TCTACATCAA GAGAGAAAAA 360
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 GCTGCCTGTA CCAATACATC CTGCACTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
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 ACAGCCCTGG AATCCCTGTA GCATGGAAGC CTGTTTGCA GTCAACCACT GGGAAACTTC 600
 AGCTACAAAT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
 55 ACCATGCACT GTATGTCTC TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720
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 TTGCAGGGAC CAGCCACGGT TGAATGCACC ACTCAAGGGC AGTGGACACA GCAAAATCCA 1080
 GTTTGTGAAG CTTTCCAGTG CACAGCCTTG TOCAACCCCG AGCGAGGCTA CATGAATTGT 1140
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 GGTTTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAAC 1260
 65 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
 GTGAGGTGTG CTCAATCCCC TATTGGAGAA TTCACTACA AGTCCTCTTG TGCTTCAGC 1380
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 TGGACAGAAG AGGTTCCCTC CTGCCAAGTG GTAAAATGTT CAAGCCTGGC AGTTCCGGGA 1500
 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCGCTGT 1560
 70 CCTGAAGGAT GGACGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620
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 CTTTCTGCTG CTGAGCTCTC CCTCCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740
 TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
 GGAAGCTACC AAAAGCCTTC TTATATCCTT TAA

75 **A12 Protein sequence:**
 Gene name: Selectin E (endothelial adhesion molecule 1)
 80 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Protein Accession #: NP_000441
 Signal sequence: 1-22
 Transmembrane domains: 555-573
 C-lectin domain: 23-139

Cellular Localization: plasma membrane

5 1 11 21 31 41 51
 MIAQSFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QORYTHLVAI QNKEEIEYLN 60
 SILSYSPSYW WIGIRKVVNV WVVVGTQKPL TEEARNWAPG EPNNRQKDED CVEIYIKREK 120
 DVGWMDERC SKKKLALCYT AACTNTSCSG HGECVETINN YTCKCDPGFS GLKCEQIVNC 180
 10 TALESPHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
 ECDAVTNPAN GFVECPQNPQ SFPWNTTCTF DCEEGFBLMG AQSLQCTSSG NWDNEKPTCK 300
 AVTCRAVRQP QNSVRCSSH PAGEFTFKSS CNFTCEBGFN LQGAQVECT TQQTQIQIP 360
 VCEAFQCTAL SNPERGYMNC LPSASGSFRT GSSCBPSCQ GFVLKGSKRL QCGPTGENDN 420
 EKPTCEAVRC DAVQPPKGL VRCASHPGE PTYKSSCAPS CEEGFELYGS TQLECTSQGQ 480
 15 WTEVPSCQV VKCSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
 SGLLPTCEAP TESNIPVLVAG LSAAGLSLLT LAPPLWLWRK CLRKAKKFVP ASSCQSLESD 600
 GSYQKPSYIL

A13 DNA SEQUENCE

20 Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Nucleic Acid Accession #: NM_001508
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
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 CCGAGATTG AGGTGGCCAC CTGGATCAAA ATCACCCCTA TTCTGGTGA CCTGATCATC 120
 TTCTGATGG GCCTTCTGGG GAACAGCGCC ACCATTGGG TCACCCAGGT GCTGCAGAAG 180
 30 AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTGGACATC 240
 TTGGTGTTC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCCTGACC 300
 ACGTCCAGT ACACCTGTG CTGCAAGCTG CACACTTCC TCTTCGAGG CTGCAGTAC 360
 GCTACGCTGC TGCAGTGTG GACACTCAGC TTTGAGCGCT ACATCGCCAT CTGTCACCCC 420
 TTCAGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTGCTCTGG 480
 35 GTCACTCCG CCGTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTG 540
 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCGG CCAACACGAG 600
 CAGCCGAGA CTTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660
 CAGTCCAGCA TCTTGGGCGC CTTCGTGGTC TACCTCGTGG TCCTGCTCTC GTAGCCCTTC 720
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 40 ACGCGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGAG 840
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 GCGTACATGA TCTCTCTCCC CTTCCTGGAG ACGTTTTTCT ACCTCAGCTC GGTTCATCAAC 1020
 CGCTCCTGT ACACGGTGTG CTGCAGCAGG TTTCGGCGGG TGTTCGTGCA GGTGCTGTGC 1080
 45 TGCCGCTGT CGCTGCAGCA CGCCAAACCC GAGAAGCGCC TGCGCGTACA TGCGCACTCC 1140
 ACCACCGACA GCGCCGCTT TGTGACGCGC CGGTGTCTCT TCGCGTCCCG GCGCCAGTCC 1200
 TCTGAAGGA GAACGTAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCGAG 1260
 TCTAAGTCCC AGTCATTGAG TCTGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAGCC 1320
 50 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

A14 Protein sequence:

55 Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Protein Accession #: NM_001508, NP_001409
 Signal sequence: none found
 Pfam domains: 7tm_1 [72-172, 224-344]
 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
 60 Cellular Localization: plasma membrane

65 1 11 21 31 41 51
 MASPSLPSSD CSQIIDHSV PEFEVATWIK ITLILVYLII FVMGLLGNLS TIRVTQVLQK 60
 KGYLQKEVTD HVMVLACSDI LVFLIGMPME FYSIWNFLT TSSYTLCKL HTPLFEACSY 120
 ATLLHLVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVN VTSALVALPL LPAMGTETPL 180
 VNVPSHRGLT CNRSSTRHHE QPETSNSIC TNLSSRWTFV QSSIFGAFVV YLVVLLSVAF 240
 70 MCWNMQVLM KSQKSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRILIV TLAVCWMPNQ 300
 IRRIMAAKP KHDWTRSYFR AYMIILPFSE TFFYLSSVIN PLIYTVSSQQ FRRVFVQVLC 360
 CRLSLQHANH ERRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTKIFL STPQSEAEPO 420
 SKSQSLSLES LEPNSGAKPA NSAAENGFOE HEV

A1 ProstateA15 DNA sequence

80 Gene name: CEBP1
 Unigene number: Hs.222399
 Probeset Accession #: AA256485
 Nucleic Acid Accession #: AJ400877
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

	GGGCTCCGCG	CACACCTCCC	CGGCGCGCGG	CGGCCACCGC	CGGCACTCCG	CGGCCTCTGC	60
	CGGCAACCGC	TGAGCCATCC	ATGGGGGTGG	CGGGCCGCAA	CGGTCGCCGG	CGGCCTCTGG	120
	CGGTGCTGCT	GCTGCTGCTG	CTGCTGCCGC	CAGTCTGCTG	GCTGGCGGGG	GCGCTCCGCG	180
5	CGGGTCGGGG	CCGTGCGCGG	GGGCGCGCAG	AGGATGTAGA	TGAGTGTGCC	CAAGGGCTAG	240
	ATGACTGCCA	TGCGAGCGCC	CTGTGTGAGA	ACACACCCAC	CTCCTACAAG	TGCTCCTGCA	300
	AGCCTGGCTA	CCAAGGGGAA	GGCAGGCAGT	GTGAGGACAT	CGATGAATGT	GGAAATGAGC	360
	TCAATGGAGG	CTGTGTCCAT	GACTGTTTGA	ATATTCCAGG	CAATTATCGT	TGCACCTGTT	420
10	TTGATGGCTT	CATGTTGGCT	CATGACGGTC	ATAATTGTCT	TGATGTGAC	GAGTGCCTGG	480
	AGAACAATGG	CGGCTGCCAG	CATACCTGTG	TCAACGTCTT	GGGGAGCTAT	GAGTGTCTGT	540
	GCAAGGAGGG	GTTTTTCCTG	AGTGACAATC	AGCACACCTG	CATTCAACGC	TGCGAAGAGG	600
	GCCTGAGCTG	CATGAATAAG	GATCACGGCT	GTAGTCAAT	CTGCAAGGAG	GCCCCAAGGG	660
	GCAGCTCGC	CTGTGAGTGC	AGGCTGGTT	TTGAGCTGGC	CAAGAACCAG	AGAGACTGCA	720
15	TCTTGACCTG	TAACCATGGG	AAOCTGGGGT	GCCAGCACTC	CTGTGAOGAT	ACAGCCGATG	780
	GCCCAGAGTG	CAGTGTCCAT	CCACAGTACA	AGATGCACAC	AGATGGGAGG	AGCTGCCTTG	840
	AGCGAGAGGA	CATCTGCTCG	GAGGTGACAG	AGAGCAACAC	CACATCAGTG	GTGGATGGGG	900
	ATAAAGCGGT	GAACGGGGGG	CTGCTCATGG	AAACGTGTGC	TGTCAACAAT	GGAGGCTGTG	960
	ACCGCACCTG	TAAGGATACT	TGACAGGTG	TCCACTGCAG	TTGTCTGTT	GGATTCACTC	1020
20	TCCAGTTGGA	TGGGAAGACA	TGTAAAGATA	TTGATGAGTG	CCAGACCCCG	AATGGAGGTT	1080
	GTGATCATTT	CTGCAAAAAC	ATCGTGGGCA	GTTTTGACTG	CGGCTGCAAG	AAAGGATTTA	1140
	AATTATTAA	AGATGAGAA	TCCTGCAAG	ATGTGGATGA	GTGCTCTTTG	GATAGGACCT	1200
	GTGACCACAG	CTGCATCAAC	CACCTGGGCA	CATTGTCTTG	TGCTTGCAAC	CGAGGGTACA	1260
	CCCTGTATGG	CTTCAACCC	TGTGGAGACA	CCATGAGTG	CAGCATCAAC	AACGGAGGCT	1320
25	GTGACGAGTG	CTGTGTGAAC	ACAGTGGGCA	GCTATGAATG	CCAGTGGCAC	CCTGGGTACA	1380
	AGCTCCACTG	GAATAAAAA	GACTGTGTGG	AAGTGAAGGG	GCTCCTGCCC	ACAAGTGTGT	1440
	CACCCCGTGT	GTCCCTGCAC	TGCGGTAAGA	GTGGTGGAGG	AGACGGGTGC	TTCTTCAGAT	1500
	GTCACCTCTG	CATTCACTCT	TCTTCAGATG	TCACCACCAT	CAGGACAAGT	GTAACCTTTA	1560
	AGCTAAATGA	AGGCAAGTGT	AGTTTGAAAA	ATGCTGAGCT	GTTCCTCCGAG	GGTCTGCGAC	1620
30	CAGCATACCC	AGAGAAAGCA	AGCTCAGTAA	AAGAGAGCTT	CGCTAGGTA	AACCTTACAT	1680
	GCAGCTCTGG	CAGCAAGTCT	CCAGGAGCCC	CTGGCCGACC	AAGCACCCCT	AAGGAAATGT	1740
	TTATCATGTG	TGAGTTTGAG	CTTGAACATA	ACCAAAAGGA	GGTGACAGCT	TCTTGTGACC	1800
	TGAGCTGCAT	CGTAAAGGGA	ACCGAGAAGC	GGCTCCGTAA	AGCCATCCGC	ACGCTCAGAA	1860
	AGGCGGTCCA	CAGGGAGCAG	TTTCACTCTC	AGCTCTCAGG	CATGAACCTC	GACGTGGCTA	1920
35	AAAGAGCTCC	CAGAAACATC	GAACGCCAGG	CAGAGTCTTG	TGGAGTGGGC	CAGGGTCATG	1980
	CAGAAAACCA	ATGTGTCACT	TGCAGGGCTG	GGACCTATTA	TGATGGAGCA	CGAGAACGCT	2040
	GCATTTTATG	TCCAAATGGA	ACCTTCCAAA	ATGAGGAAGG	ACAAATGACT	TGTGAACCAT	2100
	GCCCAAGACC	AGGAAATTTCT	GGGGCCCTGA	AGACCCGAGA	AGCTTGGAA	ATGCTGCAAT	2160
	GTGGAGGTCT	GTGTCAACCT	GGTGAATATT	CTGCAGATGG	CTTTGCACCT	TGCCAGCTCT	2220
40	GTGCCCTGGG	CAGGTTCCAG	CCTGAAGCTG	GTGGAACCTT	CTGCTTCCCC	TGTGGAGGAG	2280
	GCCTTGCCAC	CAAAATCTAG	GGAGCTACTT	CCTTTCAGGA	CTGTGAACCC	AGAGTTCAT	2340
	GTTCACCTGG	ACATTTCTAC	AACACCAACA	CTCACCGATG	TATTGTTGTC	CCAGTGGGAA	2400
	CATACGAGCG	TGAATTTTGA	AAAAATAATT	GTGTTTCTTG	CCCAGGAAAT	ACTACGACTG	2460
	ACTTTGATGG	CTCCACAAAC	ATAACCCAGT	GTAAAAACAG	AAGATGTGGA	GGGGAGCTGG	2520
45	GAGATTTTCA	TGGGTACATT	GAATCCCAAA	ACTACCCAGG	CAATTACCCA	GCCAAACCGG	2580
	AGTGTACGTG	GACCATCAAC	CCACCCCCCA	AGCGCCGCAT	CCTGATCGTG	GTCCCTGAGA	2640
	TCTTCTGCTG	CATAGAGGAC	GACTGTGGGG	ACTATCTGGT	GATGCGGAAA	ACCTCTTCAT	2700
	CCAAATCTCT	GACACATAT	GAACCTGCCC	AGACCTACGA	AGCCTCCATC	GCCTTCACCT	2760
	CCAGGTCAAA	GAAGCTGTGG	ATTCAAGTCA	AGTCCAATGA	AGGGAACAGC	GCTAGAGGGT	2820
50	TCCAGTCTCC	ATAGTGACA	TATGATGAGG	ACTACCAGGA	ACTCATTTGA	GACATAGTTC	2880
	GAGATGGCAG	GCTCTATGCA	TCTGAGAAC	ATCAGGAAT	ACTTAAGGAT	AAGAACTTAA	2940
	TCAAGGCTCT	GTGTTGATGC	CTGGCCCATC	CCGAGAACTA	TTTCAAGTAC	ACAGCCGAGG	3000
	AGTCCCGAGA	GATGTTTCCA	AGATCGTTCA	TCCGATTGCT	ACGTTCCAAA	GTGTCCAGGT	3060
	TTTGTAGACC	TTACAAATGA	CTCAGCCCAT	GTGCCATCA	ATACAAATGT	TCTGTATAG	3120
55	GGTTGGTGGG	ACAGAGCTGT	CTTCTTCTG	CATGTCAGCA	CAGTCCGGTA	TTGCTGCCTC	3180
	CCGTATCAGT	GACTCATTAG	AGTTCAATTT	TTATAGATAA	TACAGATATT	TTGGTAAATT	3240
	GACTTGTGTT	TTTCTTTCCC	AGCATCTGTG	ATGTAGACTG	AGAATGGCTT	TGAGTGGCAT	3300
	CAGCTTCTCA	CTGCTGTGGG	CGGATGTCTT	GGATAGATCA	CGGGCTGGCT	GAGCTGGACT	3360
	TTGGTCAGCC	TAGGTGAGAC	TCACTGTGCC	TTCTGGGGTC	TTAATCTCTC	TCAAGGAGTC	3420
60	TGTATGGGAA	AGGAGGCCAC	AGAATAAGCT	GCTTATTCTG	AACTTTCAGC	TTCTCTAGC	3480
	CGGCGCTCT	CTAAGGGAGC	CCTCTGCAC	OGTGTGCAGG	CTCTGACAG	GCAGAACAGG	3540
	CAAGAGGGGA	GGGAAGGAGA	CCCTGCAAG	CTCCCTCCAC	CCACCTTGAG	ACCTGGGAGG	3600
	ACTCAGTTTC	TCCACAGCCT	TCTCCAGCCT	GTGTGATACA	AGTTTGATCC	CAGGAACCTG	3660
	AGTTCTAAGC	AGTGTCTGTG	AAAAAAGGAA	GCAGAAAGAA	TTAGAAATAA	ATAAAACTA	3720
65	AGCACTTCTG	GAGACAT					

Al6 Protein sequence

Gene name: CEGP1
 Unigene number: Hs.222399
 ProbeSet Accession #: AA256485
 Protein Accession #: CAB92285
 Signal sequence: 1-31
 Transmembrane domains: none
 PFAM domains: EGF-like domains [49-84,132-167,177-213,286-321,407-442]
 CUB domain [809-918]
 Cellular Localization: may be secreted

	1	11	21	31	41	51	
80	MGVAGRNRP	AAAVLLLLL	LLPPLLLLAG	AVFPGRGAA	GPQEDVDECA	QGLDDCHADA	60
	LQNTPTSYK	CSCKPGYQGE	GRQCBIDEC	GNELNGGCVH	DCLNIPGNR	CTCFDGMFLA	120
	HDGHNCLD	ECLNNGGCG	HTCVNMGSY	ECCCKEGFPL	SDNQHTCIHR	SEGLSCMKN	180
	DBGCSHLC	APRGSVACBC	RPGFELAKNQ	RDCILTCNHG	NGGQHSCHDD	TADGPECSCH	240
	PQYQHTDGR	SCLEREDTVL	EVTSNNTSV	VDGDKRVKRR	LLMETCAVNN	GGCDRTCKDT	300

5 STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHFCRN IVGSFDCGCK KGFKLLTDEK 360
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGPTH CGDTNECSIN NGGQQQVCVN 420
 TVGSEYEQCH PGYKLHNKK DCVEVKQLLP TSVSPRVSLH CGKSGGSDGC FLRCHSGIHL 480
 SSDVTTIRTS VTFKLNKGKC SLKNAELFPE GLRPALPERK SSVKESFRYV NLTCSGKQV 540
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCOLSCIVKR TEKRLRKAIR TLRKAVHREQ 600
 FHLQLSGMNL DVAKKPPRTS ERQAESCQVC QGHAENQCVS CRAGTYDGA RERCILCPNG 660
 TFQNEEGQMT CBPCPRPGNS GALKTPAWN MSECGGLQCP GEYSADGPAP CQLCALGTFQ 720
 PEAGRTSCFP CGGLATKHQ GATSFQDCET RVQCSGPHFY NTTTHRCIRC PVGTYPQPEFG 780
 10 KNNCVSCPGN TTDFDGSN ITQCKNRRCG GELGDFGTGI ESPNYPGNYP ANTECTWTIN 840
 PPPKRRILIV VPEIFLPIED DOGDYLMVRK TSSNSVTTY BTCQTYERPI APTSRSKKLW 900
 IQPKSNEGNS ARGFQVPIVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960
 LAHPQNYFKY TAQESREMPF RSFIRLLRSK VSRFLRPYK

15 Al7 DNA sequence

Gene name: ESTs
 Unigene number: Hs.293102
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272
 Nucleic Acid Accession #: none found
 Coding sequence: 1-489 (entire sequence is an open-reading-frame)

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5 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGCGACACG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCAAGAGC AGATGGAGAG AGACCTAAAA 1560
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCCT AGGTGATGAA GACAGCCOGA 1620
 10 TOCTCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCTTG GAGCTCTGAG 1680
 TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCTTCCA TCTGATTCCA GCACAACTT 1740
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTG CCCAGGCTGG 1800
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860
 TTGCCTCAGC TTCCCAGTA GCTGGGACCA CAGTGCCCG CCACCAACC CAACTAATT 1920
 TTGTATTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
 CCTCAATGA TGTGCTGCT TCAGCCTCCC ACAGTGCTGG GATTACAGGC ATGGGCCACC 2040
 AGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
 15 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGG AAAATTCTCT 2160
 ACGAGATAAG CAGTTATGTG ACCTCACTGG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
 GCACAGCCCC AGAAGTGAGC AACTGCAGTC ACTGCACGTT TTCATCTCTA GGGACCCAGAA 2280
 CCAAAACCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
 ATGACTCGTT TAAGGCTTAT TTTCTGATG TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400
 20 TTGTCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAAAA

A20 Protein sequence:

25 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AIS38613
 Protein Accession #: BAB20077
 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 30 Tryp_SPC domain: 216-444
 Cellular Localization: not determined

35 1 11 21 31 41 51
 | | | | |
 MGENDPPAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFFP IIVIGIIALI 60
 LALAIGLGIH FDCSKYRRC SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF 120
 TAASWKTMCs DDWKGYHANY ACAQLGFPSY VSSDNLRVSS LEGQPREFV SIDHLLPDDK 180
 VTALHSHVYV REGCASGHVY TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240
 40 LCGSVITPL WITTAARCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGVKVCNT SGWGATEDGA GDASPVLNHA 360
 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSCQGD SGGPLVQQR RLWKLVGATS 420
 FGIGCAEVNK PGVYTRVTSF LDWIEQMER DLKT

A21 DNA SEQUENCE

45 Gene name: ESTs; opposite strand to TRPS1
 Unigene number: none
 Probeset Accession #: AA428090
 Nucleic Acid Accession #: AA428090
 Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 | | | | |
 ATGAAGCCCA GTTTGAAACA CTGGGCTGAT ATAAAAATGT TTTCTGAAAT AGACCAAAGG 60
 55 CAAGTTGTTG GAGAAGAAAT TCATCTACAA GTAGTATCTG TATCTTATCT TGTAGAAAAC 120
 TTTTCAGACA CAGATGATCT TATGTCCATA GTGGAGGAAT CAGACAGCTG CTACAACCGT 180
 GATTCTGTTG GCCTTCTCTG TAGAGCTGGA GACAGACTGC AACCCAAGAC AAAACCCAGA 240
 GGAAGAAACA CTAACCTCAG CCATTGCCCC AATTTCCACC TTGCTAGTTA TCAGAGTTCA 300
 CTATTGTTTA AGCTCCAGGG GTCATACTAT GGCAATCTAC TGGTGGAAAT TATTCTGAGC 360
 60 AAGTGTTTTG TTCAGCTTGC AGTATTAAAA CAAAAAAAC ATTGCCTCCA GCTGCAAGC 420
 AAGGGCATTG CCATTATGAA AGCCCCCAAA AGACTCTCTG CTATTTTCAA AACATGGAAA 480
 GAAAAAGGGA AAAAAGAAAA AAAAATAATA ATTAGAAGGA TTTGTTCCCT AATTGGGGCT 540
 CCAAAAAATC AGAATGAAG ATTGTATAAT GAGGGGAGAT ACTAATTATT TTAACCTCTC 600
 CAAGCAATC TTTGGAAGCA ATCAATTATT TATATACTTT ATGTTCTGTC TTTTGTATT 660
 65 TTTCTCTCTG GTTAAAAACA TGCAGGTGAG TCTTGCCAAC GTCCTTCTCT ATCTGGATCT 720
 GTTCTGCTCT ATTTCTCTTT CAAAGTCATC TTTTCAGGGA CTTGCCCTGA TTAATTGAT 780
 TTTAACCAAA CAAATAAGAT ATTTGATATA TTAATTAAAA CTTTTGTAGA TGATTGATTA 840
 GGAATTGCAT CATGTTTACA TGAGTATACC GAATTCRAAG TTAACCTTCA TAAGCAGGAG 900
 TTTTACACA TGTAAACATA ATCATTACCC AATACTCGAC ACTCAATATT TGATACTCAA 960
 70 CTGAATGTTT TTGAATAAAA CACATTTTFA TGTATCTCT CTGGAGAAAG TAGTATATAT 1020
 CTTTTCACAC AAAATATATC AGTGAGAGAG TGTGTTGTTA AGAAAAAAA TCAAGGACA 1080
 ACAAGTTGAG AGAGTCCAGG CTTTATCAAT ATAGTAATA ATTTTGTAGA ATGGTGATT 1140
 GATTTCACCA TTTCAATTCA GCAGAGCCTG TATATATATA TATATATATA TATATATATA 1200
 TATATATATA TATATATATA TATATTACAA TGATCTGTAT TTCTATTGCT TAGAAGGATG 1260
 75 AAAGTGAATC CATATAAACC ATACCAACGC CGTTATGTGT AACTGGTGGT AAAACTTTAT 1320
 TATTCAAGTT TAGATGTAAAC AGACATCTTT GCTGCCTGAA GATTGTTTGC ATAAGAAATA 1380
 CACCAAGAAC ATGTTTGTGA GTAGAAATGA ACATGCACTA TGAAAAACAA ATAAAAATAA 1440
 ACGAAAAAAT TTCATGTGTT GTAAGAACAG AACTATTATA GCCAACATTC TAGTATTCAA 1500
 ATCAGGACTA CAAATGTAAT TCTTTTCTCT AGCAACATGA AATCATTTCA TATGAAAGAC 1560
 80 ATTTTCTGCT GGTGAATATT GCTGTAAGTT AAATTTTACA TTGGCATTTC GAGATGTTCC 1620
 CCCCTCATGC CTCGCCCAAA GTTTTCCATG TGGTTGTCAA ATAGTCCGC

A22 Protein sequence:

Gene name: ESTs; opposite strand to TRPS1
 Unigene number: none
 Probeset Accession #: AA428090
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 113-129
 Cellular Localization: not determined

10 1 11 21 31 41 51
 MKPSLKHWD IKMFSEIDQR QVVGEEIHLQ VVSYSYLVEN FSDTDDLSI VEESDSCYNR 60
 DSVGLPGRAG DRLQPKTKPR GKTTNLHLF NFHLASYQSS LLFLQGSYY GNLLIVEPILS 120
 15 KCFVQLAVLK QKKHCLQLQS KGIAIMKAPQ RLSAIFKTNK EKGKKKKII IRRICSLIWA 180
 PKNEK

A23 DNA SEQUENCE

20 Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Nucleic Acid Accession #: AL133619
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCA GCTCGCGAC CCCGGGCTCT 60
 CGGCGCCGCG GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCGCA GAGCCGCGAG 120
 30 CTCAGGCGAGA GCGACCGCA GAAACGGAAC CTGGAACCTG AGAAAGCCT GCAGTTCCTG 180
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAA GCTCCATGAG AGATCGAGCA TCTGAAGCGG 240
 GAAACAAAGG GTGAGCCGGC GCGGGGCCCT AGGCGGGCCC TGCCCTCCCA GGCACACTCA 300
 ACACTGCCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CCTGGGCTCA 360
 GGGGGAACAC AGGACGGGGA GCCCTCCAG ACTGTCTTG CCCACCTGGC TGCACTGGCC 420
 CCTGTATGCC AAGCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGCTACCTCT 480
 35 AGCCGTGGCT GACGATGTT ATGCAGCAA GCACAGCAG TGCTGCTCTC GGGAGGCCA 540
 GGGCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGCT GCTCCCGAGA CCTCCCTCCT 600
 CCAAGTAGAG CTGAATGGG AAGGAACCCC TGGGACAGCC CTGCGCTGCG TAGATCTTTG 660
 CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCCCTAC 720
 ATGCTGGGGG CCCAGGGGAT ATGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780
 40 GCAGCAACCA TGGGACAAA GGGAGGAAGC AGAGTCTGT TTCCTTGCCA CTGTGCCAAG 840
 GCACCTCCCC ATCTGCAGAC CGGCCCCCAC CCAGCCCAGG ATCCTGGGCT GTGGTCTCAA 900
 GCTCACTTCC CATATCTTTT GGGGTCTGGG CTGACATCAG GAGGACATCT GACTGGTGGG 960
 TGGAGCCAGC CTGGGAACAT GCGAGCTGGG GCAGTGCTTA GGGCTCTCCC TCCCCAGGGA 1020
 GACATGGAGA AGGGGGTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG 1080
 45 CTGTTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CCTGCAGTGC TGGGAGCGCT 1140
 GACAGGACAC GGAAGAGGCG CATGCTTTCC CTCGGGACCT GCTGTTCAT GTGTCCCAAG 1200
 CCTCTCTGCT TTCCAGATGG CCCCTCAGGA AACCACTTT CCAGGGCCTC TGCTCCCTTG 1260
 GGGCTCTGCT SGGTCTGCAT CAACGAGTG TGGGTAGAGC CGGAGGAGCC CAGCCCTGCC 1320
 AGGCTGAAGG AGGGCTCCTC ACGACACAC AGGCCAGGAG GCAAGCGTGG GGTCTTGGG 1380
 50 GCGGTAGCG CCGACACTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440
 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGCC 1500
 TCCTTCAACA AGCAAGATTC AAAAGCTGAC GTCTCCAGGA AGGCGGACCT GGAAGAGGAG 1560
 55 CCCCTACTTC ACACAGCAA GCTGGACAAA GTTCTGGGG TACAAGGCCA GGCCAGAAAG 1620
 GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACAGGGC 1680
 AGGCAGATGG GGGCGGGGGC ACACCCGCCA ATGATCTTGC CCTTCTCCCT GCGAAAGCCC 1740
 ACCACACTTA GGCAGTGCGA AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCCTGCGA 1800
 ACCCAAGAGC TGGCGCACTT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCGACC 1860
 CCGGAGGAGG TAGCTTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCAA GGTCTCCACC 1920
 60 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCGG AGCGTGCCAT CTGCCCCGCA 1980
 CTGAAGCAGA CCCGAGGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCATGCGAG 2040
 AAGCGGCGCC TGCACTGCTC AGTGCTTGA

A24 Protein sequence:

65 Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Protein Accession #: T43457
 Signal sequence: none found
 Transmembrane domains: 303-322
 Cellular Localization: not determined

75 1 11 21 31 41 51
 MSGAGVAAGT RPPSSPTPGS RRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
 QQQHEMLAK LHEEIEHLKR ENKGEFARGP RPALPPQAHS TLPQHRNT AINSSTRILGS 120
 GGTQDGEPLQ TVLAHLAALA FVCQPSGYRF WGTWTDAAIS SRGWTMLCSQ AQHVLLSGSP 180
 GPEVIAGRQV ATGCSPLDLP PSRAEMGRNP WDSPPCARSL PQIAAVARPR ISSPMALSPH 240
 80 MLGAQGIWTH SIQSLPAIW AATMGTKGGS RVLFPCHLSK ALPHFDSGPH PAQDPGLWSQ 300
 AHFPLSLGLG LTSQGLTGG WSQPGNIAAG AVPRALPSQG DMEKGVGGP FPSRCGNSE 360
 LFWAKGSPR QPQPCSAQDA DRTRERAMLS LGTCCSMCPK PSCFPDGPSP NHLRSASAPL 420
 GARWVCINGV WVEPGGPSPA RLKEGSSRTH RPPGKRGRLA GGSADTVRSP ADSLSMSSFQ 480
 SVKISINSAN SQKARPQPG SPNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQQQARK 540

EKAESNAGA ACMGNSQHQG ROMGAGARPP MILPLPLRKP TTLROCEVLI RELWNTNLLQ 600
 TQELRHLKSL LEGSQRPAQA PEEASFPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA 660
 LKQTPKNNFA BRQKRLQAMQ KRLHRSVL

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A25 DNA SEQUENCE

Gene name: ESTs; prolactin receptor
 Unigene number: Hs.25252
 Probeset Accession #: AA057193
 Nucleic Acid Accession #: NM_000949
 Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
 15 GGAGGCTGAA ATCCCCAGAC GCGGGTTTTC TGGGCTGGGC TTTCTGCTTA CTCACCTCTT 60
 CTCCTCTTTT CTGGATTTTA CCGACCGTTC GCGAAACAGC TTTCCACACA ATGGAGCTTC 120
 ATGTCTCTGT GCAGGAAGTA CTCATGACTG GATGTGGCAG ACTTTGCTCC CTGACAAAAC 180
 TAAAGAACTC TCCTATTTCAT GGAGGCGAAC ACTGAGGATG CTTTCCACAT GAAACCTGAA 240
 20 GTGAACCTTC GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAAATGTGG 300
 CATCTGCAAC CGTTTTCCT CTGCTACTTT TTCTCAACAC CTGCCTTCTG AATGGACAGT 360
 TACCTCCTGG AAAACCTGAG ATCTTTAAAT GTGTTCTCC CAATAAGGAA ACATTACCTT 420
 GCTGGTGGAG GCTCGGGACA GATGGAGGAC TTCTACCAA TTATTCACTG ACTTACCACA 480
 GGGAAAGGAG GACACTCATG CATGAATGTC CAGACTACAT AACCGGTGGC CCCAATCTCT 540
 25 GCCACTTTGG CAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600
 CTAACACAGT GGAAGCAGT TTCTGGGATG AACTTTATGT GGACGTGACT TACATAGTTC 660
 AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAACAA GCCAGAGAGC AGAAAACCTT 720
 ACCTGTGGAT TAAATGGTCT CCACCTACCC TGATTGACTT AAAAAGTGGT TGGTTCAACG 780
 TCCTGTATGA AATTCGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTGCTG 840
 30 GGCAGCAAC AGAGTTTAAG ATTCTCAGCC TACATCCAGG ACAGAAATAC CTTGTCCAGG 900
 TTGCTGCAAC ACCAGACCAT GGATACTGGA GTGCATGGAG TCCAGCGACC TTCATTCCAG 960
 TACCTAGTGA CTTACCATG AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCTCTTCTG 1020
 CTGTCTATG TTTGATTATT GTCTGGGCAG TGGCTTTGAA GGGCTATAGC ATGGTGACCT 1080
 GCATCTTTCC GCCAGTTCTT GGGCCAAAAA TAAAGGATG TGATGCTCAT CTGTGGGAGA 1140
 35 AGGGCAAGTC TGAAGAACTA CTGAGTGCCT TGGGATGCCA AGACTTTCCT CCCACTTCTG 1200
 ACTATGAGGA CTGTCTGGTG GAGTATTAG AAGTAGATGA TAGTGAGGAC CAGCATCTAA 1260
 TGTCAGTCCA TTCAAAGAA CACCCAGTC AAGGTATGAA ACCCAATAC CTGGATCCTG 1320
 ACACTGATC AGGCGGGGG AGCTGTGACA GCGCTTCCCT TTTGTCTGAA AAGTGTGAGG 1380
 AACCCAGGCG CAATCCCTCC ACATTCATG ATCTCTGAGT CATTGAGAAG CCAGAGAATC 1440
 40 CTGAACCAAC CCACACCTGG GACCCCACTG GCATAAGCAT GGAAGGCCAA ATCCCTTATT 1500
 TTCATGTGG TGGATCCAAA TGTTCAACAT GGCCCTTACC ACAGCCAGC CAGCACAACC 1560
 CCAGATCTCT TACCACAAAT ATTACTGATG TGTGTGAGCT GGCTGTGGGC CCTGCAGGTG 1620
 CACCGGCCAC TCTGTTGAAT GAAGCAGGTA AAGATGCTTT AAAATCCTCT CAAACCATTA 1680
 AGTCTAGAGA AGAGGGAAG GCAACCCAGC AGAGGGAGGT AGAAGCTTC CATTTCTGAGA 1740
 45 CTGACCAGGA TAGCCCTCTG CTGCTGCCCC AGGAGAAAC CCCCTTTGGC TCCGCTAAAC 1800
 CCTTGGATTA TGTGGAGATT CACAAGGTCA ACAAGATGG TGCATTATCA TTGCTACCAA 1860
 AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGGAC TCCTGAGAAC AATAAGGAGT 1920
 ATGCCAAGT GTCCGGGGTC ATGGATAACA ACATCCTGGT GTTGGTGCCA GATCCACATG 1980
 CTAACAACTG GCTTGTCTTT GAAGAATCAG CCAAGAGGCG CCCACCATCA CTTGAACAGA 2040
 50 ATCAAGCTGA GAAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100
 TGGGTGGTTT GGATTACCTG GATCCCGCAT GTTTTACACA CTCCTTTTCA TGATAGCTTG 2160
 ACTAATGAAA TGATTGGTTA AAATGTGATT TTTCTTCAGS TAACACTACA GAGTACGTGA 2220
 AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAGCTC CCAGCTCCTT TCATGCTCCA 2280
 TTTTAAACCA CTTCGCTCTT TCTCCAGCAG CTGATTCCAG AACAAATCAT TATGTTTCTT 2340
 55 AACTGTGATT TGTAGATTTA CTTTGTCTG TTAGTTATAA AACTATGTGT TCAATGAAAT 2400
 AAAAGCACAC TGCTTAGTAT TCTTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAAAG 2460
 GCTTTTCATG TTTGGCATGG GACAGACGGA AATGAAATTG TCAAAATTGT TTACCATAGA 2520
 AAGATGACAA AAGAAATTT TCCACATAGG AAAATGCCAT GAAAATGTCT TTTGAAAAC 2580
 AACTGCATAA CCTTTACACT CCTGTGCCAT TTTATTAGGA TTACCCAAAT ATAACCATTT 2640
 60 AAAGAAAGAA TGCAATCCAG AACAAATTGT TTACATAAGT TCCTATACCT TACTGACACA 2700
 TTGCTGATAT GCAAGTAAGA AAT

A26 Protein sequence:

Gene name: ESTs; prolactin receptor
 Unigene number: Hs.25252
 Probeset Accession #: AA057193
 Protein Accession #: NP_000940
 Signal sequence: 1-23
 Transmembrane domains: 237-253
 FN3 domains: 28-112, 127-215
 Cellular Localization: plasma membrane

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1 11 21 31 41 51
 MKENVASATV FTLLPLIATC LLNGQLPPGK PEIPKCRSPN KETFTCWWRP GTDGGGLPTNY 60
 SLTYHREGT LMHECPDYIT GGPNSCHFGK QYTSWRTYI MMVNATQMG SSFSDLYVD 120
 VTIIVQPDFP LELAVEVKQP EDRKPYLWIK WSPPTLIDLK TGWFTLLYEI RLKPEKAAEW 180
 EIHFAQQOTE FKILSLHPGQ KYLVQVRCKP DRGVWSAWSP ATFIQIPSDP TWNDTTVWIS 240
 VAVLSAVICL IIVWAVALKG YSMVTCIFPP VPGPKIKGFD AHLLEKKGSE ELLSALGQCD 300
 FPPTSDYEDL LVEYLEVDDS EDQHLMSVHS KERPSQGMKP TYLDPDTSRG RGSCDSPSL 360
 SEKCEEPQAN PSTFYDPEVI EKPENPETH TWDPQCISME GKIPYFHAGG SKCSTWPLPQ 420

PSQHNPRSSY HNITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQOREVE 480
 SFHSETDQDT PWLLPQKEKP FGSAPLDYV BIHKVNDKGA LSLLPKQREN SGKPKKPGTP 540
 ENNKEYAKVS GVMNDNLLVL VPDPHAKNVA CFESAKEAP PSLEQNQAEK ALANFTATSS 600
 KCRLQLGLD YLDPACFTHS FH

A27 DNA SEQUENCE

Gene name: Human neurotrophin Y receptor Y1 (NPYY1)
 Unigene number: Hs.169266
 Probeset Accession #: L07615
 Nucleic Acid Accession #: NM_000909.1
 Coding sequence: 209-1363 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CATTCCCACC CTTCCTTCTT TAATAAGCAG GAGCGAAAAA GACAAATTCC AAAGAGGATT 60
 GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTTGGT AAATGGATTC CAATATCGGG 120
 AATAAGAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTTGTCTAAA 180
 ATAATCTATA ACAACCAAAAC CAATCAAAAT GAATTCACAA TTATTTTCCC AGGTTGAAAA 240
 TCATTGATGC CACTCTAATT TCTCAGAGAA GAATGCCAGC CTCTGTGCTT TTGAAAATGA 300
 TGATTGTCTT CTGCCCTTGG CCATGATATT TACCTTAGCT CTGTCTTATG GAGCTGTGAT 360
 CATTCTTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAC AAAAGGAGAT 420
 GAGAAATGTT ACCAATCATCC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTTGCCAT 480
 CATGTGTCTC CCCTTTACAT TTGCTACAC ATTAATGGAC CACTGGGTCT TTGGTGGGGC 540
 GATGTGTAAAG TTGAATCCTT TTGTGCAATG TGTTTCAATC ACTGTGTCCA TTTTCTCTCT 600
 GGTCTCTCAT GCTGTGGAAAC GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA 660
 TAATAGACAT GCCTATGTAG GTATTGCTGT GATTGGGTC CTGTCTGTGG CTCTCTCTTT 720
 GCCTTTCTCT ATCTACCAAG TAATGACTGA TGAGCCGCTC CAAATGTGAA CACTTGTATG 780
 GTACAAAGAC AATATCGTGT GCTTTGATCA ATTTCCATCG GACTCTCATA GGTGTCTTAA 840
 TACCACTCTC CTCTTGGTGC TGCAATATTG TGGTCCACTT TGTTTTATAT TTATTTGCTA 900
 CTTCAGATA TATATACGCC TAAAAAGGAG AAACAACATG ATGGACAAGA TGAGAGACAA 960
 TAAGTACAGG TCCAGTGAAG CAAAAGAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020
 ATTTGACGTC TGCTGTGCTC CTCTTACCAT CTTTAACACT GTGTTTGATT GGAATCATCA 1080
 GATCATTTGT ACCCTGCAAC ACAAATCTGT ATTCTGCTC TGCCCACTCA CAGCAATGAT 1140
 ATCCACTTGT GTCAACCCCA TATTTATGAG GTTCTGAAAC AAAAATCTCC AGAGAGACTT 1200
 GCAGTCTTTC TTCAACTTTT GTGATTTCGG GTCTCGGGAT GATGATTATG AAACAATAGC 1260
 CATGTCCACG ATGCACACAG ATGTTTCCAA AACTTCTTTG AAGCAAGCAA GCCCAGTCGC 1320
 ATTTAAAAAA ATCAACAACA ATGATGATAA TGAATAAATC TGAATACTAT TATAGCCTAT 1380
 GTCCCGGAT ACCCTGCTGT TAAAAACAAG CACAACCTGC AACATACTTT GATTACCTGT 1440
 TCTCCCAAGG AATGGGGTGT AAATCATTTG AAAATGACTA AGATTTTCTT GTCTTGTCTT 1500
 TTACTGCTTT TGTGTGATTT GTCAATAATTA CATTTGGAAC AAAAGGTGTG GGCCTTGGGG 1560
 TCTTCTGGAA ATAGTTTGA AAGACATCTT TGAAGTGTCT TTTTGTGAAT TTATGCATAT 1620
 AATATAAAGA CTTTATATCT GTACTTATG GAATGAAATT TCTTTAAAGT ATTACGATGC 1680
 GCTGACTTGT GAAGTACCTG CCATCCAATA CGGTCAATAG ATTGGGTCTT CTGATTAGA 1740
 TTAGATTAGA TTAGATTGTC AACAGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT 1800
 TAGTGTGTTA CAATAGTAAC AGTATGCAAA AGCAGCATTC AGGAGCCGAA AGATAGTCTT 1860
 GAAGTCATTC AGAAGTGGTT TGAGGTTTCT GTTTTGTGGT GGTTTTGTGT TGTTTTGTGT 1920
 TTTTTCACCC TTAAGGGAGG CTTTCATTTC CTCCCGACTG ATTGTCACTT AAATCAAAAT 1980
 TTAATAAATGA ATAAAGAAC ATACTTCTCA GCTGCAATA TTATGGAGAA TTGGGCACCC 2040
 ACAGGAATGA AGAGAGAAAG CAGCTCCCA ACTTCAAAAC CATTTTGGTA CCTGACAACA 2100
 AGAGCATTTT AGAGTAATTA ATTTAATAAA GTAAATTAGT ATTGCTGCAA ATAGCTAAAT 2160
 TATATTATTT TGAATTGATG GTCAGAGAT TTTCCATTTT TTTTACAGAC TGTTCAAGTG 2220
 TTGTCAAGCT TCTGGTCTAA TATGTACTCG AAAGACTTTC CGCTTACAAT TTGTAGAAAC 2280
 ACAAAATATG TTTTCCATAC AGCAGTGCCT ATATAGTGAC TGATTTTAACT TTTCAATGTC 2340
 CATCTTTCAC AGGAAGTAAC ACCAAGGTAC AATGTTAAAG GAATATTAC TTTACCTAGC 2400
 AGGAAAAAAT ACACAAAAAC TGCAGTACT TCATATAGCC CATTTTAACT TGTATAAATC 2460
 GTGTGACTTG TGGCGTCTTA TAAATAATGC ACTGTAAAGA TTACTGAATA GTTGTGTCAT 2520
 GTTAATGTGC CTAATTTTCA GTATCTTGTG ATCATGATTG AGCCTCAGAA TCATTGTGAG 2580
 AAATATATT TTAAGAACA AGACATACTT CAATGTATTA TACAGATAAA GTATTACATG 2640
 TGTTTGATTT TAAAGGGGCG GACATTTTAT TAAATCAAT ATTGTTTGTG CTTTTCCTGA 2700
 GGAGTCTCTT TCAATTTCTT TTTTCTCAT CCTATGACTT CCTCCGATG GT

A28 Protein sequence:

Gene name: Human neurotrophin Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds
 Unigene number: Hs.169266
 Probeset Accession #: L07615
 Protein Accession #: NP_000909.1
 Signal sequence: none found
 Pfam domains: 7tm_1 [57-91]
 Transmembrane domains: 39-61, 77-99, 118-139, 157-179, 212-234, 264-286, 300-322
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MNSTLFSQVE NHSVSNPSE KNAQLLAFEN DDCHLPLAMI FTLLALAYGAV IILGVSGNLA 60
 LIIILKQKE MRNVNLLIV NLSFSDLLVA IMCLPFTFVY TLMDEWVFE AMCKLATPPVQ 120
 CVSITVSIPS LVLIAVERHQ LIINPRGWRP NNRHAYVGIA VIWVLAVASS LPFLIYQVMT 180
 DEPPQNVTLQ AYKDKYVCFD QPPSDSHRLS YTTLLVLQY FGPLCFIFIC YFKIYIRLKR 240
 RNNMOKMRD NKYRSSETKR INIMLLSIVV APAVCWLPFT IFMTVDNNH QIIATCNHNL 300
 LFLCHLTAM ISTCVNPIFY GFLNKNFQRD LQFFNFPCDF RSRDDDYETI AMSTMTDVS 360

KTSLLKQASPV AFKKINNND NEKI

5 A29 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

10
15
20
25
30

1	11	21	31	41	51	
ATGCACACCG	TGGCTACGTC	CGGACCCAAAC	GCGTCCCTGGG	GGGCACCGGC	CAAGCCCTCC	60
GGCTGCCCGG	GCTGTGGCGC	CAACGCCTCG	GACGGCCAG	TCCCTTCGCC	GCGGGCCGTG	120
GACGCTGGC	TCGTGCCGCT	CTTCTTCGCG	GCGCTGATGC	TGCTGGGCT	GCTGGGGAAC	180
TCGCTGGTCA	TCTACGTCAT	CTGCCGCCAC	AAGCGATGC	GGACCGTGAC	CAACTTCTAC	240
ATGCCAACA	TGGCGGCCAC	GGACGTGAAC	TTCTCTCTGT	GCTGCGTCCC	CTTACGGCC	300
CTGCTGTACC	CGCTGCCCGG	CTGGGTGCTG	GCGCACTCA	TGTGCAAGTT	CGTCAACTAC	360
ATCCAGCAGG	TCTCGGTGCA	GGCCACGTGT	GCCACTCTGA	CGCCATGAG	TGTGGACCGC	420
TGTTAGCTGA	CGGTGTTCCT	GTTCGCGGCC	CTGCACCGCC	GACGCCCCG	CCTGGCGCTG	480
GCTGTGAGC	TACGATCTG	GTTAGGCTCT	GCGCGGTGT	CTGCGCCGT	GCTGCGCCCTG	540
CACCGCTGT	CACCGGGGCC	GCGCGCTAC	TGCAGTGAGG	CCTTCCCAG	CGCGCCCTG	600
GAGCGCGCT	TGCACTGTA	CAACTCTGT	GCGCTGTACC	TGCTGCCCT	GCTGCCACC	660
TGCGCTGCT	ATGCGCCAT	GCTGCGCCAC	CTGGCGCGG	TGCGCGTGC	CCCCGCGCC	720
GCGATAGCG	CCCTGCAGG	GCAGGTGCTG	GCAGAGCGG	CAGGCGCGT	GCGGCGCAAG	780
GTCTCGCGC	TGTTGGCGGC	CGTGGTCTG	CTCTTCGCG	CCTGCTGGG	CCCCATCCAG	840
CTGTTCTGT	TGCTGCAGG	GCTGGGCCCC	GCGGCTCCT	GGCACCACG	CAGCTACGCC	900
GCCTACGCG	TTAAGACCTG	GGCTCACTGC	ATGTCCTACA	GCAACTCCG	GCTGAACCCG	960
CTGCTCTAG	CCTTCTGGG	CTGCACTTC	CGACAGGCT	TCCGCGCGT	CTGCCCCCTG	1020
GCGCGCGCC	CCCCCGCGG	CCCCGACCT	CGGACCCCG	AGCCCCACAC		1080
CGGAGCTGC	ACGCGCTGG	GTCCCAACCG	GCCCCGCCA	GGGCGAGAA	GCCAGGGAGC	1140
AGTGGGCTGG	CCGCGCGCG	GCTGTGCTC	CTGGGGGAGG	ACAAGCCCC	TCTCTGA	

35 A30 Protein sequence

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA

Unigene number: Hs.208229

Protein Accession #: AI819198

Signal sequence: none found

Pfam domains: 7tm_1 [59-323]

40 Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization: plasma membrane

45
50

1	11	21	31	41	51	
MHTVATSGPN	ASWGAPANAS	GCPGCGANAS	DGFVPSRAV	DAWLVPLEFFA	ALMLLGLVGN	60
SLVIYVICRH	KPMRTVINFY	IANLAATDVT	FLCCVPFTA	LLYPLPGWVL	GDFMCKPFVNY	120
IQQVSVQATC	ATLTAMSVDR	WYVTVPFLRA	LHRRTPRLAL	AVSLSIWVGS	AAVSAPVLAL	180
HRLSPGPRAY	CSEAPPSRAL	ERAPALYNLL	ALYLLPLLAT	CACYAAMLRH	LGRVAVRPAP	240
ADSALQGQVL	AERAGAVRAK	VSRLVAAVVL	LFAACWPIQ	LFLVLQALGP	AGSWHPRSVA	300
AYALKTWAHC	MSYSNSALNP	LLYAFLGSHF	RQAFRRVPCP	APRRPRRPRR	PGSPDPAAPH	360
AEHLRLGSHP	APARAQKPGS	SGLAARGLCV	LGEDNAPL			

55 A31 DNA SEQUENCE

Gene name: CH22_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1)

Unigene number: Hs.252387

Probeset Accession #: NM_014246

Nucleic Acid Accession #: NM_014246

Coding sequence: 1-9045 (underlined sequences correspond to start and stop codons)

65
70
75
80

1	11	21	31	41	51	
ATGGCGCGCG	CGCGCGCGCC	CGTGTCTGCC	GTGCTGCTGC	TCCTGGCGCG	CGCGCGCGCC	60
CTGCGCGCGA	TGGGGCTGCG	AGCGCGCGCC	TGGGAGCGCG	GCGTACCGCG	CGGGACCGCG	120
GCCTTCGCCC	TCCGGCCCGG	CTGTACCTAC	GCGGTGGCGG	CGCTTCGAC	GCCCGGGCGG	180
CGCGGGGAGC	TGCTGGACGT	GGCGCGCGAT	GGCGCGCTGG	CAGGACGTGG	GCGGTCTCG	240
GGCGCGGGGC	GCGCGCTGCC	GCTGCAAGTC	CGCTTGGTGG	CCGCGAGTGC	CCGAGCGCGG	300
CTGAGCGCGC	GCTTGGGGGC	GCGCACGAC	CTTCCCGGCT	GCGGAGCCCG	TGCGCGGCTC	360
TGCGGAACCG	GTGCGCGGCT	CTGCGGGGCG	CTCTGCTTCC	CGGTCCCCCG	CGCTGCGCGG	420
GCGCGCGAGC	ATTGCGGCT	CGCAGCTCCG	ACCACTTAC	CGCGCTCGCG	GCTCCGCGCG	480
CGCCCCAGGC	CCCGCTGTCC	CGCGGTGCC	ATCTGCTTCC	CGCGGGCGCG	CTCGGTCCGC	540
CTGCGTCTGC	TGTGCGCCCT	GCGGCGCGCG	GCTGGGCGCG	TCCGGGTGGG	ACTGGGCTG	600
GAGCGCGCCA	CGCGGGGAC	GCCCTCCGCG	TGCGCATCCC	CATCGCGCGC	CCTGCGCGCG	660
AACTTGCGCG	AAGCCCGGCG	GGGCGCGCGG	CGACGGGCCC	GGCGGGGAC	GAGCGGCGAG	720
GGGAGCTGTA	AGTTTCGAT	GCCCACTAC	CAGGTGGGCT	TGTTTGAGAA	CGAACCGCGG	780
GGCACCCCTCA	TCCTCCAGCT	GCAACGCGAC	TACACCATCG	AGGGCGAGGA	GGAGCGGCTG	840
AGCTATTATCA	TGGAGGGGCT	GTTCGACGAG	CGTCCCGGGG	GCTACTTCGG	AATCGACTCT	900
GCCACGGCGG	CGCGGAGCAC	GGACAGCGTA	CTGGACCGCG	AGACCAAGGA	GAGCAAGCTC	960
CTCAGGGTGA	AAGCGGTGGA	CTACAGTACG	CGCGCGGCT	CGGCCACCA	CTACATCACT	1020
GTCTTGTGTA	AAGACACCAA	CGACCAAGC	CGGTCTTCG	AGCAGTGGGA	GTACCGCGAG	1080
CGCGTGGCGG	AGAACCTGGA	GGTGGGCTAC	GAGGTGCTGA	CCATCGCGCG	CAGCGACCGC	1140

	GACTGCCCCA	TCAACGCCAA	CTTGCCTTAC	CGCGTGTGG	GGGGCGCGTG	GGACGTCTTC	1200
	CAGCTCAACG	AGAGCTCTGG	CGTGGTGAGC	ACACGGGGCG	TGCTGGACCG	GGAGGAGCGG	1260
	GCGAGTACC	AGCTCTCTGT	GGAGGCCAAC	GACCAAGGGC	GCAATCCGGG	CCCGCTCAGT	1320
5	GCCACGGCCA	CCGTGTACAT	CGAGGTGGAG	GACGAGAAGC	ACAACCTACC	CCAGTTTCAG	1380
	GAGCAGAACT	ACGTGTGCCA	GGTGCCCGAG	GACGTGGGGC	TCAACACGGC	TGTGCTGCGA	1440
	GTGCAGGCCA	CGGACCCGGA	CCAGGGGCCAG	AACCGGGCCA	TTCACTACAG	CATCTCTCAGC	1500
	GGGAACGTGG	CCGGCCAGTT	CTACCTGCAC	TGCTGTAGCG	GGATCCTGGA	TGTGATCAAC	1560
	CCCTTGGATT	TGAGGATGT	CCAGAAATAC	TGCTGTAGCA	TTAAGGCCCA	GGATGGGGGC	1620
10	CGGCCCCCGC	TCATCAATTC	TTCAAGGGTG	GTGTCTGTGC	AGGTGCTGGA	TGTCAACGAC	1680
	AACGAGCCTA	TCCTTTGTAG	CAGCCCCCTC	CAGGCCACGG	TGCTGGAGAA	TGTGCCCTCG	1740
	GGCTACCCCG	TGTTGTACAT	TCAGGCGGTG	GACGCGGACT	CTGGAGAGAA	CGCCCGGCTG	1800
	CACATATCGC	TGGTGGACAC	GGCTCCAC	TTCTGGGGG	GCGGCAGCGC	TGGGCTTAAG	1860
	AATCTCTGCC	CCACCCCTGA	CTTCCCTTTC	CAGATCCACA	ACAGCTCCGG	TTGGATCACA	1920
15	GTGTGTGCCG	AGCTGGACCG	CGAGGAGGTG	GAGCACTACA	GCTTCGGGGT	GGAGGCGGTG	1980
	GACCACGGCT	CGCCCCCAT	GAGCTCTTCC	ACCAAGGTGT	CCATCACGGT	GCTGGAGCTG	2040
	AATGACAACG	ACCGGCTGTT	CAOCGAGCCC	ACCTACGAGC	TTGCTGTGAA	TGAGGATGCG	2100
	GCGGTGGGGA	CGAGCGTGT	GACCTGCAG	GCCCGCGACC	GTGACGCCAA	CAGTGTGATT	2160
	ACCTACGAGC	TCACAGCGCG	CAACACCCCG	AACCGCTTTG	CACTCAGCAG	CCAGAGAGGG	2220
20	GGGGGCTCTA	TCACCTCTGC	GCTACCTCTG	GACTACAAGC	AGGAGCAGCA	GTACGTGCTG	2280
	GCGGTGACAG	CATCCGACCG	CACACGCTCG	CACACTGCGC	ATGTCCTAAT	CAACGTCACT	2340
	GATGCCAACA	CCCAACAGGC	TGTCTTTTCA	AGCTCCCAT	ACACAGTGAG	TGTCACTGAG	2400
	GACAGGCTCG	TGGGCACCTC	CATTGCTACC	CTCAGTGCCA	ACGATGAGGA	CACAGAGAG	2460
	AATGCCCGCA	TCACCTAAGT	GATTCAAGAC	CCCGTGCCCG	AGTTCCCGAT	TGACCCCGAC	2520
25	AGTGGCACCA	TGTACACCAT	GATGGAGCTG	GACTATGAGA	ACCAGGTGCG	CTACACGCTG	2580
	ACCATCATGG	CCAGGACAAA	CGGCATCCCG	CAGAAATCAG	ACACCAACAC	CCTAGAGATC	2640
	CTCATCTCGC	ATGCCAATGA	CAATGCAACC	CAGTTCTCTG	GGGATTCTTA	CGAGGGTTCC	2700
	ATCTTTGAGG	ATGCTCCACC	CTGACCCAGC	ATCTCTCAGG	TCTCTGCCAC	GGACCGGGAC	2760
	TCAGGTCCCA	ATGGGCGTCT	GCTGTACACC	TTCCAGGGTG	GGGACGACCG	CGATGGGGAC	2820
30	TTCTACATCG	AGCCCAAGTC	CGTGTGTGAT	CGCACCCAGC	GCCGCTGGA	CCGGGAGAA	2880
	GTGGCCGCTG	ACAACTTTTG	GGCTCTGGCT	GTGGATCGGG	GCAGTCCAC	TCCCTTAGC	2940
	GCCTCGGTAG	AAATCCAGGT	GACCATCTTG	GACATTAATG	ACAATGCCCG	CATGTTTGAG	3000
	AAGGACGAAC	TGGAGCTGTT	TGTTGAGGAG	AACAACCCAG	TGGGTTCGGT	GGTGGAACAG	3060
	ATTCTGTCTA	ACGACCCCTG	TGAAGGCCCT	AATGCCCGAG	TCATGTATCA	GATTGTGGAA	3120
35	GGGACATGCG	GGCATTTCTT	CCAGCTGGAC	CTGCTCAACG	GGGACCTGCG	TGCCATGGTG	3180
	GAGCTGGACT	TTGAGGTCCG	GCGGGAGTAT	GTGCTGTGGG	TGCAGGCCAC	GTCCGCTCCG	3240
	CTGGTGAGCC	GAGCCACGGT	GCACATCTTT	CTGTTGGACC	AGAATGACAA	CCCGCTGTG	3300
	CTGCCGACT	TCCAGATCCT	CTTCAACAA	TATGTACCCA	ACAAGTCCAA	CAGTTTCCCG	3360
	ACCGGCGTGA	TCGGCTGCA	CCCGGCCCAT	GACCCGACCG	TGTGAGACAG	CCTCAACTAC	3420
40	ACCTTCTGTC	AGGGCAACGA	GCTGCGCCTG	TGTCTGTGCG	ACCCCGCCAC	GGCGGAACCTG	3480
	CAGCTCAGCG	CGGACCTGGA	CAACAAACCG	CGCTGAGAGG	CGCTCATGGA	GGTGTCTGTG	3540
	TCTGATGGCA	TCCACAGCGT	CAOCCCTTTC	TGCACCTTGC	GTGTCAACAT	CATCACGGAC	3600
	GACATGCTGA	CCAACAGCAT	CACGTGTCGG	CTGGAGAACA	TGTCCAGGGA	GAAGTTCTCTG	3660
	TCGCCGCTGC	TGCGCCCTCT	CGTGGAGGGG	GTGGCCCGCG	TGCTGTCCAC	CACCAAGGAC	3720
45	GACGTCTTCC	TCCTTCAAGT	CCAGAACGAC	ACCGACGTCA	GCTTCAACAT	CTGGAACGTG	3780
	ACCTTCTCGG	CGCTGCTGCG	TGGCGGCTC	CGGGCCAGT	TCTTCCGCTC	GGAGGACCTG	3840
	CAGGAGCAGA	TCTACCTGAA	TCGGACGCTG	CTGACCCACA	TCTCCACGCA	GCGGCTGCTG	3900
	CCCTTCTGAG	ACAACTCTCT	CCTGCGCGAG	CCCTGCGAGA	ACTACATGAA	GTGCGTGTCC	3960
	GTCTCTGCGT	TGAGCAGCTC	CGCGCCCTTC	CTCAGCTCCA	CCACCGTGTG	TTTCCGCGCC	4020
50	ATCCACCCCA	TCACAGGCGT	GCGCTGCGCG	TGCGCGCCCG	GCTTCAACGG	CGACTACTGC	4080
	GAGACGGAGA	TGCACTCTG	CTACTCCGAC	CGGTGCGGCG	CCAACGCGCG	CTGCCCGCAGC	4140
	CGCGAGGGCG	GCTACACCTG	CGAGTGTCTC	GAGGACTTCA	CTGGAGAGCA	CTGTGAGGTG	4200
	GATGCCCGCT	CAGGCGCGCT	TGCCAACGGG	GTGTGCAAGA	ACGGGGGCGC	CTGCGTGAAC	4260
	GCTGCTATCG	GCGGCTTCCA	CTGCGTGTGT	CCTCCTGGCG	AGTATGAGAG	GCCCTACTGT	4320
55	GAGGTGACCA	CCAGGAGCTT	CCCGCCCCAG	TCTTCTGTCA	CCTTCCGGGG	CCTGAGACAG	4380
	CGCTTCCACT	TCACCATCTC	CCTCACGTTT	GCCACTCAGG	AAAGGAACCG	CTTGCTTCTC	4440
	TACAAACGCC	GCTTCAATGA	GAAGCAGCAG	TTTATCGCCC	TGGAGATCGT	GGAGGAGCAG	4500
	GTGACGCTCA	CCTTCTCTCG	AGGCGAGACA	ACAACGACCG	TGGCACCGAA	GGTTCCCACT	4560
	GTTGTGAGTG	ACGGGGCGTG	GCACTCTGTG	CAGGTGCACT	ACTACAACAA	GCCCAATATT	4620
60	GGCCACCTGG	GCTTGCOCOA	TGGGCGGTCC	GGGGAAGA	TGGCGTGGT	GACAGTGGAT	4680
	GATTGTGACA	CAACCATGGC	TGTGCGCTTT	GGAAAGGACA	TGSGGAACCTA	CAGCTGCGCT	4740
	GCCCAAGGCA	CTCAGACCGG	CTCCAAGAAG	TCCCTGGATC	TGACCGGCCC	TCTACTCCTG	4800
	GGGGTGTGCC	CCAACCTGCG	AGAAGACTTC	CCAGTGACCA	ACCGGCACTT	CGTGGGCTGC	4860
	ATGCGGAACC	TGTCACTGGA	CGGCAAAAT	GTGGACATGG	CCGATTTCAT	CGCCAACTAT	4920
65	GGCACCCGGG	AAGGCTGCGC	TGCTCGGAGG	AACCTTCTGC	ATGGGAGGCG	GTGTGAGAT	4980
	GGAGGCACCT	GTGTCAACAG	GTGGAATATG	TATCTGTGTG	AGTGTCCACT	CGATTTCGGC	5040
	GGGAAGAACT	GTGAGCAAGC	CATGCCTCAC	CCCCAGCTCT	TCAGCGGTGA	GAGCGTCTG	5100
	TCCTGGAGTG	ACCTGAACAT	CATCATCTCT	GTGCGCTGGT	ACCTGGGGCT	CATGTTCCGG	5160
	ACCCGGAAGG	AGGACAGCGT	TCTGATGGAG	GCCACCACTG	GTGGGCCCAAC	CAGCTTTCCG	5220
70	CTCCAGATCC	TGAACAACTA	CCTCCAGTTT	GAGGTGTCCC	ACGGCCCTTC	CGATGTGGAG	5280
	TCGGTATGTC	TGTCCGGGTT	GCGGGTGACC	GACGGGGAGT	GGCACCACTC	GCTGATCGAG	5340
	CTGAAGAAATG	TTAAGGAGGA	CAGTGAGATG	AAGCACCTGG	TCACCATGAC	CTTGAGCTAT	5400
	GGGATGGACC	AGAACAGGCG	AGATATCGGG	GGCATGCTTC	CCGGGCTGAC	GGTAAGGAGC	5460
	GTGGTGTGCG	GAGGCGCTTC	TGAAGACAAG	GTCTCCGTGC	GCGTGGGATT	CCGAGGCTGC	5520
75	ATGCAGGGAG	TGAGGATGGG	GGGACCGCCC	ACCAACGTGG	CCACCTGAA	CATGAACAA	5580
	GCACTCAAGG	TCAGGGTGAA	GGACGGCTGT	GATGTGGAGC	ACCCCTGTAC	CTCGAGCCCC	5640
	TGTCCCGCCA	ATAGCCGCTG	CCAAGAGGCC	TGGGAGGACT	ACAGCTGCGT	CTGTGACAAA	5700
	GGGTACCTTG	GAATAAACTG	TGTGGATGCC	TGTCACTTGA	ACCCCTGCGA	GAACTAGGGG	5760
	GCTTGCCTGC	GCTCCCGCG	GGCTACGTGT	GCGAGTGTGG	GCCCACTCAC	CGCCAGTCTC	5820
80	TAGGGGCGGT	ACTGTGAGAA	CAAACTCGAC	CTTCGTGCCC	CCAGAGGCTG	GTGGGGGAAC	5880
	CCGCTCTGTG	GACCTTGCCA	CTGTGCGGTC	AGCAAGAGCT	TTGATCCCGA	CTGTAAATAG	5940
	ACCAAGGCGC	AGTGCCTAATG	CAAGGAGAAT	TACTACAAGC	TCCTAGCCCA	GGACACCTGT	6000
	CTGCCCTGCG	ACTGCTTCCC	CCATGGCTCC	CACAGCGCCA	CTTGGCAGAT	GGCCACCGGG	6060
	CAGTGTGCTC	GCAAGCCCGG	CGTCACTGGC	CGCCAGTGCA	ACCGCTGCGA	CAACCGGTTT	6120
	GCCGAGGTCA	CCAGCGCTGG	CTGTGAAGTG	ATCTACAATG	GCTGTCCCAA	AGCATTGAG	6180

	GCCGGCATCT	GGTGGCCACA	GACCAAGTTC	GGGCAGCCGG	CTGGGGTGCC	ATGCCCTAAG	6240
	GGATCCGTTG	GAAATGCGGT	CCGACACTGC	AGCGGGGAGA	AGGGCTGGCT	GCCCCCAGAG	6300
	CTCTTTAACT	GTACCAACCA	CTCCTTCGTG	GACCTCAGGG	CCATGAATGA	GAAGCTGAGC	6360
5	CGCAATGAGA	CGCAGGTGGA	CGGCGCCAGG	GCCCTGCAGC	TGGTGAGGGC	GCTGCGCAGT	6420
	GCTACACAGC	ACACGGGCAC	GCTCTTTGGC	AATGACGTGC	GCACGGGCTA	CCAGCTGCTG	6480
	GGCCAGCTCC	TTGAGCAGCA	GAGCTGGCAG	CAGGGCTTCG	ACCTGGCAGC	CACGCAGGAC	6540
	GCCGACTTTC	ACGAGGACGT	CATCCACTCG	GGCAGCGCCC	TCCTGGCCCC	AGCCACCAGG	6600
	GCGGCGTGGG	AGCAGATCCA	GCGGAGCGAG	GGCGGCACGG	CACAGCTGCT	COGGCGCCTC	6660
10	GAGGGCTACT	TCAGCAACGT	GGCACGCAAC	GTGCGGCGGA	CGTACCTGCG	GCCCTTGGTC	6720
	ATCGTCACCG	CCAACTGAT	TCTTGCTGTC	GACATCTTTG	ACAAGTTCAA	CTTTACGGGA	6780
	GCCAGGGTCC	CGCGATTGCA	CACCATCCAT	GAAGAGTTCC	CCAGGGAGCT	GGAGTCTCTC	6840
	GTCTCTCTCC	CAGCCGACTT	CTTCAGACCA	CCTGAAGAAA	AGAAGGGCCC	CCTGCTGAGG	6900
	COGGCTGGCC	GGAGGACCAC	CCCGCAGACC	ACGCGCCCGG	GGCCTGGCAC	CGAGAGGGAG	6960
15	GCCCCGATCA	GCAGGCGGAG	GCGACACCTT	GATGACGCTG	GCCAGTTGCG	CGTGGCTCTG	7020
	GTCTCATTTT	ACCGCACCCT	GGGGCAGCTC	CTGCCCGAGC	GCTACGACCC	CGACCGTCGC	7080
	AGCCTCOGTT	TGCTTCACCG	GCCCATCATT	AATACCCCGA	TGGTGAGCAC	GCTGGTGTAC	7140
	AGCGAGGGGG	CTCGCTCTCC	GAGACCCCTG	GAGAGGCCCG	TCCTGGTGGG	GTTCGCCCTG	7200
	CTGGAGGTGG	AGGAGCGAAC	CAAGCCTGTC	TGCGTGTCTT	GGAACCACTC	CCTGGCCGTT	7260
20	GGTGGGACGG	GAGGGTGGTC	TGCCCGGGGC	TGCGAGCTCC	TGTCCAGGAA	CCGGACACAT	7320
	GTGCGCTGCC	AGTGCCAGCA	CACAGCCAGC	TTTGGGTGTC	TCATGGATAT	CTCCAGGGGT	7380
	GAGAAACGGG	AGGTCTCTGC	TCTGAAGATT	GTACCTATG	CGCTGTGTCT	CTTGTCACTG	7440
	GCAGCCCTGC	TGGTGGCCTT	GGTCTCTCTG	AGCCTGGTCC	GCATGCTGCG	CTCCAACTCT	7500
	CACAGCATT	ACAAGCACCT	CGCGTGGCG	CTCTTCCTCT	CTCAGCTGGT	GTTCGTGATT	7560
25	GGGATCAACC	AGACGGAAAA	CCCGTTTCTG	TGCACAGTGG	TTGCCATCCT	CCTCCACTAC	7620
	ATCTACATGA	GCACCTTTGC	CTGGACCCCT	GTGGAGAGCC	TGCATGTCTA	CGCATGCTG	7680
	ACCGAGGTGC	GCAACATCGA	CACGGGGCCC	ATGCGGTTCT	ACTACGTCGT	GGGCTGGGGC	7740
	ATCCCCGCCA	TTGTCAACAG	ACTGGCGGTC	GGCCTGGACC	CCCAGGGCTA	CGGGAACCCC	7800
	GACTTCTGCT	GGCTGTGCTG	TCAAGACACC	CTGATTTGGA	GCTTTGCGGG	GCCCCATCGG	7860
30	GCTGTTATAA	TCATCAACAC	AGTCACTTCT	GTCTATCTCT	CAAGGGTTTC	CTGCCAAGA	7920
	AAGCACATT	ATTATGGGAA	AAAAGGGATC	GTCTCCCTCT	TGAGGACCGC	ATTCTCTCTG	7980
	CTGCTGCTCA	TCAGCGCCAC	CTGGCTGCTG	GGGCTGCTGG	CTGTGAACCG	CGATGCATCT	8040
	AGCTTTCACT	ACCTCTTCGC	CATCTTCAGC	GGCTTACAGG	GCCCCCTCGT	CCTCCTTTTC	8100
	CACCTGGTGC	TCACACAGGA	GGTCCGGAAG	CACCTGAAGG	GCGTCTCGG	CGGGAGGAAG	8160
35	CTGCACCTGG	AGGACTCCCG	CACCAACAGG	GCCACCTTGC	TGACGCGCTC	CCTCAACTGC	8220
	AACACCACT	TCGGTGAACG	GCGTGAACAT	CTGCGCACAG	ACTTGGGCGA	GTCCACCGCC	8280
	TCGCTGGACA	GCATGCTCAG	GGATGAAGGG	ATCCAGAAAG	TCGGCGTGTG	CTCTGGGCTG	8340
	GTGAGGGGCA	GCCACGGAGA	GCCAGACGCG	TCCCTCATGC	CCAGGAGCTG	CAAGGATCCC	8400
40	CCTGGGCCAG	ATTCCGACTC	AGATAGCGAG	CTGTCCCTGG	ATGAGCAGAG	CAGCTCTTAC	8460
	GCCTCTCTAC	ACTCGTCAGA	CAGCGAGGAC	GATGGGGTGG	GAGCTGAGGA	AAAAATGGGAC	8520
	CGCGCAGGG	GCGCGTCCA	CAGCACCCCC	AAAGGGGAAG	CTGTGGCCAA	CCACGTTCCG	8580
	GCCGCTGGGC	CCGACACAGG	CCTGGCTGAG	AGTGACAGTG	AGGACCCAG	CGGCAAGCCC	8640
	CGCTGAAGGG	TGGAGACCAA	GGTCAGCGTG	GAGCTGCACC	GCGAGGAGCA	GGGCAGTCAC	8700
45	CGTGGAGAGT	ACCCCCCGGA	CCAGGAGAGC	GGGGGCGCAG	CCAGGCTTGC	TAGCAGCCAG	8760
	CCCCCAGAGC	AGAGGAAGAG	CATCTTGAAG	AATAAAGTCA	CCTACCCGCC	GCGCTGACG	8820
	CTGACGAGGC	AGAGCTGAAG	GGGCCGCTC	CGGAGAAAGC	TGGCCGACTG	TGAGCAGAGC	8880
	CCCACATCCT	CGCGCAGCTC	TTCCTTGGGC	TCTGGCGGCC	CGGACTGCGC	CATCAGAGTC	8940
	AAGAGCCCTG	GGAGGGAGCC	GGGGCGTGAC	CACCTCAACG	GGGTGGCCAT	GAATGTGGGC	9000
50	ACTGGGAGCG	CCAGGGCCGA	TGGCTTCGAC	TCTGAGAAAC	CGTGAGGCAA	GCCCGTCAAC	9060
	CCACACAGGC	TGCGGCTACA	CCCTCAGACC	TTGAGAGCCA	AGGGGCCACT	GCCCTTGAAG	9120
	TGGAGTGGGC	CCAGAGTGTG	GCGTCCCCCA	TGGTGGCAGC	CCCCGCACTG	ATCATCCAGA	9180
	CACAAAGGTC	TTGGTTCTCC	CAGGAGCTCA	GGGCTGTGTA	GACCTGGTGA	CAAGTGCCAA	9240
	AGGCCACAGG	CATGAGGGAG	GCGTGGACCA	CTGGGCCAGC	ACCGCTGAGT	CCTAAGACTG	9300
55	CAGTGAAGCG	CAGAACTGAG	AGGGGACCCC	AGACTGGGCC	CAGAGGCTGG	CCAGAGTTCA	9360
	GGAAACGCGG	GCAACAGCCA	AAGACCGCGG	TCCAGCCCGG	CCAGGCGGGG	CATCTCATGG	9420
	CAGTGCAGAG	CCGTGGCTGG	CAGCCCGGGC	AGTCTTTTGC	AAAGGCACCC	CTTGTCTTAA	9480
	AATCACTTGC	CTATGTGGGA	AAGGTGGAGA	TACTTTTATA	TATTTGTATG	GGACTCTGAG	9540
	GAGGTGCAAC	CTGTATATAT	ATTGCATTGG	TGCTGACTTT	GTTATCCCGA	GAGATCCATG	9600
	CAATGATCTC	TTGCTGTCTT	CTCTGTCAAG	ATTGCACAGT	TGTACTTGAA	CTGTCATGAT	9660
60	GTTGACGAAA	CTGTGCCCCC	AGCAGATCAA	AGGTGGGAAA	TACGTACGCA	GTGGGGCTAA	9720
	AACCAAGCGG	CTAGAAGCCC	TACAGCTGCC	TTGCGCCAGG	AAGTGAGGAT	GGTGTGGGCC	9780
	CTCCCCCGCG	GCCCCCTGGG	TCCCCAGTGT	TGCGTGTGTG	TGCGTTTGTG	CTCTGCTGCC	9840
	ATCTGCCCCG	GCTGTGTGAA	TTCAAGACAG	GGCAGTGCAG	CAGTAGGCAG	GTGTGAGGAG	9900
	CCCTGCTGAG	GTCACGTGTG	GGCAAGGTTG	CCACAGGCT	GTCTTTTTC	ACCTGGTCTAT	9960
65	TCTGTGACCA	CCACCCCTCT	CCCTCACCGC	CTCCAGGTG	GCCCCGGAGC	TGCAGGTGGG	10020
	GATGGCTTTG	TCTTTTGTCT	CTGCTCCCGG	TGGGACCTGG	GACCTTAAAG	CGTTGCAGGT	10080
	TCCTGATTTG	GACAGAGGTG	TGGGGCCTTC	CAGGCGGTTA	CATACCTCCT	GCCTATCTTC	10140
	TAACCTCTCT	AGACTGCGAG	GATCTCCAGG	CAGGGTCTCT	CCCTCTGGAG	TCTGACCAAT	10200
	TACTTCAATT	TGCTTCAAAT	GGCCAAATTG	GCAGAGGAGC	AAAGCCACAG	CCACACTCTT	10260
70	CAACGGTTAC	CAAACCTGTT	TTGGAAATTC	ACACCAAGGT	CGGGCCCACT	GCAGGCAGCT	10320
	GGCACAGCGT	GGCCCGAGGG	GCTGTGGAAC	GGGTCCCGGA	ACTGTACAGC	ATGTTTGATT	10380
	TTAGCGTTTC	CTTTGTTCTT	CAAAACAGGT	GCCCAATAAA	GTGATCAGCA	CAGCTGCTTC	10440
	CAATAGGAG	AAACCATAAA	ATAGGATGAA	AATCAAGTAA	AATGCAAGAA	TGTCCACACT	10500
	GTTTTAAACT	TGACCCCTGAT	GAAATGTGA	GCACTGTTAG	CAGATGCCTA	TGGGAGAGGA	10560
75	AAAGCGTATC	TGAAATGGT	CCAGGACAGG	AGGATGAAAT	GAGATCCGAG	AGTCTCTACA	10620
	CCTGAATGAA	TATACATGT	GCTTACCAG	GTGAGTGGTC	TTTGAAGAT	AAAAAACTCT	10680
	AGTCCCTTTA	AAAGTTTGCC	CCTGGCGTTT	CCTAAGTACG	AAAAGGTTTT	TAAGTCTTCG	10740
	AACAGTCTCC	TTTCTAGACT	TTAACAGGAT	TCTGCCCTCT	GAGGTGTAA	TTTTTTGTTT	10800
	TATTTTTCCT	CAGCTACTCC	ACAGCCAACA	TACGAGGTG	TAAATTTTAA	TTTGATCAGA	10860
80	ACTGTATACA	AAAAACAATT	GTCACTTTTA	TTGAGATGGG	AAAAATGTAA	ACCTATTTTT	10920
	ATTACTTAAG	ACTTATATGG	AGAGATTAGA	CAGTGGAGGT	TTTTAACAGA	ACGTGTATTT	10980
	ATTAAATGTT	AAAACACTTG	AATTACAAAT	GAGAAGAGTC	TACAAATAAT	TAAATTTTTT	11040
	GAATTTGTAC	TTCTGCGGTG	CTGGTTTTC	TCCACAAACA	CCCCCGCCCC	TCCCCATGCC	11100
	CAGGGTGGCC	GTGGAGAGGA	CGGTTTACGG	ACGTGCAGCT	GAGCTGTCCG	TGTCCCATGC	11160
	TCCCTCAGCC	AGTGGAACGT	GCCGGAACCT	TTTGTCCATT	CCCTAGTAGG	CCTGCCACAG	11220

CCTAGATGGG CAGTTTITGT CTTTCACCAA ATTTGAGGAC TTTTITTTTT TGCCATTATT 11280
 TCTTCAGTTT TCITTTCTTG CACTGATCTT TCTCCTCTCC TTCTGTGACT CCAGTGACTC 11340
 AGACGTTAGA CCTCTTGATG TTTTCCCACT GGTCCCTGAG GCTCTGTTC

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A32 Protein Sequence

Gene name: CH22_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSRL), Hs.252387
 Unigene number: NP_055061
 Protein Accession #: 1-20
 Signal sequence: 250-344, 358-449, 464-556, 570-678, 692-780, 794-883, 897-990, 1004-1092, 1110-1199
 Cadherin domains: Laminin_EGF [2003-2048], 7tm_2 [2465-2708]
 Pfam domains: 2407-2460
 Latrophilin/GPS domains: 1219-1238, 2473-2492, 2507-2522, 2529-2547, 2616-2634, 2659-2675, 2687-2704
 Transmembrane domains: plasma membrane
 Cellular Localization:

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1	11	21	31	41	51	
MAPPPTVLP	VLLLLAAAA	LPAMGLRAAA	WEPRVPGGTR	APALRPGCTY	AVGAACTPRA	60
PRELLDVGRD	GRLAGRRRV	GAGRPLPLQV	RLVARSAPTA	LSRRLRARTH	LPCCGARARL	120
CGTGARLCOA	LCFVPGGCA	AAQHSALAAP	TTLPACRCPP	RPRPRCPGRP	ICLPGGGSVR	180
LRLLCALRRA	AGAVRVGLAL	EAATAGTPSA	SPSPSPPLPP	NLPEARAGPA	RRARRGTSGR	240
GSLLKPFMPNY	QVALFENEP	GTLLQLLHAH	YTIAGEEERV	SYMEGLFDE	RSRGYFRIDS	300
ATGAVSTDSV	LDRETKETHV	LRVKAVDYST	PPRSATTYIT	VLVKTNDHS	FVFEQSEYRE	360
RVRENLEVG	EVLITRASDR	DSPINANLRY	RVLGGANDVP	QLNBSGVS	TRAVLDREEA	420
AEYQLLVEAN	DQGRNPGPLS	ATATVYIEVE	DENDNYPPQS	EQNYVVQVPE	DVGLNTAVLR	480
VQATDRDQGG	NAAIHYSILS	GNVAGQFYLE	SLSGILDVIN	PLDFEDVQKY	SLSIKAQDGG	540
RPLINSGV	VSVQVLDVND	NEPIFVSSPF	QATVLENVPL	GYPVHHQAV	DADSGENARL	600
HYRLVDAST	FLGGSGAGPK	NPAPTDFPFP	QIHNSSGWIT	VCARLDREBV	EHSYFGVEAV	660
DHGSPPMSSS	TSVSITVLDV	NDNDFVFTQP	TYELRLNEDA	AVGSSVLTQ	ARDRDANSVI	720
TYQLTGGNTR	NRPALSSQRG	GGLITLALPL	DYKQEQYVL	AVTASDGRS	HTAHVLINVT	780
DANTHRPFVQ	SSHYTVSVSE	DRPVGTSIAT	LSANEDTGE	NARITYVIQD	PVPQFRIDPD	840
SGTMYTMMEL	SGYENQVAYTL	TIMAQDNGIF	QKSDTTTLEI	LILDANDNAP	QFLMDFYQGS	900
IFEDAPPSTS	ILQVSATDRD	SGPNRLLYT	FQGGDDGDGD	FYIEPTSGVI	RTQRRLDREN	960
VAVYNLWALA	VDRGSPTPLS	ASVEIQVITL	DINDNAPMPE	KDELELFVEE	NNPVGSVVAK	1020
IRANDPDEGP	NAQIMYQIVE	GDMRHFQQLD	LLNGDLRAMV	ELDFEVRRREY	VLVVQATSAP	1080
LVSRATVHIL	LVQNDNPPV	LPDFQILFNN	VYTNKNSFP	TGVIGCIPAH	DFVSDSLNY	1140
TFVQGNELRL	LLLDPATGEL	QLSRDLNDR	PLEALMEVS	SDGIHVSATP	CTLRVTIITD	1200
DMLTNSITVR	LENMSQEKPL	SPLALPVEG	VAAVLSTTKD	DVFVFNQND	TDVSSNLANV	1260
TFSALLPGGV	RQGFPSSEDL	QEYIYLNRTL	LTITSTQVRL	PFDDNICLRE	PCENYMKCVS	1320
VLRFDSAPP	LSSTTVLFRP	IHPINGLRRC	CPPGFTGDYC	ETEDLCYSD	PCGANRCRS	1380
REGGYTCBCF	EDPTGEHCEV	DARSGRCANG	VCKNGGTCVN	LLIGGFHCVC	PPGEYERFVC	1440
EVTTTSFPFQ	SFTVFRGLRQ	RFHFTISLTP	ATQERNGLLL	YNGRFNEKHD	FIALIVDEQ	1500
VQLTFSAGET	TTTVAPKVPS	GVSDGRWHSV	QVQYNNKPN	GHLGLPHGPS	GEKMAVTVTD	1560
DCDTTMAVRP	GKDIGNYSCA	AQGTQTGSKK	SLDLTGPLLL	GGVFNLPEDF	PVHNRQFVGC	1620
MRLNSVDGKN	VDNAGFIANN	GTREGCAARR	NFCDGRRCON	GGTCVNRWNN	YLCECLRFGR	1680
GKNCQAMPH	PQLFSGESV	SWSDLIHII	VFWVLGLMFR	TRKEDSVLME	ATSGGPTSF	1740
LQILNNYLQF	EVSHGPSDVE	SVMLSGLRVT	DGEWHLLIE	LGNVKEDSEM	KHLVTMTLDY	1800
GMDQNKADIG	GMGPGLTVRS	VVGGADEK	VSVRRGFRGC	MQGVRMGGTP	TNVATLNMNN	1860
ALKVRVKGDC	DVDDPCTSSP	CFPNRCHDA	WEDYSCVCDK	GYLGINCUDA	CHLNPCENMG	1920
ACVRSFSGSP	GYVCEGSPSH	YGPYCNKLD	LPCPRGWMGN	PVCGPCHCAV	SKGFPDPCNK	1980
TNGQQCKEN	YKLLAQDTC	LPDCDPPHGS	HSRTCDMATG	QCACKPGVIG	RQCNCRDNPF	2040
AEVTTLGCEV	IYNGCPKAF	AGIWWPQTKF	GQPAAVPCPK	GSVGNVAVRH	SGEKGWLPPE	2100
LFNCTIISFV	DLRAMNEKLS	RNETQVDGAR	ALQLVRLARS	ATQHTGTLP	NDVRTAYQLL	2160
GHVLQHSWQ	QGFDLAATQD	ADPHEDVIHS	GSALLAPATR	AAWEQIQORSE	GGTAQLLERL	2220
EGYFSNVAVR	VRRYTLRPPV	IVTANMILAV	DIFDKFNFTG	ARVPRFTDTH	ERFPRELESS	2280
VSPADFPFRP	PEKEGPIILR	PAGRRITPQT	TRPGPGTERE	APISRRRRHP	DDAGQFAVAL	2340
VIIYRTLQGL	LPERYDPRR	SLRLPHRPII	NTPMVSTLVY	SEGAPLPRPL	ERFVLVEFAL	2400
LEVEERTKPV	CVFVNHSLAV	GGTGGWSARG	CELLSRNRTH	VACQCSHTAS	PAVLMDISRR	2460
ENGEVLPKLI	VYAASVLSL	AALLVAFVLL	SLVRMLRSNL	HSIHKLAVA	LPLSQLVFEVI	2520
GINQTNPFPL	CTVVAILLHY	IYMTFAWTL	VESLHVYRML	TEVRNIDTGP	MRFYVVGWG	2580
IPAVITGLAV	GLDPQGYGNP	DFCWLSQLDT	LIWSFAGPIG	AVIIINTVTS	VLSAKVSCQR	2640
KHHYKKGKI	VSLRLTAFL	LLLSATWLL	GLLAVNRDAL	SPHYLFAIPS	GLQGPVLLF	2700
HCVLNQEVRL	HLKGLVGRK	LHLEDSATTR	ATLLTRSLNC	NTTFDGDGDM	LRTDLGESTA	2760
SLDSIVRDEG	IQKLGVSSGL	VRGSHGEPDA	SLMPRSCKDP	PGHSDSDSSE	LSLDEQSSSY	2820
ASSHSDSED	DGVGAEEKWD	PARGAVHSTP	KGDVAVNHVP	AGWPDQSLAE	SDSEDPGSKP	2880
RLKVETKVS	ELHREBQGS	RGEYPPDQES	GGAARLASSQ	PPEQRKGILK	NKVYTPPPLT	2940
LTEQTLKGR	REKLADCEQS	PTSSRTSSLG	SGGPDCAITV	KSPGREPRGR	HLNGVAMNVR	3000
TGSAQADGSD	SEKP					

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A33 DNA SEQUENCE

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3
 Unigene number: Hs.198252
 Probeset Accession #: X95876
 Nucleic Acid Accession #: X95876
 Coding sequence: 69-1175 (underlined sequences correspond to start and stop codons)

80

1	11	21	31	41	51	
CCAACCAAA	GCACCAAGC	AGAGGGGCG	GCAGCACACC	ACCCAGCAGC	CAGAGCACCA	60
GCCACGCCAT	GGTCCTTGAG	GTGAGTGACC	ACCAAGTGCT	AAATGAGGCC	GAGGTGCGG	120

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CCCTCCTGGA GAACTTCAGC TCTTCTATG ACTATGGAGA AAACGAGAGT GACTCGTGCT 180
GTACCTTCCC GCCTTGCCCA CAGGACTTCA GCCTGAACCT CGACCGGGCC TTCTTGCCAG 240
CCCTCTACAG CCTCTCTTTT CTGCTGGGGC TGCTGGGCAA CGGCGCGGTG GCAGCCGTGC 300
TGCTGAGCCG GCGGACAGCC CTGAGCAGCA CCGACACCTT CCTGCTCCAC CTAGCTGTAG 360
CAGACAAGCT GCTGGTGTCT ACACTGCCGC TCTGGGCAGT GGAGCGTGCC GTCCAGTGGG 420
TCTTTGGCTC TGGCCTCTGC AAAGTGGCAG GTGCCCTCTT CAACATCAAC TTCTACGCAG 480
GAGCCCTCCT GCTGGGCTGC ATCAGCTTTG ACCGCTACCT GAACATAGTT CATGCCACCC 540
AGCTCTACCG CCGGGGGGCC CCGGGCCGCG TGACCTCAC CTGCTGGCT GTCTGGGGGC 600
TCTGCTGCTT TTTGCGCTC CCAGACTTCA TCTTCTGTG GGCCACCAC GACGAGCGCC 660
TCAACGCCAC CCACTGCCAA TACAACCTCC CACAGGTGGG CCGCACGGCT CTGCGGGTGC 720
TGCACTGTGT GGTGCTGCTT CTGCTGCCCC TGCTGGTCTT GGCCACTGTC TATGCCACA 780
TCTTGGCGGT GCTGGGCTGT TCCAGGGGCC AGCGGCGCT GCGGGCCATG CGGCTGGTGG 840
TGGTGGTGTG GGTGGGCTTT GCCCTCTGCT GGACCCCTTA TCACCTGGTG GTGCTGGTGG 900
ACATCTCAT GGAACCTGGC GCTTTGGCCC GCAACTGTGG CCGAGAAAGC AGGGTAGACG 960
TGCCCAAGTC GGTCACTCTA GGCTTGGGCT ACATGCACTG CTGCCTCAAC CGCTGCTCT 1020
ATGCTTTTGT AGGGGTCAAG TTCGGGAGC GATGTGGAT GCTGCTCTTG CGCCTGGGCT 1080
GCCCAACCA GAGAGGGCTC CAGAGGCAGC CATGCTCTT CCGCGCGGAT TCATCTGTGT 1140
CTGAGACCTC AGAGGCTCTT TACTCGGGCT TGTGAGGCGC GAATCCGGGC TCCCTTTTCG 1200
CCCACAGTCT GACTTCCCGG CATTCAGGCT TCCTCCCTCC CTCTGCCGGC TCTGGCTCTC 1260
CCCAATATCT TCGCTCCCGG GACTCACTGG CAGCCCCAGC ACCACAGGT CTCCCGGAA 1320
GCCACCTCTC CAGCTCTGAG GACTGCACCA TTGCTGCTCC TTAGTGCCA AGCCCATCC 1380
TGCCGCCGGA GGTGGCTGCC TGGAGCCCCA CTGCCCTTCT CATTTGAAAT CTAAGAACTC 1440
ATCTTCCCCA AGTGGGGGA GTACAAGGCA TGGCGTAGAG GGTGCTGCC CATGAAGCCA 1500
CAGCCGAGC CTCCAGCTCA GCAGTGAAGT TGGCCATGGT CCGCAAGACC TCTATATTG 1560
CTCTTTTATT TTTATGCTTA AAATCCTGCT TAAAACTTTT CAATAAACAA GATCGTCAGG 1620
ACCAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA BHCLITERAT 1680
UREBHCBLAS TPBHCORTHO LOGUESMOUS ECKRMYLEV SERQVLDASD PAFLEENSTS 1740
PYDYGENESD FSDSPPCQPD FSLNFDRTFL PALYSLFLFL GLLNGAVAA VLLSQRTALS 1800
STDFTLLHLA VADVLLVTL FLWAVDAVQ WVFGPGLCKV AGALFNINFY AGAPILLACIS 1860
FDRYLSIVHA TQYRRDPRV RVALTCIVVW GLCLLFLALPD FYLSANYDQ RLNATHCQYN 1920
FPQVGRALR VLQVLVAGFL PLVMAYCYA HILAVLLVSR GQRFRFRMRL VVVVAAFAV 1980
CWTFYHLVVL VILMDVGV LARNCGRESHV DVAKSVTSQM GYMHCCLNPL LYAFVGVKFR 2040
EQMMMLFTRL GRSDQRPQR QPSSSRRESS WSETTEASYL GL

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A34 Protein sequence

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3
 Unigene number: Hs.198252
 Protein Accession #: P49682
 Signal sequence: none found
 Pfam domains: 7tm_1 [70-318]
 Transmembrane domains: 57-78, 92-113, 129-147, 169-190, 222-243, 257-275, 307-323
 DRY box: 148-149
 Cellular Localization: plasma membrane

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1 11 21 31 41 51
| | | | |
MVLEVSDEHQV LNDAEVAALL ENFSSSYDYG ENESDSCTTS PPCQDPFSLN PDRAFLPALY 60
SLLFLLGLLG NGAVAVALLS RRTALSSDT FLLHLAVADT LLVLTPLWA VDAAVQWVFG 120
SGLCKVAGAL FNINFYAGAL LLACISFDYR LNTVHATQLY RRGPPARVTL TCLAVWGLCL 180
LFLALPFIPL SAHDERLINA THCQYNFPQV GRTALRLVLQ VAGFLLPLL V MAYCYAHILA 240
VLLVSRGQRR LRAMRLVVVV VVAFALCWT P YHLVVLVDIL MDLGALARNC GRESRVDAK 300
SVTSGLYMH CCLNPLLYAF VGVKFRERMW MLLRLGCPN QRLQRPSS SRRDSSWSET 360
SEASYSGL

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A35 DNA SEQUENCE

Gene name: Differentially expressed CO16 gene (clone MGC:5257)
 Unigene number: Hs.69517
 Probeset Accession #: AA447522
 Nucleic Acid Accession #: BC001291
 Coding sequence: 44-541 (start and stop codons are underlined)

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1 11 21 31 41 51
| | | | |
GGGGGGCGCG CGCGCTGACC CTCCTGGGCG ACCGCTGGGG ACGATGGGCG TGCTGCGCTT 60
GCTGCTGGTC GTGGCCCTAC CGGGGTGTG GACAGACGCC AACCTGACTG CGAGACAACG 120
AGATCCAGAG GACTCCCGAG GAACGGACGA GGGTGACAAT AGAGTGTGGT GTCATGTTTG 180
TGAGAGAGAA AACACTTTTG AGTGCCAGAA CCCAAGGAGG TGCAATGGA CAGAGCCATA 240
CTGCGTTATA GCGGCGGTGA AAATATTTC ACCTTTTTC ATGGTTGGA AGCAGTGCTC 300
CGCTGGTTGT GCAGCGATGG AGAGACCCAA GCCAGAGGAG AAGCGGTTTC TCCTGGAAGA 360
GCCCATGCC TTTCTTTACC TCAAGTGTG TAAATTOGC TACTGCAATT TAGAGGGGCC 420
ACCTATCAAC TCATCAGTGT TCAAGAATA TGCTGGGAGC ATGGGTGAGA GCTGTGGTGG 480
GCTGTGGCTG GCCATCTCC TGCTGCTGGC CTCCATTGCA GCGGCGCTCA GCCTGTCTTG 540
AGCCACGGGA CTGACACAGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTTGTC 600
ACCTGTGCA TTAACCTGT TTTCTGTGA TTACCTCTTG GTTTGACTTC CCAAGGTCTT 660
GGGATGGGAG AGTGGGGATC AGGTGCAGTT GGCTCTTAAC CCTCAAGGGT TCTTTAACTC 720
ACATTACAGG GAAGTCCAGA TCTCTGAGT AGTGATTTTG GTGACAAGTT TTTCTTTG 780
AAATCAAAACC TTGTAACCTA TTTATTGCTG ATGGCCACTC TTTTCTTGA CTCCCTCTG 840
CCTCTGAGGG CTGAGTATT GATGGGAGG GAGGCCTAAG TACCACTCAT GGAGAGTATG 900
TGCTGAGATG CTTCCGACCT TTCAGGTGAC GCAGGAACAC TGGGGGAGTC TGAATGATTG 960
GGGTGAAGAC ATCCCTGGAG TGAAGGACTC CTCAGCATGG GGGGCACTGG GGCACACGTT 1020
AGGGCTGCC CCATTCAGT GGTGGAGGCG CTGTGGATGG CTGCTTTTCC TCAACCTTTC 1080

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5 CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTTG AAGAACTTA GACTTCACCC 1140
 ACCAGCTGGC ACAGGTGCAC AGATTCATAA ATTCCACAC GTGTGTGTTT AACATCTGAA 1200
 ACTTAGGGCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260
 CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCACCC AAAAACAAAT ACAAGGGGAC 1320
 TTCAAAGTT CACGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA

10 A36 Protein sequence:
 Gene name: Differentially expressed CO16 gene (clone MGC:5257)
 Unigene number: Hs.69517
 Probeset Accession #: AA447522
 Protein Accession #: AAH01291
 Signal sequence: 1-17 (first underlined sequence)
 Transmembrane domain: 146 - 162
 Cellular localization: plasma membrane

20 1 11 21 31 41 51
 MALLALLLVV ALPRVWTDAN LTARQRDPED SQRTEGDNR VVCHVCEREN TFECQNPERRC 60
 KWTEPYCVIA AVKIFPRPFM VAKQCSAGCA AMERPKPEEK RFLLEEFMPF FYLKCKKIRY 120
 CNLEGGPPINS SVFKEYAGSM GESCGGLWLA ILLLLASIAA GLSL

25 A37 DNA SEQUENCE
 Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

35 1 11 21 31 41 51
 AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCGCTGTG 60
 CCTGTGCTGCT AGCAGCGCGG CGGAGAGGCA GCTGCTCCCC GGGAACTCACT TCACCAATGA 120
 GTGCAACATA CCGAGCAACT TCATGTGCAG CAATGGAACG TGCACTCCCG GCGCCTGGCA 180
 GTGTGACGGG CTGCGTGAAT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
 GTCGAATATG GGCCCAACCT TCTTCCCTCG TGCCAGCGCG ATCCATTGCA TCATTGGTCC 300
 CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
 AAACCCCTCG CTTTGTCTCA CCGCCCGCTA CCACTGCAAG AACGGCTCT GTATTGACAA 420
 GAGCTTCATC TCGATGGAG AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
 AAGTTCTCAA GAACCCGCGA GTGGGCGAGT GTTTGTGACT TCAGAGAACC AACCTGTGTA 540
 TTACCCGACG ATCACTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
 CCGCTGTGCA AATGGTCTTG ACCACGAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
 GCACCGGCTG CAGCACCCCT TGCTGTCTGT CCGCCTGGTG GTCCTGGACC ACCCCACCA 720
 CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
 GAATGCGTGG GAAGTAGGCT CCCACCCCTC CTACTCCGAG GCCTTGTCTGG ACCAGAGGCC 840
 TGCGTGGTAT GAACCTCCCT CACCGCCCTA CTCTCTGAC ACGGAATCTC TGAACCAAGC 900
 CGACCTGCCC CACTTCCGCT CCGGTCGCG GAGTGCCAAC AGTGCCAGCT CCGAGGCAGC 960
 50 CAGCAGCCTC CTGAGCGTGG AAGACACCA CCAACGCCCC GGGCAGCCTG GCCCCAGGA 1020
 GGGCACTGCT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080
 AGTTATTCCA AAGTGCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTG TAACAATTG 1140
 TGCTCATGGG AAGCTCTTTA AGCACTGTGA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
 55 AACTATCTCT GCATTCCTCT CCTCCCCAG ACTTCAGAGA TGTTTTCTG GGTCTCAGT 1260
 TGACATGATC TGTGTGCGT CTTTCTGTCT AGGTCACTCT TCCCTTGGGA CCGAGATCA 1320
 CACCCCTATT TTTCACATTA TTCTGTTTCT GTTGAGAGA CAGCATATAA AACAGTATTG 1380
 AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
 CGCTGAGCCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTGGGTTAG 1500
 60 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAATT CCAATTGAGC 1560
 ATCAAAACCT GCTTTGCACA ATCCTATTGG ATGCCCCAG TTCAGCAGAG TCAGTGGCCA 1620
 AAGAAAACCT TGGAGCTGAG TAACACCCCT CAGCAGTCCG AACGTTATTT TGGTTTGTG 1680
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 65 GAGCCCTCTC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860
 TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCACAGCTG 1920
 ACCCTGCGCT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980
 GTATGTCCCT GTGGCCCA CAACAGCCTGT CTTGCTCATT CATGCAGCCT CAACACTGGC 2040
 CTCCAAAGTT CCTTAACAC TTGCAAAGTC CTTTTTACCT GTGCATTGGG ACTTGAGGAC 2100
 70 ACTGGTTTCT ATCAGAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160
 CTGCACTGTG CAGCTCTCTC TTCCCAAGGT OCCAATACCA GCACCTCTAG TTAGAGTTAG 2220
 GGTCAAGGCT AGGCTCTCTC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
 AGACAATTG GAGTCAAGAT TTCCATTGG GATCTATTTT AAATCTTTTA GAAATGCATT 2340
 TGAAACAGTG TGTGTGTTTT TTCCCTTCTA GTTAAGGGAC TATTTATATG TGTATAGGAA 2400
 75 AGCTGTCTCT TTTTGTGTTT TTCTTTTAA AAGGTCCAAA GAAAGATGCA AAAGGAGATC 2460
 ACACCTCTGC CCGCTGTGAC CCGGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
 ACATTGTGTC ATGTGTGCAC TTTGAGGTTA TTATTATCA AGTTCCTGAA GGAAGCAGAA 2580
 AGAGGCACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTT 2640
 TTCTCTGTGT CCACTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACGTT 2700
 80 AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATAGGAA CCAGGTAGAG 2760
 CCACTCCGGG CAGCTGTAC CCATTGAGAA CTTCTTTCCG CAGCTGAGA AATGTTCACT 2820
 AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAG TGGCATTAG 2880
 TGATCTGTGT CTGTAGACTT TTTCTTCTTT TTTTAAACAA ATCCAAAGGA TGTATACGAA 2940
 AAGCTAGCCA CTGTTATTTT GTTTTGTGTT AAAAAAAGA AAGAAAGAAA 3000

AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAAGAA CTTTGTATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120
 CATTTTCATCT CTTGTAGATC AGAAGGGCTT TATTTCTCCC TTGTATGGGG CCCCTTCTTC 3180
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTTAGT 3300
 AGATAAGGGA TGCTACTAA TGCTTTTTTA AAACAAACAG GCACATTTT ATTATAGATT 3360
 TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CCACAACAG 3540
 AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTA GCATTAAATT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
 TTTTAAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720
 GAAAGGTGTG GTGTCGTGTC TTTTGTGTTT TTGGTTAGGC TTGTTTTTGT TTTTAAATT 3780
 TTATACTTTC TAATAAATTT GCAGTTTCAT TCTTCTCTGT TGTGCAAAWG GWMCTAMARM 3840
 AAMMAAAAC AWYWTGGGG GGGCTTGGGC CTCGAAAAA GTTTTAAACA CCACTTCGGG 3900
 TGGGGCGCGG GGGCCACAGT AGGTACGCGG ACCACGCGGG CCCAAACGGG ACCCCAGAAG 3960
 GAAACCCCTGG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAAA ACGCGCGGG 4020
 GGAAACCGCA GAGTGTTCG TAAACCAAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

A38 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MNLLGLPLCLL LSSAAESQLL PGNFTNECN IPGNFMCNSG RCIPGAWQCD GLPDCFDKSD 60
 EKECEPKAKSK CGPTFFPCAS GIHCIIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
 KNGLCIDKSF ICDGQNNQD NSDEBSCSS QEPGSGQVVF TSENQLVYYP SITVYIIGSS 180
 VIFVLVALL ALVLHHRQRK NNLMTLFFVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240
 YVASQAEQNA SEVGSPPSYS EALLDQRPAN YDLPPPPYSS DTESLNQADL PFYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEV

A39 DNA sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGCTGCTG GCTTCTTGAT GAGTCCCAGT ACCCAGCACA GAGCACAGTA CACTCCCAGA 60
 GGAAAGAAAC TTCCGTGGGA GGCCTCCATC GGTGCGCACA CTTCCGAGG GCGAGGCAGC 120
 GACCGGGAGA GGGAGAGCCG GCGGGAGGCT GCGGGGCTCC TGTGGGACCG CGCTGCAGCC 180
 GGGAGCCGCG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGAATCCGCG CCAGCAGCAG 240
 CCGCGGCGCG CCGCAGCTGG GCAAGCTCCC GGGACTGCGG CTGGGGCGCG GCAGGACCT 300
 CGCCTGCGCT CTGGACGTTT CCGGGGAGAG GTCCGGTTGC CAGTGAACCC TCCAGAGGCT 360
 TCGGAGCAGC AGCCCGCGGG GCCTTCTGAC TGCCATCCGA GATTTCATC AGCGAGTGCA 420
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACCGGGA TGGCTTAGGA 480
 GCTCTCTGAC CTAGGGCCCG GCTCTCTGCG CTCTGGGCG TCGCGGAGA GGGGAGTGGC 540
 CCGCGCGGAA AGCGCGCGCG GACAGTCAGT GACGAGGCCG GGGGTCGCC GGGGCCACGA 600
 CTTCTCGGAG ACCGTCTGCG GCTCTCTGGA GAGCGCTGTG CGCGGCCAG GGTGGTGCCA 660
 TGTGGGGCGC TCGCGCTCG TCGCTCTCCT CATCTGGAA CGCGCTTCG CTCCTGCAGC 720
 TGCTGCTGGC TCGCTGCTG GCGCGGGGGG CAGGGGCCCA GCGCGAGTA CTCCTCAGCG 780
 TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTGCAAGCG 840
 GGCGAGCCCA CCATCTGCTG CGGAGCTGCG GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
 GCGCGCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960
 CCGGCGGACA AAGAGCGGGC CCGACGGCTC GGCAGGGCTT CATGCTTAG GGGTACCCAA 1020
 GGAGACGGCG AGGGTGGCGC CCCACCGCTG AGGGCTTGGC AGCGGTGCTC CCTTGAAGGC 1080
 TCCCGAAGAG GAAGGCGAGT CTTAGGGGCT TTCCCGGGGC TGCTGCCCGG TGCCAGACGC 1140
 CGCGGATTCC CATCTTCTCC ACGGGCGGCG CCTCTCCGCC TGCAGCGGCC CGCTTGGCCC 1200
 ATCTAGTGC CGTTCCTCAT TGTGGCTCC GTGTTTGTGG CCTTTATCAT CTTGGGGTCC 1260
 CTGGTGGCAG CCGTGTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCCA GCAGAGCCGA 1320
 GCGCCAGGGG GTAAACCGCTT GATGAGAGCC ATCCCATGTA TCCCATGTC CAGCACTCC 1380
 CGGGGGTCTG CTTACGCCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACCTC 1440
 GGGGCGCGGG CGCCGCCAAC AAGTTCACAG ACCAAGTGTG GCTTGGCGGA AGGGACCATG 1500
 AACAACTGTG ATGTCAACAT GCGCAGCAAT TTCTCTGTGC TGAAGTGTCA GCAGGCCACC 1560
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCOCCAT ACGTGGGGTA CAGGTGCGAG 1620
 CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCCTGGCTAC 1680
 AGGCAGATTC AGTCCOCCCT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740
 ACTGTATAAC CGAGAGTCAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
 GATTCTCGAG GTGGAGTTC GCACATGTGG GTGGTATTTA TGGCAGGATT CCTTGGGATG 1860
 GCTTCATTGG CCCCAGACT GTATGAAAC ATCTCGAAT TAGCATTCTT GGATATGTTT 1920
 CATCCAGGGT ATCATTGATT TATGATGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980
 TTGCTGATGG GTGTATAACA AATGCTTGAG TCGAAGTGC CCTTGAGATA TGGTTGACGA 2040
 AAGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100

5 TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160
 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCAGGC TGGAGTGAG 2220
 TGGTGCATC TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCCCTGCCTC 2280
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCAT GGCTAATTTT TTGTATTTT 2340
 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGGTGGTCTC ACTCTCTGA CCTCAAGCAA 2400
 TCTGCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
 TGAGCCTTTT TTTTCTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520
 ATTCTAAAG GAAACCTGTT TGAACCTGTT GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
 10 GGCACACCTT AATTTTCATT TAAAAAGATA TATATATTTT GTCTATTTT GTGCTTTTGG 2640
 GGGCCTATTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700
 TTAATAAGAG ACTGAAATAA ATTGTATAGT TACTTAACCTA ATGAAGACAT TTCAGAACTC 2760
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAATT CATCCCTTC 2820
 TTGATTGTAT CTTAATTTTC TGGCTTAAAG GTGACATCTG AGAGGTAATG CATTCTTTT 2880
 TATATTGAAA TCATAAACTA TCACCCGCTG CTCTCTGAG TTACTTTTAA TTTTGCTTG 2940
 15 TGGTTATGGT TTGGCCTTTT CTCTGTTTGT GTTTTCAGAG CCCCATGTCT ATATAGTCTC 3000
 GAGTGCAAGT AATTACTATA CTGTAAATG AAGATCAGTA TTCTGCTCA GATCTGATAA 3060
 AAAAAATTTT TTGCTTTTGT TATAAAAAAT CAAGAAATG TGTACAAAG ATACTTAGTA 3120
 TAGCTCCTCA GCCATAAACC GAGACTGGG ATGAAATTTA AACCAGATAC GATTTACTTT 3180
 20 GCAGATCATA AGGCTTTTTA TACTCTTGT ATCAAAATGG CTATTTTTC AGGCACTAAG 3240
 GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCTTTT CTCTCCAC ACTGTTCTTG 3300
 ATTTCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATCA TTGCCAATGT TCCAAATAT 3360
 CAAATCAAG TGAATTTAT TGTGTGTTCT TACTTATAT AAAAAAGAT AACTTTAAG 3420
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTA ACAAATCGCT 3480
 25 GTATGTTATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTTCTATT 3540
 TGTTCATGA CTGAAATAAT TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACCTA 3600
 TTTTAAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAATA TTTTATGATG 3660
 TGAATAAAAA AAAAAAATA AAAAAAATA

30 **A40 Protein sequence**
 Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 35 Transmembrane domains: 402-424
 Cellular localization: not determined

40 1 11 21 31 41 51
 MLSGFLMSPS TQHRAQYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLMDRAAA 60
 GEAEKGNRGE PPAWIRAQQQ PKPPPAGQAP GTAAGGADQP RLPRGRSRGR VRLPVKPEA 120
 SGRQPRGSD CIPRFPSSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG 180
 45 PRGKRGRGTVS DEARGSPGPR LLGDRPALSG DALSAFVVPV CGALAARPSF HPGTPLRSCS 240
 CCLWRKRRRG RPSGGEYCHG WLDAGQVMRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300
 ARLDQGGCND DRQQGAGEPG RADKDGPRRL GRASCLRGTD GDGEGAPPPV RAWQRCSEGE 360
 SPKGRQLLRA PPGLLPRARR RGFPSPPRGG PSLQRPALP IYVPLIVGS VFVAPIILGS 420
 LVAAACRCRL RPKQDPQQR AEGGNRLMET IPMIPSASTS RGSSSRQSST AASSSSSANS 480
 50 GARAPPTRSQ TNCCLPEGTN NNVVNMPTN FSVLNCQQAT QIVPHQGGYL HPPYVGYTVQ 540
 HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQRMYPV TV

A41 DNA SEQUENCE:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 55 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
 CTACACTCAG CTTTGGGTCT CTGCTCTTA CTGCTCACAG TTTCTTCAA CCTTGCCATT 120
 65 GCAATAAAAA AGGAAAAGAG GCTCCTCAG ACACCTCAA GAGGATGGGG AGATGACATC 180
 ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
 ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGCC 300
 CAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
 GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
 70 GACCTTCTTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTTAACAG ATTGTACACA 480
 TATGAGCCTC GGGATTTACC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540
 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAGAAGT CAAATTTTAT 600
 GAGAAAAACC TCTGGACAT TGACAAATCA TAAATGTGCA AGTATATAGA TTTTGTATA 660
 75 TTACTATTTA GTTTTTTAA TGTGTTTGA ATAGTCTTAT TAAATAAAT GTTTTTTAA 720
 TCTGAAAAAA AAAAAAATA AAAAAAATA

A42 Protein sequence:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 80 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

1 11 21 31 41 51
5 MMLHSALGLC LLVLTSSNL AIAIKKEKRP POTLSRGWGD DITWVQTYEE GLFYAQKSKK 60
PLMVIHLED CQYSQALKKV PAQNEEIQEM AQNKPFIMNL MHETDKNLS PDGQYVPRIM 120
FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

10 A43 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: NS1919
Nucleic Acid Accession #: AF189723
15 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
20 ATGATTCCTG TATTGACATC AAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGA GAAGTATATT 180
TCTCAGTTTA AAAATCCCCT TATTATGCTG CTTCCTGGCTT CTGCAGTCAT CAGTGTTTTA 240
ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300
25 GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTGAAG AATTGAGTAA ACTGTGCCA 360
CCAGAATGCC ATGTGTGCGG TGAAGAAAAA TTGGAGCATA CACTTGGCCG AGACTTGGTT 420
CCAGGTGATA CAGTTTGCCT TTCTGTTGGG GATAGAGTTC CTGCTGACTT ACGCTTGT 480
GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTCT 540
AAGGTGACAG CTCTTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600
30 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTGTTCAT TGGAAACAGGA 660
GAAAAATCTG AATTGGGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
CTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780
ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAG ATATCCTGGA AATGTTTACT 840
ATTAGTGTA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTTGT GGTCAAGTGT 900
35 AGCTAGCTC TTGGTGTAT GAGAATGGTG AAGAAAGGG CCATTGTGAA AAAGCTGCCT 960
ATGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTCG AACACTGACG 1020
AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT 1080
GGAGTTGCT ATAAATCAAT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATT 1140
TATAACCCAG CTCTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
40 AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260
ATGGGCTCTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320
GAGCAAAAGT GGATGGCTGT TAAGTGTTGA CACGAACAC AGCAGGACAG ACCAGAGATT 1380
TGTTTTATGA AAGGTGCTTA CGAACAAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
GGCAGAGCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAAG GAAGGCACGC 1500
45 ATGGGCTCAG CGGACTCAG AGTTCCTGCT TTGGCTTCTG GTCTGAACT GGGACAGCTG 1560
ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
ACACACTTCA TTGCCCTCAG AGTATCAATA AAAATGATTA CTGAGATTAC ACAGGAGACT 1680
GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCAAAAA CTTCCAGTC AGTCTCAGGA 1740
GAAGAAATAG ATGCAATGGA TGTTTACAGC CTTTCAAAA TAGTACCAA GGTTCAGTA 1800
50 TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGTACA GAAGAAAGGT 1860
TCAGTTGTAG CCAATGACAG AGATGGAGTA AATGATGCGA TTGCTCTGAA GGCTGCAGAC 1920
ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGA AAGAGGCAGC AGACATGATC 1980
CTAGTGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040
AATAACATTA AAAATTTGCT TAGATTCCAG CTGAGCAAGA GTATAGCAGC ATTAACTTTA 2100
55 ATCTCATGG CTACATTAAT GAATTTTCTT AATCTCTCA ATGCCATGCA GATTTTGTGG 2160
ATCAATATTA TTATGGATGG ACCCCAGCT CAGAGCCTTG GAGTAGAAC AGTGGAATAA 2220
GATGTCAATC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGTACTA AAACCTTGATA 2280
CTTAAATATG GTTTTTCATC AATAATCAT GTTTGTGGGA CTTTGTGTGT CTTCTGGCGT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
60 TTTTITGACA TGTTCATGCT ACTAAGTCC AGATCCCAGA CCAAGTCTGT GTTTGAGATT 2460
GGAATCTGCA GTAATAGAAT GTTTTGCTAT GCAGTTCTTG GATCCATCAT GSGACAATTA 2520
CTAGTTATTT ACTTTCCTCC GCTTCAGAA GTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
65 AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700
CTTGAAGTAT GA

A44 Protein sequence:

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
70 Probeset Accession #: NS1919
Protein Accession #: AAF27813
Signal sequence: none found
Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
75 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
Cellular Localization: not determined

1 11 21 31 41 51
80 MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FRGMNEFDIS EDEPLWKYI 60
SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVTV AFQOYRSEK SLEELSKLVP 120
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSIDES SLTGETTPCS 180
KVTAPOPAAT NGDLASRSNI AFMGTILVRCG KAKGVVITG ENSEFGEVFK MMQABEAPKT 240
PLQKSMDDLQ KQLSPYSFGI IGIIMLVGWL LGKIDLEMTF ISVSLAVAAI PEGLPFIVTV 300

5 TLALGVMRMV KKRAIVKILP IVBTIGCCNV ICSDKTGTLT KNEMTVTHIP TSDGLHAEVT 360
 GVGYNQFGEV IVDGTVVHGF YNPVAVSRIVE AGVCVNDABI RNTLMGKPT EGALIALAMK 420
 MGLDGLQQDY IRKAEYFPSS EQNMMAVKCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK 480
 10 GQTLTLTQQQ RDVYQEKAR MGSAGLRVLA LASGPGLGQL TPLGLVGIID PPRTGVKEAV 540
 TLLASGVSI KMITGDSQET AVAIASRLGL YSKTSQSVSG EBIIDAMDVOQ LSQIVPKVAV 600
 FYRASPRHMK KIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVMAGTGT DVCKEAAADMI 660
 LVDDDFQTIM SAIEBKGIIY NNINVFVRFO LSTSIALLTL ISLATLMNFP NPLNAMQILW 720
 15 INIIMDPPA QSLGVBPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780
 ELRDNVITPR DTTMTPTCFV FDFMFNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL 840
 LVYIFPPLQK VFQTESLSIL DLLFLGLTSS SVCIVABIIK KVERSREKIQ KHVSTSSSF 900
 LEV

A45 DNA sequence

15 Gene name: ESTs
 Unigene number: Hs.157601
 Probeset Accession #: W07459
 Nucleic Acid Accession #: AC005383
 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

20
 25
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1 11 21 31 41 51
 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60
 TTTATTTCG AGACCTGGGC CGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACCTC 120
 CCTGCGCGTA GTTCTCCGGA CCTCAGCCGG GTCCGGTCTG GCCGCCCTCT CCCAGGAGAG 180
 ACAAAACAGT GTCCACACGT GCAGCCCGGC CCCGGGCGCC CCTCCTGTGA TCCCGTAGCG 240
 CCCCCTGGCC CGAGCCCGGC CCGGCTCTGT GAGTAGAGCC GCCCGGCGAC CGAGCGCTGG 300
 TCGCCGCTCT CCTTCCGTTA TATCAACATG CCCCCTTTCC TGTGTCTGGA GGCCGCTCTG 360
 GTTTTCCCTGT TTTCCAGAGT GCGCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAAGCAA 420
 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480
 ATCATGTTC TGTAGATGG GTCTAACAGC GTCCGGAAGG GGAGCTTTGA AAGGTCCAAG 540
 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600
 GCATTCCAGT TCAGTTCAC TCCTCATCTG GAATTCCTCT TGGATTCTTT TCAACCCCAA 660
 CAGGAAGTGA AGGCAAGAAAT CAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720
 CTGTGCTCTGA AATACCTTCT GCACAGAGGG TTGCCTGGAG GCAGAAATGC TTCTGTGCC 780
 CAGATCCCTCA TCATGTCAC TGATGGGAAG TCCACGGGGG ATGTGCACT GCCATCCAG 840
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGG TCAGGTTTCC CAGGTGGGAG 900
 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCAGC TGCTGTGGC TGAGCAGGTG 960
 GAGGATGCCA CCAACGGGCT CTTCAGCACC CTGAGCAGCT CGGCCATCTG CTCCAGCGCC 1020
 ACGCCAGACT GCAGGGTGA GGCTCACCCC TGTGAGCACA GGAAGCTGGA GATGGTCCGG 1080
 GAGTTGCTG GCAATGCCCC ATGCTGAGGA GGATCGCGGC GGACCTTCG GGTGCTGGCT 1140
 GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTTCG CACTGCTTAC 1200
 AGGACCACCT GCCCAGGCCC CTGTGACTCG CAGCCCTGCC AGAATGAGG CACATGTGTT 1260
 CCAGAGGAC TGGACGGCTA CCAAGTGCCT TGCCCGCTGG CCTTTGAGG GGAGGCTAAC 1320
 TGTGCGCTGA AGCTGAGCCT GGAATGCAGG GTGACCTCC TCTTCTGCT GGACAGCTCT 1380
 GCGGGCACCA CTCTGGACGG CTCTGCTGG GCCAAAGTCT TCGTGAAGCG GTTTGTGGCG 1440
 CGCTGCTGA GCGAGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500
 CTGGTGGCG TGCTGTGGG GGAGTACCAG GATGTGCTG ACCTGTCTG GAGCCTGAT 1560
 GGCATTCCCT TCGTGTGGG CCCACCTCG ACGGGCAGTG CCTTGGGCA GCGCGCAGAG 1620
 CTGGCTTGG GAGAGCGCAC CAGGACCGGC CAGCTAGAGT GGTGTTTTC 1680
 CTCCTGAGT CACTCTCCA GGATGAGGTT GCGGGCCGAG CGCTCACAGC AAGGGCGGCA 1740
 GAGCTGCTCC TGCTGGTGT AGGCAGTGAG GCGTGCAGG CAGAGCTGGA GGAGATCCA 1800
 GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAATCCCT 1860
 GAGCTGCAG GGAAGCTGTG CAGCCGCGAG CGCCAGGGT GCCGACACA AGCCCTGGAC 1920
 CTGCTCTTCA TGTGGACAC CTCTGCCCTCA GTAGGGCCCG AGAATTTTC TCAGATGAG 1980
 AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCCGC 2040
 CTGGTGGTGT ATGCGAGCCA GGTGCAACT GCCTTCGGGC TGGACACCAA ACCCACCCTG 2100
 GCTGCGATGC TCGGGCCCAT TAGCCAGGCC CCTACCTAG GTGGGTGGG CTCAGCCGCG 2160
 ACCGCCCTGC TGCACATCTA TGAACAAAGT ATGACCGTCC AGAGGGGTGC CCGGCTTGGT 2220
 GTCCCCAAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCT 2280
 GCCCAGAAAG TGAGGAACAA TGGCATCTCT GTCTTGGTGG TGGGGTGGG GCCTGTCTTA 2340
 AGTGAGGGT TGCGGAGGCT TGCAAGTCCC CGGATTCCT TGATCCAGT GGCAGCTTAC 2400
 GCGACCTGC GGTACCAACA GGAAGTGTCT ATTGAGTGGC TGTGTGAGA AGCCAAGCAG 2460
 CCAGTCAACC TCTGCAAAAC CAGCCCGTGC ATGAATGAGG GCAGCTGGT CCTGCAGAA 2520
 GGGAGCTACC GCTGCAAGT TCGGGATGGC TGGGAGGGCC CCCACTGCGA GAAACGCTGAG 2580
 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATT TTAGAGAGCC CCTGAGGCAC 2640
 ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT ACCCTCCCA GCAACTACAG AGAAGGCTG 2700
 GGCACTGAAA TGGTGCTTAC CTTCTGGAAT GTCTGTGCCC CAGGTCTTGA GAATGTCTG 2760
 TTCCCGCTGT GGCAGGAGAC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820
 ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCAACCAACA AACGATGTT TTAAGAGTT 2880
 TTGATGTGTA AGTAAATACC CACTTCTGT ACCTGCTGTG CCTGTTGAG GCTATGCTT 2940
 CTGCCACCTT TCCCTTGAGG ATAACAAAGG GGTCTGAAG ACTTAAATTT AGCGGCTG 3000
 OGTTCTTTG CACACAATCA ATGCTGCCCA GAATGTTGTT GACACAGTAA TGCCAGCAG 3060
 AGGCTTTTAC TAGAGCATCC TTTGGAGCGC GAAGGCCAAG GCCTTCAAG ATGGAAGCA 3120
 75 CAGCTTTTTC CACTTCCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAGGGGG 3180
 CTTGAGGGAC GTTTTGACT TCTTGGGAC CAATTAACCA GCTTGGTTGA TGATGGGGA GGGCTGAGT 3240
 GGTCTCAGAC GGAATGTGAC CAAATTAACCA GCTTGGTTGA TGATGGGGA GGGCTGAGT 3300
 TGTGATGGG CCCAGTCTG GAGGGCCAG TAAATCGTT CTGAGTGTG AGCAGTGTCC 3360
 80 ACCTTGAAG TCTTC

A45 Protein sequence

Gene name: ESTs

Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGF domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

10 1 11 21 31 41 51
 | | | | |
 MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
 SVKGSGSPERS KHFAITVCDG LDISPERVRV GAFQPSSTPH LEPLDSFST QQEVKARIKR 120
 MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
 15 FAVGVFRPPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD 300
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
 RAKVFKRFV RAVLSEDSRA RVGVATYSRE LLVAVFVGEY QDVPLDVNSL DGIFPRGGPT 420
 20 LTGSLRQAA ERGFGSATRT QDRPRRVVV LTESHSEDE VAGPARHARA RELLLLVGS 480
 EAVRAELEI TGSPKHMVY SDPQDLFNQI PELQKLCRSR QRPGRCTQAL DLVFMLOISA 540
 SVGPENFAQM QSFVRSICALQ FEVNPDTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 APVLGGVGS A GTALLHIYDK VMTVQRGARP GVPKAVVVLIT GGRGAEDAAV PAQKLNNNGI 660
 SVLVVGVGFPV LSEGLRRLAG PRDSLHVA A YADLRVHQDV LIEWLCGEAK QPVNLCKPSP 720
 25 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
 RTPPSNYREG LGTEMVPTFW NVCAPGP

COLON

30 A47 DNA SEQUENCE:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 35 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
 | | | | |
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
 CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGCTCAGAG TTTCTTCCAA CCTTGCCATT 120
 GCAATAA AAA AGGAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
 ACTTGGGTAC AAACCTTAGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
 45 ATGGTTATTC ATCACCCTGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGCCC 300
 CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
 GAAACCACTG ATAAGAATT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
 GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
 TATGAGCTTC GGGATTATAC CCTATTGATA GAAAACATGA AGAAAGCAIT AAGACTTATT 540
 50 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAGAGAAGT CAAATTTCAT 600
 GAAGAAAAAC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660
 TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAA 720
 TCTGAAAAA AAAAAAAAAA AAAAAAAAAA

55 A48 Protein sequence:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 60 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

65 1 11 21 31 41 51
 | | | | |
 MMLHSALGLC LLLVTSSNL AIAIKKEKRP PQTLRSGWGD DITWVQTYEE GLFYAQKSKK 60
 PLMVIIHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHEITDKNLS PDGQVPRIM 120
 70 FVDPSTLVRA DIAGRYNRL YTYEPRDLPL LIENMKALR LIQSEL

A49 DNA SEQUENCE
 Gene name: G protein-coupled receptor 56
 75 Unigene number: Hs.6527
 Probeset Accession #: AA478599
 Nucleic Acid Accession #: NM_005682
 Coding sequence: 163-2244 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
 | | | | |
 CGGCAGCAGG GTCTCGCTCT GTACACAGG CTGGAGTGCA GTGGTGTGAT CTTGGCTCAT 60
 CGTAACCTCC ACCTCCCGGG TTCAAGTGAT TCTCATGCCT CAGCCTCCCG AGTAGCTGGG 120
 ATTACAGGTG GTGACTTCCA AGAGTGACTC CGTCGGAGGA AAATGACTCC CCAGTCCGCTG 180

	CTGCAGACGA	CACTGTTCTC	GCTGAGTCTG	CTCTTCTGG	TCCAAGGTGC	CCAAGGACAG	240
	GGCCACAGGG	AAGACTTTTG	CTTCTGCAGC	CAGCGGAACC	AGACACACAG	GAGCAGCCTC	300
	CACTACAAC	CCACACACGA	CCTGCGCATC	TCCATCGAGA	ACTCCGAAGA	GGCCCTCACA	360
5	GTCCATGCC	CTTTCCCTGC	AGCCCCACCT	GCTTCCCGAT	CCTTCCCTGA	CCCCAGGGGC	420
	CTCTACCACT	TCTGCTCTA	CTGGAACCGA	CATGCTGGGA	GATTACATCT	TCTCTATGGC	480
	AAGCGTGACT	TCTTGCTGAG	TGACAAAGCC	TCTAGCCTCC	TCTGCTTCCA	GCACAGGAG	540
	GAGAGCCTGG	CTCAGGGCCC	CCCGCTGTTA	GCCACTTCTG	TCACCTCCTG	GTGGAGCCTC	600
	CAGAACATCA	GCCTGCCAG	TGCGGCCAG	TTCACCTTCT	CCTTCCACAG	TCCTCCCCAC	660
10	AGGGCCGCTC	ACAATGCCTC	GGTGGACATG	TGCGAGCTCA	AAAGGGACCT	CCAGCTGCTC	720
	AGCCAGTTCC	TGAAGCATCC	CCAGAAGGCC	TCAAGGAGGC	CCTCGGCTGC	CCCCGCCAGC	780
	CAGCAGTTGC	AGAGCCTGGA	GTCGAAACTG	ACCTCTGTGA	GATTCAATGG	GGACATGGTG	840
	TCCTTGGAGG	AGGACCGGAT	CAACGCCACG	GTATGGAAGC	TCCAGCCAC	AGCCGGCCTC	900
	CAGGACCTGC	ACATCCACTC	COGGCAGGAG	GAGGAGCAGA	GCGAGATCAT	GGAGTACTCG	960
	GTGCTGCTGC	CTCGAACACT	CTTCCAGAGG	ACGAAAGGCC	GGAGCGGGGA	GGCTGAGAAG	1020
15	AGACTCCTCC	TGGTGGACTT	CAGCAGCCAA	GCCCTGTTC	AGGACAGAA	TTCCAGCCAA	1080
	GTCTGGGTG	AGAAGGTTT	GGGGATTTG	GTACAGAA	CCAAAGTAGC	CAACCTCAG	1140
	GAGCCCGTGG	TGCTCACTTT	CCAGCACCG	CTACAGCCGA	AGAATGTGAC	TCTGCAATGT	1200
	GTGTTCTGGG	TTGAAGACCC	CACATTGAGC	AGCCCGGGC	ATTGGAGCAG	TGCTGGGTGT	1260
20	GAGACCGTCA	GGAGAGAAAC	CCAAACATCC	TGCTTCTGCA	ACCACTTGAC	CTACTTTGCA	1320
	GTGCTGATGG	TCTCTCGT	GGAGGTGGAC	GCCGTGCACA	AGCACTACCT	GAGCCTCCTC	1380
	TCTTACGTGG	GCTGTGTGCT	CTCTGCCCTG	GCCTGCCTTG	TCACCATTCG	GCCTACCTC	1440
	TGCTCCAGGG	TGCCCTGCG	GTGCAGGAG	AAACCTCGGG	ACTACACCAT	CAAGGTGCAC	1500
	ATGAACCTGC	TGCTGGCGT	CTTCTGCTG	GACACGAGCT	TCCTGCTCAG	CGAGCCGGTG	1560
25	GCCTTGACAG	GCTCTGAGGC	TGGCTGCCGA	GCCAGTGCCA	TCTTCTGCA	CTTCTCCCTG	1620
	CTCAGCTGCC	TTTCTCGGAT	GGGCTCGAG	GGGTACAACC	TCTACCGACT	GCTGGTGGAG	1680
	GTCTTTGGCA	CCTATGTCCC	TGGCTACCTA	CTCAAGCTGA	GCGCCATGGG	CTGGGGCTTC	1740
	CCCATCTTTC	TGCTGACGCT	GGTGGCCCTG	GTGGATGTGG	ACAATATG	CCCCATCATC	1800
	TTGGCTGTGC	ATAGGACTCC	AGAGGGCGTC	ATCTACCTTC	CCATGTGCTG	GATCCGGGAC	1860
30	TCCTGTGCTA	GCTACATCAC	CAACCTGGGC	CTCTTACGCC	TGGTGTTCCT	GTTCAACATG	1920
	GCATGTGCTA	CCACCATGGT	GGTGCAGATC	CTGCGGCTGC	GCCCCACAC	CCAAAGTGG	1980
	TCACATGTGC	TGACATGCT	GGGCTCAGC	CTGTCTCTTG	GCCTGCCCTG	GGCCTTGATC	2040
	TTCTTCTCCT	TTGCTTCTGG	CACCTTCCAG	CTTGTCTGCT	TCTACCTTTT	CAGCATCATC	2100
	ACCTCCTTCC	AAGGCTTCT	CATCTTCATC	TGCTACTGGT	CCATGCGGCT	CGAGGCCCGG	2160
35	GGTGGCCCTC	CCCTCTGAA	GAGCACTCA	GACTGCGCCA	GGCTCCCAT	CAGCTCGGGC	2220
	AGCACCTGCT	CCAGCGCAT	CTAGGCCTCC	AGCCCACTG	CCCATGTGAT	GAAGCAGAGA	2280
	TGCGGCTCG	TGCGACATG	CCTGTGGCCC	CCGAGCCAGG	CCCAGCCCCA	GGCCAGTCAG	2340
	CCGACAGACT	TGGAAGCCCC	AACGACCATG	GAGAGATGGG	CCGTGCCAT	GGTGGACGGA	2400
	CTCCCGGGGC	TGGGGCTTTT	GAATTGGCCT	TGGGGACTAC	TGGGCTCTCA	CTCAGCTCCC	2460
40	ACGGGACTCA	GAAGTGGGCC	GCCATGTGCT	CTAGGGTACT	GTCCCCACAT	CTGTCCCAAC	2520
	CCAGCTGGAG	CCAGTGTCTC	TCCTTACAAC	CCCTGGGGCC	AGCCTCATTG	CTGGGGGCCA	2580
	GGCCTTGGAT	CTTGAGGGTC	TGGCACATCC	TTAATCTCTG	GCCCCGCTCT	GGGACAGAAA	2640
	TGTGGCTCCA	GTGCTCTGCT	CTCTCGTGGT	CACCTGAGG	GCACCTCTGCA	TCCTCTGTCA	2700
45	TTTAACTCTC	AGGTGGCACC	CAGGGCGAAT	GGGGCCGAGG	GCAGACCTCT	AGGGCCAGAG	2760
	CCCTGGCGGA	GGAGAGGCC	TTTGCCAGGA	GCACAGCAGC	AGCTCGCTTA	CCTCTGAGCC	2820

A50 Protein sequence

50	Gene name:	G protein-coupled receptor 56
	Unigene number:	Hs.6527
	Protein Accession #:	NM_005682.1
	Signal sequence:	1-26
	GPS domain:	342-394
55	Pfam domain:	7tm_2[400-665]
	Transmembrane domains:	410-432, 446-468, 482-504, 517-539, 575-597, 608-630, 638-659
	Cellular Localization:	plasma membrane

60	1	11	21	31	41	51	
	MTPQSLQTT	LPLLSLLFLV	QGAHGRGHRE	DFRFSQRNQ	THRSSLHYKP	TPDLRISIE	60
	SEALTVHAP	FPAAHPASRS	FPDPRGLYHF	CLYWNRHAGR	LHLLYGRKDP	LLSDKASSLL	120
	CFQHEESLA	QGPPLLATSV	TSWNSPQNIS	LPSAASFTPS	FHSPPHTAAH	NASVDMCEKL	180
65	RDLQLLSQFL	KHPQKASRRP	SAAPASQQLQ	SLESKLTSVR	FMGDMVSFEE	DRINATVWKL	240
	QPTAGLQDLH	IHSRQEEQES	EIMEYSVLLP	RTLFTQTKGR	SGEAEKRLLL	VDFSSQALPQ	300
	DKNSSQVLGE	KVLGIUVQNT	KVANLTFPVV	LTFQHLQPK	NVTLCQVFWV	EDFTLSSPGH	360
	WSSAGCSTVR	RETQTSFCFN	RLTYFAVLNV	SSVEVDAVHK	HYLSLLSYVG	CVVSALACL	420
	TIAYLCSRVR	PLPCRKRPRD	YTIKVMNLL	LAVFLDTSF	LLSEPVALTG	SEAGCRASAI	480
70	FLHFSLLTCL	SWMGLBSYNL	YRLVVEVFGT	YVPGYLLKLS	AMGWGFPPIPL	VTILVALVDVD	540
	NYGPIILAVH	RTPEGVIYPS	MCWIRDSLVS	YITNLGLFSL	VFLPNMAMLA	TMVVQILRLR	600
	PHTQKNSRVL	TLGLSLVLG	LFWALIFFSF	ASGTFQLVVL	YLFSTITSFQ	GFLPIPIWTS	660
	MRLQARGGPS	PLKNSDCAR	LPISSGSTSS	SRI			

A51 DNA SEQUENCE

75	Gene name:	Hypothetical protein FLJ20063
	Unigene number:	Hs.5940
	Probeset Accession #:	AA053660
	Nucleic Acid Accession #:	AA053660
80	Coding sequence:	218-1360 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
CCCCATGAC	TTTGACAGC	TACTTCACTG	CTTCCCCCA	ATTAGTACAC	ATAGTCTCTC	60

5 CACAATTCCT ACACCTGCTC CCCCCATAAT CAGTACACAT AGTTCCTCCA CAATTCCTAT 120
 ACCTACTGCT GCAGACAGTG AGTCAACCAC AAATGTAAT TCATTAGCTA CCTCTGACAT 180
 AATCACCCTC TCATCTCCAA ATGATGGATT AATCACAATG GTTCTCTCTG AAACACAAAG 240
 TAACAATGAA ATGTCCCCCA CCACAGAAGA CAATCAATCA TCAGGGCTC CCACCTGGCAC 300
 CGCTTTATGG GAGACCAGCA CCCTAAACAG CACAGGTCCC AGCAATCCTT GCCAAGATGA 360
 TCCCTGTGCA GATAATTGCT TATGTGTAA GCTGCATAAT ACAAGTTTTT GCCTGTGTTT 420
 AGAAGGGTAT TACTACAACT CTTCTACATG TAAGAAAGGA AAGGTATTCC CTGGGAAGAT 480
 TTCAGTGACA GTATCAGAAA CATTTGACCC AGAAGAGAAA CATTCCATGG CCTATCAAGA 540
 10 CTTGCTATAGT GAAATTACTA GCTTGTTTAA AGATGTATTT GGCACATCTG TTTATGGACA 600
 GACTGTAAAT CTTACTGTAA GCACATCTCT GTCAACAGA TCTGAAATGC GTGCTGATGA 660
 CAAGTTTGTG GATGTAACAA TAGTAACAAT TTTGGCAGAA ACCACAAGTG ACAATGAGAA 720
 GACTGTGACT GAGAAAAATTA ATAAAGCAAT TAGAAGTAGC TCAAGCAACT TTCTAAACTA 780
 TGATTTGACC CTTGGTGTGG ATTATTATGG CTGTAACAGG ACTGCGGATG ACTGCTCTCA 840
 15 TGGTTTAGCA TGGGATTGCA AATCTGACCT GCAAGGCCT AACCACAGA GCCCTTCTG 900
 CGTTGCTTCC AGTCTCAAGT GTCCTGATGC CTGCAACGCA CAGCACAAGC AATGCTTAAT 960
 AAAGAAGAGT GGTGGGGCCC CTGAGTGTGC GTGCGTGCCC GGCTACCAGG AAGATGCTAA 1020
 TGGGAAGTGC CAAAAGTGTG CATTGTGCTA CAGTGGACTG GACTGTAAAG ACAAAATTCA 1080
 GCTGATCCTC ACTATTGTGG GCACCATCGC TGGCATTGTC ATTCTCAGCA TGATAATTGC 1140
 20 ATTGATTGTC ACAGCAAGAT CAAATAACAA AACGAAGCAT ATTGAAGAAG AGAAGTTGAT 1200
 TGACGAAGAC TTTCAAATTC TAAAACTGCG GTCCACAGGC TTCACCAATC TTGGAGCAGA 1260
 AGGGAGCGTC TTTCCTAAGG TCAGGATAAC GGCTCCAGA GACAGCCAGA TGCAAAATCC 1320
 CTATTCAAGA CACAGCAGCA TGCCCCGCC TGAATTAGG AATCATAAGA ATGTGGAAAC 1380
 CGCCATGGCC CCCAACCAAT GTACAAGCTA TTAATTAGAG TGTTTAGAAA GACTGATGGA 1440
 25 GAAGTGAGCA CCAAGTAAAG TCTGGCCTCC GGGGTTTTTC TTCCATCTGA CATCTGCCAG 1500
 CCTCTCTGAA TGGAAAGTGT GAATGTTTGC AACGAATCCA GCTCACTTGC TAAATAAGAA 1560
 TCTATGACAT TAAATGTAGT AGATGCTATT AGCGCTTGTC AGAGAGGTGG TTTTCTTCAA 1620
 TCAGTACAAA GTACTGAGAC AATGGTTAGG GTTGTTTTCT TAAATCTTTT CTGGTAGGG 1680
 CAACAAGAAC CATTTCATAT CTAGAGGAAA GCTCCCGAGC ATTGCTTGCT CCTGGGCAAA 1740
 30 CATTGCTCTT GAGTTAAGTG ACCTAATTCC CTTGGGAGAC ATACGCATCA ACTGTGGAGG 1800
 TCCGAGGGGA TGAGAAGGGA TACCCACCAT CTTTCAAGGG TCACAAGCTC ACTCTCTGAC 1860
 AAGTCAGAAAT AGGGACACTG CTTCTATCCC TCCAATGGAG AGATTCTGGC AACCTTTGAA 1920
 CAGCCAGAGC CTTGCAACCT AGCCTCACCC AAGAAGACTG GAAAGAGACA TATCTCTCAG 1980
 CTTTTCAGG AGGCGTGCTC GGGAAATCCAG GAACCTTTTG ATGCTAATTA GAAGGCCTGG 2040
 35 ACTAAAAATG TCCACTATGG GGTGCACTCT ACAGTTTTTG AAATGCTAGG AGGCAGAAAG 2100
 GGCAGAGAGT AAAAAACATG ACCTGGTAGA AGGAAGAGAG GCAAGAGAAA CTGGGTGGGG 2160
 AGGATCAATT AGAGAGGAGG CACCTGGGAT CCACCTTCTT CCTTAGGTCC CCTCTCCAT 2220
 CAGCAAAAGGA GCACCTCTCT AATCATGCCC TCCGAAGAC TGGCTGGGAG AAGGTTTAAA 2280
 AACAAAAAAT CCAAGAGTAA GAGCCTTAGG TCAGTTTGAA ATTGGAGACA AACTGTCTGG 2340
 40 CAAAGGGTGC GAGAGGGAGC TTGTGCTCAG GAGTCCAGCC GTCCAGCCTC GGGGTGTAGG 2400
 TTTCTGAGGT GTGCATTGGG GGCTCAGCC TTCTCTGGTG ACAGAGGCTC AGCTGTGGCC 2460
 ACCAACACAC AACCAACAC ACACAACCAC ACACAACAAT GGGGGCAACC ACATCCAGTA 2520
 CAAGCTTTTA CAAATGTTAT TAGTGTCTT TTTTATTCT AATGCCTTGT CCTCTTAAAA 2580
 GTTATTATTAT TTGTTATTAT TATTGTCTT TGACTGTTAA TTGTGAATGG TAATGCAATA 2640
 45 AAGTGCCTTT GTTAGATGCT GAAAAAATA AAAAAAATA AAAAAAATA A

A52 Protein sequence:

Gene name: Hypothetical protein FLJ20063
 50 Unigene number: Hs.5940
 Probeset Accession #: AA053660
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 289-311
 55 EGF domain: 45-74
 SEA domain: 80-196
 Cellular Localization: plasma membrane

60 1 11 21 31 41 51
 | | | | |
 MVSFETQSNN EMSPTTEDNQ SSGPPTGTAL LETSTLANSTG PSNPGQDDPC ADNSLCVKLH 60
 NTSFCLCLEG YYVNSSTCRK GKVPFGKISV TVSETFDPEE KHSMAVQDLH SEITSLFKDV 120
 FGTSVYQGTV ILTVSTSLSP RSEMRADDFK VDVITVITLA ETTSDEKTV TEKINKAIRS 180
 65 SSSNPLNYDL TLRCDYGCN QTADDCLNGL ACDCKSDLQR PNPQSPFCVA SSLKCPDACH 240
 AQHKQCLIKK SSGAPEACAV PGYQEDANGN CQKCAFYSG LDCKDKFQLI LTIVGTIAGI 300
 VILSMILALI VTARSNNKTK HIEBENLIDE DFQMLKLRSF GFTNLGAEBS VPPKVRITAS 360
 RDSQMNPYS RHSSMPRPDY

A53 DNA SEQUENCE

70 Gene name: TMFRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 75 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
 | | | | |
 ACCGGGCACC GGAAGGCTCG GGTACTTTCT TTTCTTAATTA GGTATGCCCC GTGTGAGCCA 60
 GGAAGGGCTG GTGTTTATGG GAAGCCAGTA AACTGTGTGC CTACTATCTC TTCCGTGGTG 120
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCGGATGTC 180
 AGAGGTCTCT AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240

5 TCATCCGAT CGCTTTTGG CCTTGATGAT TTGAAATAA GTCTGTGTC ACCAGATGCA 300
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCAGCTGC 420
 TCAGGGAAGT ACAGATGTGC CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA OGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACGCAATGT TGCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720
 10 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCCCTCG GCCACGTGGT TACCTTGCAG TGACACAGCT GTGGTCATAG AAGGGCTAC 840
 AGCTCAOGCA TCGTGGGTGG AACATGTCC TTGCTCTGC AGTGGCCCTG GCAGGCCAGC 900
 CTTGAGTTCC AGGGTACCA CCGTGTGCGG GGCTCTGTCA TCACGCCCTC GTGGATCATC 960
 ACTGCTGCAC ACTGTGTTA TGACTTGATC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020
 15 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTGG TGGAGAAGAT TGTCTACCAC 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GCGCGGCCCA 1140
 CTCAGCTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACCTCCCC 1200
 GATGAAAAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
 TCCCTGTGCC TGAACCAAGC GCGCGTCCCT TTGATTTCCA ACAAGATCTG CAACCAACAGG 1320
 20 GACGTGTACG GTGGCATCAT CTCCCTCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCGCTGTGCT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGCGACCA CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCG AGGTGATGAA GACAGCCCGA 1620
 25 TCCTCCCTCG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
 TTCGGGCACT AGTAGCAGCG CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACCTT 1740
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTGT CCCAGGCTGG 1800
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCGCTT CCGTGGTTCA AGCGATTCTC 1860
 TTGCTCAGC TTCCTCAGTA GCTGGGACCA CAGGTGCGCG CCACACACCC CAACATAATT 1920
 30 TTGTATTTT AGTAGAGACA GGGTTTCACT ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
 CCTCAATGA TGTGCTGCT TCAGCCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040
 ACGCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTCTG 2100
 AGGGCGGCTT TCCCACTGGT TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCTCG 2160
 ACGAGATAAG CAGTTATGTG AOCTCACGTG CAAAGCCACC AACGCCACT CAGAAAGAC 2220
 35 GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCACTT TTTCTCTCTA GGGACCAGAA 2280
 CCAACCCAC CCTTCTTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
 ATGACTCGTT TAAGGCCTAT TTTTATGATT TCTTTGTAGC ATTTGGTGTCT TGACGTATTA 2400
 TTGTCCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAAAAA

40 A54 Protein sequence:
 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 45 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 Tryp_SPC domain: 216-444
 Cellular Localization: plasma membrane

50
 1 11 21 31 41 51
 | | | | |
 55 MGENDPFAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFFP IIVIGIILI 60
 LALAIGLGIH FDCSGKYRCR SSFKCIBLIA RCGVSDCKD GEDEYRCVRV GGQNAVQLQVF 120
 TAASWTKMCS DDWKGHYANV ACAQLGPPSY VSSDNLRVSS LEGQFREBFV SIDHLLPDDK 180
 VTALHHSVTV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPF QASLQFQGYH 240
 LCGSVITPL WITTAARCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCMT SGWGATEDGA GDASPVLAHA 360
 60 AVPLISNKC NHRDVYGGII SPSMLCAGYL TGGVDSQGD SGGPLVCQER RLWKLVGATS 420
 FGIACAEVKN PGVYTRVTSF LDWIEHQMER DLKT

65 A55 DNA SEQUENCE
 Gene name: Putative G protein-coupled receptor GPCR150
 Unigene number: Hs.97101
 Probeset Accession #: AA215333
 Nucleic Acid Accession #: NM_014373
 Coding sequence: 322-1338 (underlined sequences correspond to start and stop codons)

70
 1 11 21 31 41 51
 | | | | |
 GTGGCTCGA GGTGGTGGCA GGGCGGCCCC CTGCAGTCCG GAGACGAACG CACGGACCGG 60
 GCCTCCGGAG GCAGGTTCGG CTGGAAGGAA CCGCTCTCGC TTCGTCTTAC ACTTGCACAA 120
 75 ATGTCTCCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAATGC AAGGAACCAA 180
 AAATAACATA ATTGAAGGCA GTAAAAGTGA AATTAAATAG GAAGATCATC AGTCAAGGAA 240
 GACCCACTGG AGAGGACAGA AAATGAAGCA GTGTTTTATC ATGTGTATTT CAGCAGGTCT 300
 TCTTGAATTT TAATAAAAA TAATGACTGCT CTCTCTTCTG AGAAGTCTCT TTTTCAGTAC 360
 CAGTTACGTC AAACAAACCA GCCCTAGAC GTTAACTATC TGCTATTCTT GATCATACTT 420
 80 GGGAAAATAT TATTAAATAT CCTTACACTA GGAATGAGAA GAAAAACAC CTGTCAAAAT 480
 TTTATGGAAT ATTTTGTGAT TTCCTAGCA TTCGTTGATC TTTTACTTTT GGTAAACATT 540
 TCCATTATAT TGTATTTTCT GGATTTTGTG CTTTAAGCA TTAGTTTCTC TAAATACCAC 600
 ATCTGCCTAT TTAATCAAT TATTTCTTTT ACTTATGGCT TTTTGCATTA TCCAGTTTCT 660
 CTGACAGCTT GTATAGATTA TTGCTGAAT TTCTCTAAAA CAACCAAGCT TTAATTTAAG 720
 TGTCAAAATAT TATTTTATTT CTTTACAGTA ATTTTAATTT GGAATTCAGT CCTTGCTTAT 780

	GTTTTGGGAG	ACCCAGCCAT	CTACCAAAGC	CTGAAGGCAC	AGAATGCTTA	TTCTGTCAC	840
	TGTCCTTTCT	ATGTCAGCAT	TCAGAGTTAC	TGGCTGTCAT	TTTTCATGGT	GATGATTTTA	900
	TTTGTAGCTT	TCATAACCTG	TTGGGAAGAA	GTTACTACTT	TGGTACAGGC	TATCAGGATA	960
5	ACTTCCATATA	TGAATGAAAC	TATCTTATAT	TTTCTTTT	CATCCACTC	CAGTTATACT	1020
	GTGAGATCTA	AAAAAATATT	CTTATCCAAG	CTCATTGTCT	GTTTTCTCAG	TACCTGGTTA	1080
	CCATTGTATC	TACTTCAGGT	AATCATTGTT	TTACTTAAAG	TTGAGATTCC	AGCATATATT	1140
	GAGATGAATA	TTCCCTGGTT	ATACTTTGTC	AATAGTTTTT	TCATTGCTAC	AGTGTATTGG	1200
	TTTAATGTCT	ACAAGCTTAA	TTTAAAAGAC	ATTGGATTAC	CTTTGGATCC	ATTGTGCAAC	1260
10	TGGAAGTGCT	GCTTCATTCC	ACTTACAATT	CCTAATCTTG	AGCAAATTGA	AAAGCCTATA	1320
	TCAATAATGA	TTTGTTAATA	TTATTAATTA	AAAGTTACAG	CTGTCATAAG	ATCATAATTT	1380
	TATGAACAGA	AAGAACTCAG	GACATATTAA	AAAATAAACT	GAACATAAAC	AACTTTTGCC	1440
	CCCTGACTGA	TAGCATTTCA	GAATGTGTCT	TTTGAAGGGC	TATACCAATT	ATTAAATAGT	1500
	GTTTTATTTT	AAAAACAATA	TAAATCCAAG	AAGTTTTTAT	AGTTATTTCAG	GGCACTATATA	1560
15	TTACAAATAT	TACTTTGTGA	TTAACACAAA	AAGTGATAAG	AGTTAACATT	TGGCTATACT	1620
	GATGTTTGTG	TTACTCAAAA	AAACTACTGG	ATGCAAACTG	TTATGTAAT	CTGAGATTTC	1680
	ACTGACAAC	TTAAGATATC	AACCTAAACA	TTTTTATTAA	ATGTTCAAAT	GTAAGCAAGA	1740
	AAAAAAAA						
20	<u>A56 Protein sequence</u>						
	Gene name:		Putative G protein-coupled receptor GPCR150				
	Unigene number:		Hs.97101				
	Protein Accession #:		NP_055188				
	Signal sequence:		none found				
25	Transmembrane domains:		23-45, 59-81, 97-119, 138-160, 184-206, 241-263, 276-297				
	Cellular Localization:		plasma membrane				

	1	11	21	31	41	51	
30	MTALSSSENC	FQYQLRQTNQ	PLDVNYLLPL	IILGKILLNI	LTLGMRKNT	CQNFMEYFCI	60
	SLAFVLLLL	VNISIIILYFR	DFVLLSIRFT	KYHICLPTQI	ISFTYGLFHY	PVFLTACIDY	120
	CLNFSKTTKL	SFKCQKLFYF	FTVILINISV	LAYVLGDPPI	YQSLKAQWAY	SRHCPPYVSI	180
	QSYWLSFFMV	MILFVAFITC	WEEVTTLVQA	IRITSYMNET	ILYPPFSSHS	SYTVRSKKIF	240
35	LSKLIYCFIS	TWLFVPLLVQ	IIVLLKVQIP	AYIEMNIPWL	YFVNSFLIAT	VYWFNCHKLN	300
	LKDIGLEPLD	FVNWKCCFIP	LITPNLEQIE	KPISIMIC			

	<u>A57 DNA SEQUENCE</u>						
	Gene name:		ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]				
40	Unigene number:		Hs.19322				
	Probeset Accession #:		AA088458				
	Nucleic Acid Accession #:		AA088458				
	Coding sequence:		862-1995 (underlined sequences correspond to start and stop codons)				

	1	11	21	31	41	51	
	GCCCTTGGAC	ACTGACATGG	ACTGAAGGAG	TAGAATGGAG	CACGAGGACA	CTGACATGGA	60
	CTGAAGAAAA	AGGAGCTGGA	GCAGGAGAAG	GAGGTGCTGC	TGCAGGGTTT	GGAGATGATG	120
50	GCGCGGGGCC	GCGACTGGTA	CCAGCAGCAG	CTGCAACGAG	TGCAGGAGCG	CCAGCGCCGC	180
	CTGGGCCAGA	GCAGAGCCAG	CGCCGACTTT	GGGGCTGCAG	GGAGCCCCCG	CCCCTGGGGG	240
	CGGCTACTGC	CCAGAGTACA	AGAGGTGGCC	CGGTGCTTGG	GGGAGCTGCT	GGCTGCAGCC	300
	TGTGCCAGCC	GGGCGCTGCC	CCCGTCTTCC	TCCGGGCCCC	CCTGCCCTGC	CCTGACGTCC	360
55	ACCTCACCCC	CGGTCTGGCA	GCAGCAGACC	ATCCTCATGC	TGAAGGAGCA	GAAACGACTC	420
	CTCACCCAGG	AGGTGACCGA	GAAGAGTGAG	CGCATCAAGC	AGCTGGAGCA	GGAGAGTGG	480
	GCGCTCATT	AGCAGCTGTT	TGAGGCCGCG	GCCCTGAGCC	AGCAGGACGG	GGGACCTCTG	540
	GATTTCACCT	TCATCTAGTC	CTTGTGGGCC	GCGTGGGCCC	CCAGGGCCAG	CCTGGCACTC	600
	AGCCCTTCGA	GGGTGGGCGC	CCCATCGCAC	CCACCTCTCT	TGGCTGGAGA	CCCGCGGAG	660
	GCCGAGGCAC	AGTCCCGGAG	TGGGGGCGCT	CCTGCGCCCC	TTGCCAGATG	GGCTCCCCAG	720
60	GCTTGCCCCC	GGCTGGTCCC	CGCACCGAGC	GCTTGACTCC	GTTTGGGCTC	CTGGTTGTTG	780
	ACATGGGCTG	GGGGCTCTCT	TGAGTCCGCA	TAGTCCGCG	CTACTACTGG	CCGCTGTCTG	840
	TGGACAGTGG	GGTACCCCTC	CATGAGTTAG	CGTCCCCCG	TTTCCAGCGG	TGCCCGCCCTG	900
	GGTCCCATCT	TCAGGGAAAG	GCACTGCCCA	CGCCAGGCTG	CACTTCCAAC	AACGGGCAGC	960
65	AGAGGGGCGG	GGGCGGCTCC	GACGCGGGTC	CAAGGGCAGC	TTCCCGCTCA	ACCAGGGCAC	1020
	CAGGACGAGG	TGGCTGTAGC	TOGGACGGAC	GGAAGTAGAT	GGAGGGGGTG	GGGACGGCCT	1080
	GTAAGCGGGG	GGTGCTTGCC	TGGCTGGGGA	GCCCCAGGGA	TAGCGGTGCG	ACTTCAGGTT	1140
	CTGGCCAAAG	CTGAGGGACC	CTGGCTGCAG	CGGATCGGCA	CGCCGGGTGG	GCGAGAGCTT	1200
	GGCCTGCATG	TGCCTCCAC	AGACCTCGGG	GTGATGGCCT	TCCCTCTCTT	GGCCGGGACG	1260
70	TTGCCCCACG	TTGAGTCCCA	CACAACATCC	TGTGAGCCTG	GCTCCCCAGG	AGGGCCCCCA	1320
	GACAGCTCCC	AGGCAAGTCA	TAGGCAAAAGC	CTGTTTCCCC	CGACTCAGGA	TTTCCAAGCC	1380
	CTGGGGTCTT	GCTCACCCCC	CTTTGCTCTC	ACGCCACGCC	TGTCCCCAGG	TTTCACTGGG	1440
	GAGAGGCCAC	CTCCCTCAGC	CAAGGAAAAAC	GAGAACCCCC	AGGGTACAGG	AGGAGGCTGG	1500
	GGCAGGTCCC	CTGGGTGTC	ACTCCCTCAG	CCCCTGCCCA	GGCCCACTCC	CGCTGGTGCT	1560
75	GGAGTAGCSA	CTGGTGGGGG	GGCCCTGTCT	AGCCCAACCT	GGAGGGTCCC	AGTGTCACTA	1620
	GAACACAGGG	CACGGCAACA	GCACTGATGG	GTCTGTCAGC	CCAGGGCCCC	CGATGCGGGG	1680
	TCAGTGTGTG	TGGGGCGCAG	GGCCTCCGAT	GCGGGGTGAG	TGCGTGGGGG	GCGCAGGGCC	1740
	CCGATGCGG	GGTCAGTGGG	TGGGGGGCGC	AGGGCCCCCT	CGTGTCCAGG	GCACTTTGGT	1800
	ACACTGTCCC	ACAAGGCACC	TGTCTCAGAG	GAGGGGCCCT	GGCAGGCAGC	GTGGCAACTC	1860
80	CCTTCCGGAG	CCCAGCTCCA	TGCTAACCTG	CCCACAGCAA	CCCCACAGAG	CCCATTTCCC	1920
	TGCTGCACCT	GGTCTGCAGG	GGTGTCCAG	GACAGGCCCA	AGTCAGCCCA	GCACTGCAGT	1980
	GCCCTCTCAC	CTGGAAGATG	GGAGTGGGCT	TTCCAGGGGA	CATAAGGATG	TCAGGCTGGG	2040
	ACCTCTCTGG	CAGGAAGAGG	TGCAGGTCTT	GAGGGCTCTG	GCCCCACAGC	CCCAGCACCC	2100
	AGGTGGAAGT	CAGCGCAGTG	GGTGGGCCAG	TGGCAGCCAG	GGAGAAGCCC	CCCGTCAGCA	2160
	GGCTGGGGTC	TGCCACCACG	GGCTTCCCCA	CGTCTGCCCT	TGAGGGTGCC	TGCCATGCCC	2220

5	TGGGGGATCC	TGGCATCTTT	ACTGGACTGG	AAGCAGGAGA	CAGAACAGTG	TCTGTCCCGG	2280
	GGTGACTTCA	TCAGGAGACC	GCCCACATAG	AGCTGGACCC	CGCAGCTGAA	GCGGAAATGT	2340
	GAGACAGGCT	GGCACCCTCG	GAATAACTGC	CTTTACGCC	TGGTGTTCGG	TGCAAGGTGA	2400
	AAAGAAATAG	GTCTCTCCAG	TTTACAGCTT	GAAATCAGGC	TAGTGAAGTG	CCCTGGAGAC	2460
	CACGAGGGGA	GAATTTAAAG	GCCCCGGCTG	GCAGGGTCTA	GOTGGCTGGC	AGAGGCACAT	2520
	GCAGACCCTG	CCTGGAGCCT	GCCCTAGGAC	GCTGGGGCGG	TCAGTCTCCG	TGCAGGATGT	2580
	GAGCAGCGTC	CTTGGGCTCT	ATCCGCGAGG	TGCCAGTAGC	GTGTGCAAGT	ACATACACGT	2640
	CGGTGACAC	TGTGATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTG	TCCTTGGGGG	2700
10	CAGAAAGTGC	CCAGATTGAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GCCTCAGGA	2760
	TTTGTGTGTG	ATCAAGTTCC	AAGGAAAGG	AACATCTCAG	CCGGGCGTGG	TGGTTCACGC	2820
	CTGGAATCCC	AGCATTGAG	GCCAGGAGTT	CCAGAGCAGC	CTGGGCAACG	CAGTGAGAGA	2880
	CCCCATCTCT	ACAARAAAAA	AAAAAGAAAG	AAAGAAATG	AGAGATCCAG	GTTTAAAAAT	2940
	TCATAAACAC	CACAAGGAAA	CAATACACTA	TGAGACCCAG	CAGAAGCAAC	AGATTGACTC	3000
15	TAGACCCAGA	TACTAGAATT	ATCAGAGAGA	ATATAAAGTA	ACAGTGTTTT	ATATATCTAA	3060
	AGAAATAAAA	GAGATTTCTG	GAACATGAA	AAAAAA			

A58 DNA sequence

	Gene name:	ESTs
	Unigene number:	Hs.157601
20	Probeset Accession #:	W07459
	Nucleic Acid Accession #:	AC005383
	Coding Sequence:	328-2751 (underlined sequences correspond to start and stop codons)

25	1	11	21	31	41	51	
	GACAGTGTTC	GCGGCTGCAC	CGCTCGGAGG	CTGGGTGACC	CGCGTAGAAG	TGAAGTACTT	60
	TTTATTATTC	AGACCTGGGC	CGATGCCGCT	TTAAAAACG	CGAGGGGCTC	TATGCACCTC	120
	CCTGGCGGTA	GTCTCTCCGA	CCTCAGCCGG	GTGCGGTGCT	GCCGCCCTCT	CCGAGGAGAG	180
30	ACAAACAGGT	GTCCACAGTG	GCAGCCGCGC	CCCGGGCGCC	CCTCCTGTGA	TCCCGTAGCG	240
	CCCCCTGGCC	CGAGCCGCGC	CCGGGTCTGT	GAGTAGAGCC	GCCCGGGCAC	CGAGCGCTGG	300
	TGCGCGCTCT	CCTTCCGTTA	TATCAACATG	CCCCCTTTCC	TGTGTCTGGA	GGCGGTCTGT	360
	GTTTTCTCTG	TTTCCAGAGT	GCCCCCATCT	CTCCCTCTCC	AGGAAGTCCA	TGTAAGCAAA	420
	GAAACCATCG	GGAAGATTTC	AGCTGCCAGC	AAAATGATGT	GCTGCTCCGC	TGCAGTGGAC	480
35	ATCATGTTTC	TGTTAGATGG	GTCTAACAGC	GTGCGGAAGG	GGAGCTTTGA	AAGGTCCAAG	540
	CACCTTTGCCA	TCACAGTCTG	TGACGGTCTG	GACATCAGCC	CCGAGAGGGT	CAGAGTGGGA	600
	GCATTCCAGT	TCAGTTCCAC	TCCTCATCTG	GAATTCCTCC	TGGATTCAAT	TTCAACCCAA	660
	CAGGAAGTGA	AGGCAAGAAAT	CAAGAGGATG	GTTTTCAAGG	GAGGGCGCAC	GGAGACGGAA	720
	CTTGCTCTGA	AATACCTTCT	GCACAGAGGG	TTGCTCGGAG	GCAGAAATGC	TTCTGTGCCC	780
40	CAGATCCCTCA	TCATCGTCAC	TGATGGGAAG	TCCACGGGGG	ATGTGGCACT	GCCATCCAA	840
	CAGCTGAAGG	AAAGGGGTGT	CACGTGTGTT	GCTGTGGGGG	TCAGGTTTCC	CAGGTGGGAG	900
	GAGCTGCATG	CACTGGCCAG	CGAGCCTAGA	GGGCAGCAGG	TGCTGTTGGC	TGAGCAGGTG	960
	GAGGATGCCA	CCAAAGCGCT	CTTCAGCACC	CTCAGCAGCT	CGGCCATCTG	CTCCAGCGCC	1020
	ACGCCAGACT	GCAAGGTGGA	GGCTCACCCC	TGTGAGCACA	GGACGCTGGA	GATGGTCCGG	1080
45	GAGTTCGCTG	GCAATGCCCC	ATGCTGGAGA	GGATGCGCGC	GGACCCCTGC	GGTGTGGCT	1140
	GCACACTGTC	CCTTCTACAG	CTGGAAGAGA	GTGTTCTTAA	CCCACCTGTC	CACCTGTCTC	1200
	AGGACCACCT	GCCCAGGGCC	CTGTGACTCG	CAGCCCTGCC	AGAATGGAGG	CACATGTGTT	1260
	CCAGAAAGAC	TGGAAGGGTA	CCAGTGCCCT	TGCCCGCTGG	CCCTTGGAGG	GGAGGCTTAA	1320
	TGTGCCCTGA	AGCTGAGCCT	GGAATGCAGG	GTGCACTCC	TCTTCTGCTG	GGACAGCTCT	1380
50	GCGGGCACCA	CTCTGGAGCG	CTTCTGCGGG	GCCAAAGTCT	TCGTGAAGCG	GTGTTGTGGG	1440
	GCGGTGCTGA	GCGAGGACTC	TGGGGCCCGA	GTGGGTGTGG	CCACATACAG	CAGGGAGCTG	1500
	CTGGTGGGCG	TGCTGTGGGG	GGAGTACCA	GATGTGCTGG	ACCTGGTCTG	GAGCCTCGAT	1560
	GGCATTCCCT	TCCGTGTGGG	CCCCACCCCT	ACGGGCACTG	CCTTGGCGCA	GGCGGCAGAG	1620
	CGTGCTCTTG	GGAGCGCCAC	CAGGACAGGC	CAGGACCGGC	CACGTAGAGT	GGTGGTTTGG	1680
55	CTCACTGAGT	CACACTCCGA	GGATGAGGTT	GCGGGCCCG	GCGTCAACGC	AAGGGCGCGA	1740
	GAGCTGTCTC	TGCTGGGTGT	AGGCAGTGAG	GCCGTGCGGG	CAGAGCTGGA	GGAGATCACA	1800
	GGCAGCCCAA	AGCATGTGAT	GGTCTACTCG	GATCCTCAGG	ATCTGTTCAA	CCAAATCCCT	1860
	GAGCTGCAGG	GGAAGCTGTG	CAGCCGGCAG	CGGCCAGGGT	GCCGGACACA	AGCCCTGGAC	1920
	CTGCTCTTCA	TGTTGGACAC	CTCTGCCTCA	GTAGGGCCCG	AGAATTTTGC	TCAGATGCAG	1980
60	AGCTTTGTGA	GAAGCTGTGC	CCTCCAGTTT	GAGGTGAACC	CTGACGTGAC	ACAGGTCCGC	2040
	CTGGTGGTGT	ATGGCAGCCA	GGTGCAGACT	GCCTTGGGGC	TGGACACCAA	ACCCACCCCG	2100
	GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	CCCTACCTAG	GTGGGGTGGG	CTCAGCCGGC	2160
	ACCGCCCTGC	TGCACATCTA	TGACAAAGTG	ATGACCTCC	AGAGGGGTGC	CCGGCCTGGT	2220
	GTCCCAAGAG	CTGTGGTGGT	GCTCACAGGC	GGGAGAGGGG	CAGAGGATGC	AGCGGTTCTC	2280
65	GCCCAGAAGC	TGAGGAACAA	TGGCATCTCT	GTCTTGTGCG	TGGGCGTGGG	GCCTGTCTTA	2340
	AGTGAGGGTC	TGCGGAGGCT	TGCAGGTCCC	CGGGATTCCC	TGATCCACGT	GGCAGCTTAC	2400
	GCGACCTGCG	GGTACCACCA	GGACGTGCTC	ATTGAGTGGC	TGTGTGGAGA	AGCCAAGCAG	2460
	CCAGTCAACC	TCTGCAAAAC	CAGCCCGTGC	ATGAATGAGG	GCAGCTGCGT	CCTGCAGAA	2520
	GGGAGCTACC	GCTGCAAGTG	TGCGGATGGC	TGGGAGGGCC	CCCACTGCGA	GAACCGTGAG	2580
70	TGGAGCTCTT	GCTCTGTATG	TGTGAGCCAG	GGATGGATTG	TTGAGACGCC	CCTGAGGCAC	2640
	ATGGCTCCCG	TGCAGGAGGG	CAGCAGCGGT	ACCCCTCCCA	GCAACTACAG	AGAAAGGCGT	2700
	GGCACTGAAG	TGGTGCCTAC	CTTCTGGAAT	GTCTGTGCC	CAGGTCTCTA	GAATGTCTGC	2760
	TTCCCGCGGT	GGCCAGGACC	ACTATTCTCA	CTGAGGGAGG	AGGATGTCCC	AACTGCAGCC	2820
	ATGCTGCTTA	GAGACAAGAA	AGCAGCTGAT	GTCAACCCCA	AACGATGTTG	TTGAAAGATT	2880
75	TTGATGTGTA	AGTAAATACC	CACCTTCTGT	ACCTGCTGTG	CCTTGTGTAG	GCTATGTCTA	2940
	CTGCCACCTT	TCCTTTGAGG	ATAAACAGGG	GGTCTGTAAG	ACTTAAATTT	AGCGGCGCTA	3000
	CGTTCTCTTG	CACACAATCA	ATGCTGCCCA	GAATGTGTTT	GACACAGTAA	TGCCAGCAGC	3060
	AGGCCCTTAC	TAGAGCATCC	TTTGGACGGC	GAAGGCCAAG	GCCTTTCAAG	ATGGAAAGCA	3120
	GCAGCTTTTC	CACCTTCCCA	GAGACATTCT	GGATGCATTT	GCATTGAGTC	TGAAAGGGGG	3180
80	CTTGAGGGAC	GTTTTGTGAT	TCTTGGGCGC	TGCCCTTTGT	GTGTGGAAGA	GACTTGGAAA	3240
	GGTCTCAGAC	TGAATGTGAC	CAATTAAACA	GCTTGGTTGA	TGATGGGGGA	GGGGCTGAGT	3300
	TGTGCATGGG	CCAGGTCTG	GAGGGCCACG	TAAATCGTTT	CTGAGTCGTG	AGCAGTGTCC	3360
	ACCTTGAAGG	TCTTC					

A59 Protein sequence

Gene name: ESTs
 Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGM domains: 49-223; 341-518; 529-706
 BGF domains: 298-333; 715-748
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
15  MPPFLLEAV CVFLPSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
    SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQPSSTPH LEFPLDSFST QQEVKARIKR 120
    MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGTV 180
    FAVGVPRFPR BELHALASEP RQGHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
    PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPPGCD 300
    SPPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
    RAKVFVKRFV RAVLSDSRA RVGVATYSRE LLVAVFVGEY QDVDPDLVWSL DGIPFRGGPT 420
    LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTSHSEDE VAGPARHARA RELLLLGVGS 480
    EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGLCSR QRPGRCTQAL DLVFMLD TSA 540
    SVGPENPAQM QSFVRSCALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
    APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVL T GGRGAEDAAV PAQKLNRNGI 660
    SVLVVGVGPFV LSEGLRRLAG PRDSLHVAA YADLRVHQDV LIEWLCEGAK QPVNLCKPSP 720
    CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
    RTPPSNVYREG LGTEMVPTFW NVCAPEGP
  
```

A60 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
40  ATGTTCACAG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60
    AAACCCCGTA TCCCATGGA GACCTTCAGA AAGTGGGGA TCCCATCAT CATAGCACTA 120
    CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180
    TACTTCTCTT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
    CTGGAAGTTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
    GCAGTGGCAG TCCGCTCTCT CAAGGACCGA TCCCACTGTC AGGTGCTGGA CTGCGCCACA 360
    GGGAACTGGT TCTCTGCTCT TTTGCAAC TTTACAGAAG CTCTCGCTGA GACAGCCTGT 420
    AGGCAGATGG GCTACAGCAG CAACCCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCTG 480
    GATCTGGATG TTGTTGAAT CACAGAAAC AGCCAGGAGC TTGCTATGCG GAACCTCAAGT 540
    GGGCCTCTGC TCTCAGGCTC CTGCTCTGCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
    AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
    AGCATCCAGT ACACAAACA GCACGCTCTGT GGAGGGAGCA TCCTGGACCC CCACCTGGTC 720
    CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCACTGGAA GGTGCGGGCA 780
    GGCTCAGACA AACTGGGCGC CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCATTTGA 840
    TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGTGCAT GTTCCCACTC 900
    ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCCCTT TTGATGAGGA GCTCACTCCA 960
    GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
    GACATACATG TCAGAGGCTC AGTCCAGGTC ATTGACAGCA CACGGTGCAT TGCAGACGAT 1080
    GCGTACACAG GGAAGTCAC CAGAAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG 1140
    GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
    GTGGGCTACG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
    AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
  
```

A61 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLa domain: 54-94
 Tryp_SPC domain: 204-429
 Cellular Localization: plasma membrane/ER

```

1      11      21      31      41      51
|      |      |      |      |      |
75  MLQDPDSQPF LNSLDVKPLR KPRIPMTFPR KVGIPITIAL LSLASIIIVV VLIKVILDKY 60
    YFLCGQPLHF IPRRLCDGE LDCPLGEDEE HCVKSPPEGP AVAVRLSKDR STLQVLDSAT 120
    GWNFSACFDN FTEALAEATC RQMGYSSEKPT FRAVEIGPDQ DLDVVEITEN SQELEMNRNS 180
    GPCLSGSLVS LHCLACGKSL KTRPVVGEE ASVDWSPHQV SIQYDKQHVC GGSILDPHWV 240
    LTAHCFRKH TDVFNKVR A GSDKLSFPPS LAVAKIIIE FNFMPKDN D IALMKLQFPL 300
    TFSGTVRPIC LPPFDEELTP ATPLIWIGW FTQNGGKMS DILLQASVQV IDSTRCNADD 360
    AYQGEVTEKM MCAIGPEGGV DTCQGDSSGP LMYQSDQHEV VGIWSWGYGC GGPSTPGVYT 420
    KVSAYLNWII NVWKAEI
  
```

A62 DNA SEQUENCE

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Nucleic Acid Accession #: none found
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

10
 15
 20
 25
 30

1	11	21	31	41	51	
CCAAACAGAT	TTGCAGATCA	AGGAGAACCC	AGGAGTTTCA	AAGAAGCGCT	AGTAAGGTCT	60
CTGAGATCCT	TGCACTAGCT	ACATCCTCAG	GGTAGGAGGA	AGATGGCTTC	CAGAAGCATG	120
CGGCTGCTCC	TATTGCTGAG	CTGCCTGGCC	AAAACAGGAG	TCCTGGGTGA	TATCATCATG	180
AGACCCAGCT	GTGCTCCTGG	ATGGTTTAC	CACAAGTCCA	ATTGCTATGG	TTACTTCAGG	240
AAGCTGAGGA	ACTGCTCTGA	TGCCGAGCTC	GAGTGTCACT	CTTACGGA	CGGAGCCAC	300
CTGSCATCTA	TCCTGAGTTT	AAAGGAAGCC	AGCACCATAG	CAGAGTACAT	AAGTGGCTAT	360
CAGAGAAGCC	AGCCGATATG	GATTTGGCTG	CACGACCCAC	AGAAGAGGCA	GCACTGGCAG	420
TGGATTGATG	GGGCCATGTA	TCTGTACAGA	TCCTGGTCTG	GCAAGTCCAT	GGGTGGGAAC	480
AAGCACTGTG	CTGAGATGAG	CTCCAATAAC	AACTTTAA	CTTGGAGCAG	CAACGAATGC	540
AACAAGCGCC	AACAATTCTCT	GTGCAAGTAC	CGACCATAGA	GCAAGAATCA	AGATTCTGCT	600
AACCTCTGCA	CCAGCCCCGT	CCTCTTCTT	TCTGCTAGCC	TGGCTAAATC	TGCTCATTAT	660
TTCAAGAGGG	AAACCTAGCA	AACTAAGAGT	GATAAGGGCC	CTACTACACT	GGCTTTTATA	720
GGCTTAGAGA	CAGAAACTTT	AGCATTGGGC	CCAGTAGTGG	CTTCTAGCTC	TAAATGTTTG	780
CCCCGCCATC	CTTTCCACA	GTATCCTTCT	TCCCTCCTCC	CCTGTCTCTG	GCTGTCTCGA	840
GCAGTCTAGA	AGAGTGATCC	TCCAGCCTAT	GAACAGCTG	GGTCTTTGGC	CATAAGAAGT	900
AAAGATTTGA	AGACGAGAAG	AAGAACTCA	GGAGTAAGCT	TCTAGACCCC	TTCACTTCTT	960
ACACCTTCTT	GCCTCTCTC	CATTGCTG	ACCCCAACCC	AGCCACTCAA	CTCTGCTTGT	1020
TTTTCTCTTT	GGCCATAGGA	AGGTTTACCA	GTAGAATCCT	TGCTAGGTTG	ATGTGGGCCA	1080
TACATTCCTT	TAATAAACCA	TTGTGTACAT	AAGAGAAAAA	AAAAAAAAAA	AAAAAAAAAA	

A63 Protein sequence:

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Protein Accession #: none found
 Signal sequence: 1-22
 Transmembrane domains: none found
 C-type lectin domain: 47-156
 Cellular Localization: secreted

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1	11	21	31	41	51	
MASRSRLRL	LLSCLAKTGV	LGDIIMRPS	APGWFYHKS	CYGYPRKLR	WSDAELECO	60
YNGAHLASI	LSLKEASTIA	EYISGVQRS	PIWIGLEHDP	KRQWQWIDG	AMLYRSWSG	120
KSMGGNKHCA	EMSSNNFLT	WSSNECNKQ	HFLCKYRP			

A64 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

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1	11	21	31	41	51	
GCGGAACACC	GGCCCGCGT	CGCGGCAGCT	GCTTCACCCC	TCTCTCTGCA	GCCATGGGGC	60
TCCTCTGTGG	ACCTCTGCG	TCTCTCTCTC	TTCTCCAGGT	TTGCTGGCTG	CAGTGGCGG	120
CCTCOGAGCC	GTGCGCGGG	GTCTTCAGGG	AGGCTGAAGT	GACCTTGGAG	GCGGAGGCG	180
CGGAGCAGCA	CGCCGCGCAG	CGCTGGGGGA	AAGTATTCAT	GGGCTGCCCT	GGGCAAGAGC	240
CAGCTCTGTT	TAGCACTGAT	AATGATGACT	TCACTGTGCG	GAATGGCGAG	ACAGTCCAGG	300
AAAGAAGGTC	ACTGAAGGAA	AGGAATCCAT	TGAAGATCTT	CCCATCCAAA	CGTATCTTAC	360
GAAGACACAA	GAGAGATTGG	GTGGTTGCTC	CAATATCTGT	CCCTGAAAAT	GGCAAGGGTC	420
CCTTCCCCCA	GAGACTGAAT	CAGCTCAAGT	CTAATAAAGA	TAGAGACACC	AAGATTTTCT	480
ACAGCATCAC	GGGCGCGGG	GCAGACAGCC	CCCTTGAGGG	TGTCTTCGCT	GTAGAGAAGG	540
AGACAGGCTG	GTGTGTTTGG	AATAAGCCAC	TGGACCGGGA	GGAGATTGCC	AAGTATGAGC	600
TCCTTTGGCCA	CGCTGTGTCA	GAGAATGGTG	CCTCAGTGGG	GGACCCCATG	AACATCTCCA	660
TCATCTGTAC	CGACCAAGAT	GACCAACAGC	CCAAGTTTAC	CCAGGACACC	TTCCGAGGGA	720
GTGTCTTAGA	GGGAGTCCTA	CCAGGTACTT	CTGTGATGCA	GGTGACAGCC	ACAGATGAGG	780
ATGATGCCAT	CTACACCTAC	AATGGGGTGG	TTGCTTACTC	CATCCATAGC	CAAGAACCAA	840
AGGACCCACA	CGACCTCATG	TTCACAATTC	ACCGGAGCAC	AGGCACCATC	AGCGTCATCT	900
CCAGTGGCCT	GGACCGGGAA	AAAGTCCCTG	AGTACACACT	GACCATCCAG	GCCACAGACA	960
TGGATGGGGA	GGGCTCCACC	ACCAOCCGAG	TGGCAGTAGT	GGAGATCCCT	GATGCCAATG	1020
ACAATGCTCC	CATGTTTGGC	CCCCAGAAGT	ACGAGGCCCA	TGTGCTGAG	AATGCACTGG	1080
GCCATGAGGT	GCAGAGGCTG	ACGGTCACTG	ATCTGGAGCG	CCCCAATCA	CCAGCGTGGC	1140
GTGCCACCTA	CCATTATCAT	GGCGGTGAAG	ACGGGGACCA	TTTACCATC	ACCAOCCACC	1200
CTGAGAGCAA	CCAGGGCATC	CTGACAAACA	GGAAGGGTTT	GGATTTTGAG	GCCAAAAACC	1260
AGCACACCTT	GTACGTTGAA	GTGACCAACG	AGGCCCTTTT	TGTGCTGAAG	CTCCCAACCT	1320
CCACAGCCAC	CATAGTGGTC	CACGTGGAGG	ATGTGAATGA	GGCACCCTGT	TTTGTCCAC	1380
CCTCCAAAGT	CGTTGAGGTC	CAGGAGGGCA	TCOCCACTGG	GGAGCCTGTG	TGTGTCTACA	1440
CTGCAGAAGA	CCCTGACAAG	GAGAATCAAA	AGATCAGCTA	CGCATCCTCT	AGAGACCCAG	1500

CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC 1560
 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
 ATGGAAGCCC TCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
 ACCATGGCCC AGTCCCTGAG CCCCCTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC 1740
 5 ACCTGCTGAA CATCACGGAC AAGGACCTGT CTCCCCACAC CTCCCCCTTC CAGGCCCAGC 1800
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACTT TCTCTGTCTG 1920
 ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
 10 ATGTGAAAC CTGCCCTGGA CCTGGAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
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 TCAGGAGGCC CCTCTACTC CCAGAAGATG ACACCGTGA CAACGTCTT TACTATGGCG 2160
 AAGAGGGGCC TGGCGAAGAG GACCAAGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
 AGGCCAGGCC GGAGGTGGTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
 15 AGSCGGCTAA CACAGACCCC ACAGCCCCG CCTACGACAC CCTCTTGGTG TTCGACTATG 2400
 AGGCGACGG CTCCGACGCC GGTCCCTGA GCTCCCTCAC CTCTCGGCC TCCGACCAAG 2460
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGCTT CAAGAAGCTG GCAGACATGT 2520
 ACGGTGGCGG GGAGGACGAC TAGGCGGCTT GCCTGCAGGG CTGGGGACCA AACGTGAGGC 2580
 CACAGAGCAT CTCCAAGGGG TCTCAGTTC CCCTTCAGCT GAGGACTTGG GAGCTTGTC 2640
 20 GGAAGTGGCC GTAGCAACTT GCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
 TCCTTAGCCT TTCAAGATGG AGGAATGTGG GCAGTTTGA CTTAGCACTG AAAACCTCTC 2760
 CACCTGGGCC AGGGTTGCC CTAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCTAATA 2820
 TGCTCAACCC TGTGTCTCTG GCCTGGGCTT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAATGGA ACCTTCTTAG GCCTCTCTGT GCAACTTAAT TTTTCTTTT AATGCTATCT 2940
 25 TCAGAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCAGAG GCTGCTGGGC CCACTGGCCG 3000
 TCCTGCAATT CTGGTTTCCA GACCCCAATG CCTCCCATC GGATGGATCT CTGCTTTT 3060
 ATACTGAGTG TGCTTAGGTT GCCCCTTATT TTTTATTTC CTGTTGCGT TGCTATAGAT 3120
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAAGCTTTT TATTAAAGAA A

A65 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 35 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675 (second underlined sequence)
 Cellular localization: plasma membrane

1 11 21 31 41 51
 MGLPRGFLAS LLLQLQVCWLQ CAASEPCRAV FREAEVTL EA GGAEQEPGQA LGKVFMGCPG 60
 QEPALFSTDN DDFTVRNGET VQERRSLKER NFLKIPPSKR ILRRHKRDWV VAPISVPENG 120
 45 KGPPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLN KPLDREEIAK 180
 YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYTNV GVVAYSISHQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TMDGDGSGTT TAVAVVEILD ANDNAPMFDQ QKYBAHVPEV AVGEHVQLRT VTDLDAPNSP 360
 50 AWRATLYING GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEFVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLAMPD DSGQVTAAGT LDREDEQFVR NNIYEVMLVA MONGSPPTTG TGTLLLLTLD 540
 VNDHGVPVPEP RQITICNQSE VRHVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660
 55 GAVLALLFL LVLLLVVRKK RKIKEPLLLP EDDTRDNVFP YGEBGGGEED QDYDITQLHR 720
 GLEARPEVRL RNDVAPTIIP TPMYRPRPAN PDEIGNPIE NLKAANTDEPT APPYDTLLVF 780
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

A66 DNA SEQUENCE

60 Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Nucleic Acid Accession #: AF189723
 65 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGATTCCTG TATTGACATC AAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
 ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
 70 TTTCTAGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
 TCTCAGTTTA AAAATCCCTT TATTATGCTG CTTCCTGGCT CTGCACTCAT CAGTGTTTTA 240
 ATGATCAGT TTAGATATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTATACGTT 300
 GCCTTTGTTT AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
 75 CCAGATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGGCCG AGACTTGGTT 420
 CCAGGTGATA CAGTTTGCCT TCTGTGTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTTT 480
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTCTT 540
 AAGGTGACAG CTCTCAGGCC AGCTGCAACT AATGGAGATC TTGATCGAG AAGTAACATT 600
 80 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTGTTCAT TGAACAGGA 660
 GAAATTTCTG AATTGTGGGA GGTTTTAAAT ATGATGCAAG CAGAGAGGCC ACCAAAAACC 720
 CCTCTGACA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780
 ATAGGAATCA TCATGTTGGT TGGCTGTGTA CTGGGAAAAA ATATCCTGGA AATGTTTACT 840

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ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCCATTGT GGTACAGTG 900
ACGCTAGCTC TTGGTGTAT GAGAAATGGT AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 950
ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCTG ATAAAACTGG AACACTGACG 1020
AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT 1080
GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATTTC 1140
TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAAAT 1200
AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260
ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTAGCTCT 1320
GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
TGTTTTATGA AAGGTGCTTA CGAACAAAGT ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAAG GAAGGCACGC 1500
ATGGGCTCAG CGGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCTGAACT GGGACAGCTG 1560
ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
ACAACACTCA TTGCCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTTC ACAGGAGACT 1680
GCAGTTGCAA TCGGCTGCTT TCTGGGATTG TATTCCAAAA CTTCACAGTC AGTCTCAGGA 1740
GAAGAAATAG ATGCAATGGA TGTTCAGCAG CTTTCACAAA TAGTACCAAA GGTTCAGTA 1800
TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTOGCTACA GAAGAACGGT 1860
TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920
ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980
CTAGTGGATG TTGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGAGTTTAT 2040
AATAACATTA AAAATTTCGT TAGATTCCAG CTGAGCAGCA GTATAGCAGC ATTAACCTTA 2100
ATCTCATTGG CTACATTAAT GAACCTTCTT AATCTCTCTA ATGCCATGCA GATTTTGTGG 2160
ATCAATATTA TTATGGATGG ACCCCAGCTC CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
GATGTCAATC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTTGATA 2280
CTTAAATATC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTTG CTCTGGCGGT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACACAA TGACCTTCAC ATGCTTTGTG 2400
TTTTTTGACA TGTTCATGTC ACTAAGTCC AGATCCCAGA CCAAGTCTGT GTTTGAGATT 2460
GGACTCTGCA GTAATAGAAAT GTTTTGCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA 2520
CTAGTTATTT ACTTCTCTCC GCTTCAGAA GTTTTCAGCA CTGAGAGCCT AAGCATACTG 2580
GATCTGTTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTGA GTTCGACATC ATCATCTTTT 2700
CTTGAAGTAT GA
  
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A67 Protein sequence:
 Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Protein Accession #: AAF27813
 Signal sequence: none found
 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
 Cellular Localization: not determined

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1      11      21      31      41      51
|      |      |      |      |      |
MIPVLTSKKA SELPVEVAS ILQADLQNL NKCEVSHERRA FHGWNEFDIS EDEPLWKKYI 60
SQFKNLIML LLASAVISVL MHQFDDAVSI TVAILIVTV APVQEYRSEK SLEELSKLVP 120
PECHCVREK LEHTLARDLV PGDTVCLSVG DRVPADLRFP EAVDLSDIES SLTGETTFCPS 180
KVTAQPPAAT NGDLASRSNI APMGTLVRCG KAKGVVIGTG ENSEFGEVFK MQQAEAPKT 240
PLQKSDLLG KQLSFYSPGI IGIIMLVGWL LKQDILEMPT ISVSLAVAAI PEGLPFIVTV 300
TLALGVMRMV KKRRAIVKLEP IVETLGCCNV ICSDKTGLTL KNEMTVTHIP TSDGLHAEVT 360
GVGYNQFGEV IVDGDVVHGP YNPVSRIVE AGCVNDNAVI RNTLMGKPT EGALIALAMK 420
MGLDGLQDY IRKAEYFPSS EQKMAVKCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK 480
GQTLTLTQQQ RDVYQQEKAR MGSAGLRVLA LASGPGLQL TFLGLVGTID PPRTGVKEAV 540
TTLIASGVSI KMITGDSQBT AVAIASRLGL YSKTSQSVSG BEIDAMDVQV LSQIVPKVAV 600
PYRASPRHM KIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMQGTGT DVCKEADMI 660
LVDDPRTIM SAIEBGRGIY NNIKNFVRFO LSTSIALTL ISLATLMNFP NPLNAMQLW 720
INIIMDGPPA QSLGVEFVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFW 780
ELRDNVITPR DTTMTPTCFV PFDMPNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMQGL 840
LVYFPPLOK VFQTESLSIL DLLFLGLTS SVCIVAEIIE KVERSRREKIQ KHVSTSTSSSF 900
LEV
  
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A68 DNA SEQUENCE
 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Nucleic Acid Accession #: NM_001719
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CGGAGCGCGG GGTAGCGCGT AGAGCGGCG 120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCGCACAG CTTCGTGCGG CTCTGGGCAC 180
CCCTGTTCTT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAAAGAG GTGCACTCGA 240
GCTTCATCCA CGCGCGCTCC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTCT GCTGCACTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
GCCAGGGCTT CTCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGCGCA 480
GCCTGCAAGA TAGCCATTTC CTCACGAGC CGACATGGT CATGAGCTTC GTCAACCTCG 540
TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACACCA TCAGAGATTG CGGTTTGATC 600
TTTCCAAGAT CCCAGAAAGG GAAGCTGTCA CGGCGCGCA ATTCCGAGAT TACAAGGACT 660
  
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ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCTCGG 780
AGGAGGGCTG GCTGTGTTT GACATCACAG CCACAGCAA CCACTGGGTG GTCAATCCGC 840
GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
AGTTGGCGGG CCGATTGGG CGGCAGGGG CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960
TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGCTC CAGGGGAGC AACACAGCGCA 1020
GCCAGAACC CGTCCAGACG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTAGCGCGCC TACTACTGTG 1200
AGGGGGAGTG TGCCCTTCCCT CTGAACCTCT ACATGAACGC CACCAACCA GCCATCGTGC 1260
AGACGCTGGT CCACTTCATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCACGCG 1320
AGCTCAATGC CATCTCCGTC CTCTACTTGG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCAGAA TTCAGACCTC 1440
TTGGGGCCAA GTTTTCTGG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCCCTTTG TGAGACCTTC CCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
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TCTTCAAGC TGTGACAGCA AACCTAGCA GGAAGAAAA ACAACGCATA AAGAAAAATG 1680
GCCGGGCCAG GTCATTGGCT GGAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
TTATGAGCGC CTACACGCCA GGCCACCCAG CCGTGGGAGG AAGGGGCGT GGCAGGGGT 1800
GGGCACATG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAACG AATGAATG

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A69 Protein sequence:
Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number: Hs.170195
Probeset Accession #: BE616633
Protein Accession #: NP_001710.1
Signal sequence: 1-30
Pfam domains: TGFb_propeptide [37-281]
Transmembrane domains: none found
Cellular Localization: secreted

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1 11 21 31 41 51
| | | | |
MHVRSRAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQE REMQREILS 60
ILGLPHRPRP HLQCKNSAP MFMLDLNLYM AVBEGGGPGG QGFSYPYKAV PSTQGPPLAS 120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREFRFDL SKIPEGEAVT AAEFRIYKDY 180
IRERFNETF RISVYVQLQE HLGRESDLFL LDSRTLWASE EGWLVDITA TSNHWVNP 240
HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
QNRSKTPKQK EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWQDWIIA PEGYAAAYCE 360
GECAPPLNSY MNATNHAIQ TLVHFNPET VPKPCCAPTQ LNAISVLYFD DSSNVILWKY 420
RNMVVRACGC H

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Cervical

A70 DNA sequence
Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.87223
Probeset Accession #: AA250737
Nucleic Acid Accession #: NM_001203
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGAACGGGCG AGTGGGAGA CCGCGGCGCT 60
GAGGAACGGG GAGCCGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTCTTTAGAT 120
GTGAAGAGAA AGGAAGATCA TTTCATGCCT TGTGATAAAA GGTTCAGACT TCTGCTGATT 180
CATAACCATI TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA 300
AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCAACCCCGG TCCAAAGGTC 360
TTGCGTGTGA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGACGACA 420
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480
GGTTGCCTAG GACTAGAAGG CTCAGATTTT CAGTGTGCGG ACATCCCAT TCCTCATCAA 540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600
CTGCCTCCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660
ATATCTGTGA CTGCTCTGAG TTTGCTCTTG GTCTTATCA TATTATTTTG TTACTTCCGG 720
TATAAAAGAC AAGAAACCCG ACCTCGATAC AGCATTTGGT TAGAACAGGA TGAACCTTAC 780
ATTCCTCTTG GAGATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840
TCAGGCTCTC CTCTCTGCTG CCAAGGAGCT ATAGCTAAGC AGATTGAGT GGTGAAACAG 900
ATTGGAAAGG GTGGCTATGG GGAAGTTTGG ATGGGAAAGT GGCGTGCGCA AAAGGTAGCT 960
GTGAAGTGT TCTTCAACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
ACAGTGTGTA TGAGGATGTA AAACATTTTG GGTTCATCTG CTGCAGATAT CAAAGGGACA 1080
GGGTCTGCTG GAGCTTGTGA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
TATCTGAAGT CCACCAACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200
AGTGGCTTAT GTCAATTACA CACAGAAATC TTTAGTACTC AAGGCAACCC AGCAATTGCC 1260
CATCGAGATC TGAAAAGTAA AAACATTTCT GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320
GACCTGGGCC TGGCTGTGTA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
ACTCGAGTTG GCACCAACCG CTATATGCCT CCAGAAAGTG TGAACGAGAG CTTGAACAGA 1440
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTTCC CTTTGGGAG 1500
GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGAAGAAAT ACCAGCTTCC TTATCATGAC 1560
CTAGTCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620

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5 CGCCCCATCAT TCCCAAACCG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAACTC 1680
ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740
ACACTTGCCA AAATGTGAGA GTCCCAGGAC ATTAAGCTCT GATAGGAGAG GAAAAGTAAG 1800
CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA 1860
TAAGCATCCA CAGTACAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAC 1920
CTTTCAGGGA GGCACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
TCTGTTTGTG GCGGAGAGAA CCGTTGGGTA ACTTGTTCAT GATATGATGC AT

10 A71 Protein sequence
Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.72472 / Hs.87223
Probeset Accession #: AA250737 / U89326
Protein Accession #: NP_001194
Signal sequence: 1-13
Transmembrane domains: 128-144
PFAM domains: activin_receptor [30-111], protein kinase [204-491]
Cellular Localization: plasma membrane

20 1 11 21 31 41 51
MLLSRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFTMIEED 60
DSGLPVVTSIG CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD 120
25 GPIHRRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180
BQSQSSSGSGS GLPLLVRQTI AKQIQMKVQI GKGRYGEVNM GKWRGEKVAV KVFFTTTERAS 240
WFRTEIYQOT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
MLKLAYSSVS GLCHLHTEIF STQKPAIAH RDLKSKNIVL KKNGTCCIAI LGLAVKFISS 360
TNEVDIPFNT RVGTRKYMPP EVLDESLNRN HFQSYIMADM YSFGILLWEV ARRCVSGGIV 420
30 EYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHPAS 480
RLTALRVKKT LAKMSSESQDI KL

Bladder
A72 DNA SEQUENCE
Gene name: Homo sapiens type II membrane serine protease mRNA
35 Unigene number: Hs.63325
Probeset Accession #: AA411502
Nucleic Acid Accession #: NM_016425
Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
ATGTTACAGG ATCCTGACAG TGATCAACT CTGAACAGCC TGATGTCAA ACCCCTGCGC 60
AAAACCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
45 CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCTCATCA AGGTGATTCT GGATAAATAC 180
TACTTCCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
CTGGACTGTC CCTTGGGGGAG GGACGAGGAG CACTGTGTCA AGAGCTTCCC GGAAGGGCCT 300
GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCACACTGC AGTGCTGGA CTCGGCCACA 360
50 GGGAACTGGT TCTCTGCCGT TTTGCAAC TFCACAGAAG CTCTGCTGA GACAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTGCGATGCG GAACCTCAAGT 540
GGGCCCTGTC TCTCAGGCTC CTGCTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGCCC TTGGCAGGTC 660
55 AGCATCCAGT ACACAAAC GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
CTCAGCGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
GGCTCAGACA AACTGGGAGC CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
TTCAACCCCA TGACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
60 GCCACCCAC TCTGGATCAT TGGATGGGGC TTACGAAGC AGAATGGAGG GAAGATGTCT 1020
GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
GGTACCCAGG GGGAAAGTAC CGAGAAGATG ATGTGTGTCG GCATCCCGGA AGGGGGTGTG 1140
GACACCTGCC AGGGTACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
GTGGGCACTG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
65 AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

A73 Protein sequence:
Gene name: Homo sapiens type II membrane serine protease mRNA
70 Unigene number: Hs.63325
Probeset Accession #: AA411502
Protein Accession #: NP_057509
Signal sequence: none found
Transmembrane domains: 31-53
LDLa domain: 54-94
75 Tryp_SPC domain: 204-429
Cellular Localization: plasma membrane/ER

80 1 11 21 31 41 51
MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY 60
YFLOGQPLHP IPRKQLCDGE LDCPLGEDEE HCVKSPFPEG AVAVRLSKDR STLQVLD SAT 120

5 GNPFSACFDN FTBALAETAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
 GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWPMQV SIQYDKQHV C GGSILDPHWV 240
 LTAARCFRKH TDVFNWVKRA GSKLGSFSS LAVAKIIIE FNPMPKND IALMKLQFPL 300
 TFSGTVRPIC LPFFDEELTP ATPLWIIWG FTKQNGGKMS DILLQASVQV IDSTRQADD 360
 AYQGEVTEKM MCAGIPEGGV DTCQGDSSGP LMYQSDQMHV VGIVSWGYC GGPSTPGVYT 420
 KVSAYLWIIY NVWKAEL

A74 DNA SEQUENCE

10 Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

15 1 11 21 31 41 51
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 20 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
 CTGGGCCAGA GCAGAGCCAG CGCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTCGG GGGAGCTGCT GGCTGCAGCC 300
 TGTGCCAGCC GGGCCCTGCC CCGTCTCTCC TCCGGGCCCC CCTGCCCTGC CTGACGTCC 360
 25 ACCTCACCCC CGGTCTGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTGG 480
 GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540
 GATTCCACCT TCATCTAGTC CTGTGGGGCC GCGTGGGGCC CCAGGGCCAG CCTGGCACTC 600
 AGCCCTTCGA GGGTGGGGCC CCGATCGCAC CCACCTCTC TGGCTGGAGA CCCCAGGAG 660
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 30 GCCTGCCCCC GCGTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG 780
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 35 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGTG GGAACGGCTC 1080
 GTAAGCGGGG GGTGCTCTGC TGGCTGGGGA GCGCCAGGGA TAGCGGTCCG ACTTCAGGTT 1140
 CTGGCCAAAG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200
 GGCTCTCATG TGCTCCCAAG AGACCCCTGG GTGATGGCCT TCCCCCTCTT GGCGGGGAGC 1260
 TTGCCCCACG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCGAGG AGGGCCCCCA 1320
 40 GACAGCTCCC AGGCACGTC TAGGCAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC 1380
 CTGGGGTCTC GCTCACCCCC CTTTGTCTCT ACGCCAGGCC TGTCCCCAGG TTTCACTGG 1440
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 GGCAGGTCCC CTGGGTGTC ACTCCCTCAG CCGCTGCCCA GGCCCACTCC CGCTGGTGCT 1560
 45 GGAGTACGCA CTGGTGGGGG GGCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTACCA 1620
 GAACCGGGG CAGGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680
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 50 CCTTCGGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCACAGAG CCACATTOCC 1920
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 55 GGTGGGGTCT TGCCACCAGG GGCCTCCCCA CGTCTGCTT TGAGGGTGGC TGCCATGCCC 2220
 TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280
 GGTGATCTAG TCGGAGAGAG GCCCACAATG AGCTGGACCC CGCAGCTGAA GCGGAAATG 2340
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 60 CAGAGGGGGA GAATTTAAAG GCGCCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520
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 GAGCAGCGTC CCGGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACAGT 2640
 GCGTGACAC TGTGATGACA CCGGAAATG TCTCAGGATG TTGAATGTG TCCTGGGGG 2700
 CAGAAGTGT CCGAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCTCAGGA 2760
 65 TTTTGTGTG ATCAAGTTCC AAGGAAAAGG AACATCTCAG CCGGGCGTGG TGGTTACGCG 2820
 CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
 CCCATCTCT ACAAAAAAAA AAAAAGAAAG AAAGAAATG AGAGATCCAG GTTTAAAAAT 2940
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
 TAGACCCAGA TACTAGAAAT ATCAGAGAGA ATATAAAGTA ACAGTGTTTT ATATATCTAA 3060
 70 AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

A75 DNA SEQUENCE

75 Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
 Unigene number: Hs.227948
 Probeset Accession #: AB035089
 Nucleic Acid Accession #: AB035089
 Coding sequence: 9845-10219 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
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 GGCATGCGAG CCATCGGGGA AAATCCATAG TGCAGATAAA GCAAGGAGGA AGAAGAAGGA 60
 CAGTTCTAGT AAAAGGGAGA ACATCAATAT AGGATGTTTC TTAGCAATAG AAAAAGAAGG 120
 CCAAGAGGAA TTAGGGAGAG AGTTATAAGA GATCAGCAAG GGGACAGGGT TAGATTGGT 180
 TTGTTTGAA AGCATACAGT AAATATGATG TCTGTCCCTG GCAGTGTTGG CAGAGTAGGA 240

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	AAGAAAGGAA	AGCTAGTTAG	TCTTGTCTCG	AGGTTGTTC	ATGTATACAT	ATCTATATCT	420
5	GTAGACAGAA	TCCTTGGGAA	TACAGTAATT	GACATATATT	CTGTTATTTG	ATGCTTGAAA	480
	AATCTCCTCC	ACTAACCCAGT	TTCCCTATAG	ATTGCCACAA	GCACATAATA	AGAAACAATA	540
	AATAAAATGT	TCTCTTGACT	TTGTTACTTA	ACAATGCTGA	GAAAACTTTA	CAGCCTTCAT	600
	AAGGAAGTGA	GGTCCAGGAA	AATCTAGGAG	ATATTTCTTA	ACCAATCTAT	AAAGGCATTA	660
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10	GGATTCCTGG	AGCCAATGAA	GTTGGTGAT	GTTTATGAAA	TATCAAGAGA	CATAAGTTGG	780
	CAAGTGTTC	TATGCAAAAA	CTTCTTGGAA	TTTCTGAGTT	CTCTGTGGCA	ATATATGACA	840
	TCAGGATATG	TCCAGTCTCA	CACACCAGGA	TATGTCTTT	CTAGCCTGTC	TATCACAATG	900
	TAGGAGAAT	ATTTAGGAAC	AGAAAAAAT	GCCTGAAATG	ATTTCTCAT	TGAACTCATC	960
	CAAGCTTTCT	CTAAATTTAA	GCAAACTCCT	GGTCATTTTC	AGTTAGTACC	TTTCTTAAAG	1020
15	TTCAACCTTC	AGGGCAAAACC	TCCGTGCCTC	AGACGTTTAC	CCATAGTCTG	AAATTTCTCT	1080
	CCATAGCTTG	ACTTCCCTGTA	ACCCCGGTTT	GTCTCAGCTT	GTTATCCTGT	TTTTTTCTTC	1140
	CCTCCATTCC	CAGGATGAGC	TTGTTGCTTC	TGTCCTATGA	GACATTAGAT	TCCTTTTCTT	1200
	TGGTACCCGA	GTAAATCCAT	CCTACTCCAA	TAGAGGAAGG	TCCATTTTGT	TCTTATAGCG	1260
	CTGGAATGAG	ACTCAGCTGA	GAAGACCAT	ATTCAATTTT	GGAAATCTTT	ATCTCAGATA	1320
20	TTTCTCTCTC	TTTCTTTTTC	TTCTATCTTT	GGATTTTITAG	TCCATCAACG	CCCCATTAGT	1380
	CTATTCCCGG	ACTTCAATCA	GGGAACCTTAT	ACCTCTTAAA	CTCATTGAGA	GACTCAAAAC	1440
	ATATATATTT	ATACAGGAGA	CCTAAGAAGA	GCATGTCTTG	GGGGTTGAGG	AAACAGGCAG	1500
	GTGAGAAAT	TCCAGATTGG	AAACACAGCT	TCCTTTCTCC	CATCCAGCCC	CTACTTTTCAG	1560
	CCTATGTGTT	TCTGGCACCT	TGTTGTAGAT	AAATCTCCCT	TGACTTTTGT	ATGTGCTGAG	1620
25	AAAACAAACT	CAGGGCTGTT	GTTAAAAAGG	GCCCATGACA	ATACCAAGTG	TTGGGGAGAA	1680
	TGTGGAGAAA	TCGAACTCT	ATTCACGCTC	GGTTGGAATG	CACACTTGTG	CAGAATTCTA	1740
	TGGAGAAGAG	TCTGGCATTT	CCTCAAAATG	TTAACCTTGA	TTTACCATAT	GACCCAGCGA	1800
	TTTCATTCTAT	AGGTTTATAC	TCAAAAGAAA	TGAAGAAATA	TGCCATGCAA	AAAAATGTAC	1860
	ATGAAAGGTC	ACAAACATCAT	TATTCATAAT	AGTAAAAGGA	TGGAACAAC	ACAAATGTCC	1920
	ATCAACTTAT	GATTAAGAAA	AATCTGGTCT	ATTCATAGAA	TGGAATATTA	TTGACCCACA	1980
30	AAAGGAATG	ATGTACTGAT	CCATGCAATG	ATGTGGACAA	ACCATGAAAA	TAACACTAGA	2040
	TTAAAGAAGC	CAGTCACAAA	AGGACTTACT	GTATGATTCC	ATTTACCTGA	AATGTTTGGG	2100
	ATAGGCAAT	CCATAGAAAC	AGGAGGTAGA	TTCTCTGGTT	CCAGGGTCTC	CAGGAAGGGA	2160
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35	TATATAAAT	ATATGTTAAT	AAAAAGGGGG	TCCACAAAAC	AAACAGCCCC	CCACTCTGGT	2340
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	ATTCCTTCAG	TTACAAGATA	TTCCAGGGGA	AACACTGGAA	TGAGTCTGAA	GCCAGGTGCT	2460
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40	CTTCATTTT	AAATGTAAAA	TTAGAAAGCT	GCCATTTAAA	ATGGCCCGTC	TGTTTCAATT	2580
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	AAACATACCT	GAGACTGGCA	AGAAAAAGAG	GTTTAAATGG	GCTTAGAGTT	CCACGTGATT	2700
	GGGGAGGCGT	CAGAATCACA	GTAGGAGGCA	AAAGTTATTC	TTACATGGTG	GCTGCAAGAG	2760
	AAGATGAGGA	AGAGCAAAA	GAAGAAACCC	CTGATAAAC	CATCGATCT	CCTGAGGCTT	2820
45	ATTAACATAT	ATGAGAATAG	CACAAGAAAG	ACCGGCCCCC	ATGATTCAAT	TACCTCTACC	2880
	TGGGTCCCTC	CAATAACATG	TGGAAATTTCT	GGTAGATACA	ATTCAGTTG	AGATTGGGTT	2940
	GGGAACACAG	CCAAACCAT	TCACTCAGCA	AGGCAGATAA	CTTTCTCACT	GAGCCTATGC	3000
	AACAGAAAC	CATCTGGGAT	GGTGTGAAG	GGCAGAGGAA	GTGACTGGTA	GGATCACTGC	3060
	CAAGCTGAG	CATCTGGGAT	AAGGCAATAG	AATCCTATTC	TCCATAGTAT	GCTATAAGAT	3120
	ACTGAAGTAC	ACTTCTTCAC	TATCTCTTTG	GACTTAGAAT	TAGCACTACA	TTCTTTGTTA	3180
50	TACAGAAAA	TTACTAAGGA	AATTCATAGG	ATGACAAAA	CTTTCAGAAC	TGAAAAACAG	3240
	GAAATGTAA	CTTTTGTGTT	CTTTGGTATT	OGAAGTATGC	CTAAAAAGCA	ATGCAAAATC	3300
	CAAGAAAAAG	ATGGTGGGGT	TTTGTGTTGT	TTGTTTGTGT	TTTGTGTTTA	CAGCTGGAGT	3360
	AGAATACAAA	GGGATGGAGT	TGAACAAAT	GAGAGGAAAT	TGGAATTCTA	AACTTATTTCT	3420
55	CATTGGCAAT	AGAAAGGCAC	CTACATGTAT	TTACATGAG	CCGGTGACTG	CTGACTTGCA	3480
	TTCTTATTTT	TTCCCTATAG	ATTAAAAAGG	AGGTACAATG	GTAGAACTGT	AATCCTGTCC	3540
	TTTGTCTATA	TTTTCATAT	TCATAAGGT	GAGTGTATGC	CCGCTTGTA	AATCTGAAGT	3600
	TGAGTAACCT	CAATACTATA	CCACAGAGGG	AAAGGCAGCA	AGAGGAGAGG	CATAAATTTA	3660
	GGATCTCACC	CTTCATTCCA	CAGACACACA	CAGCCTCTCT	GCCCACTCTC	GCTTCTCTTA	3720
60	GGAAACACAG	TAGAGCTTTC	AAGCCTCTCC	AGCTTAATAA	CATGAATTAT	TTTTGAGAAAT	3780
	AATAATGATA	CTGTGTTCTA	TATCATGCAT	CTCCTGCATT	CTGTCTGATT	ATATTTTACT	3840
	TATTTGCGCA	GAGCAAAAT	AAAATAACCTA	TTTCATCTGA	TTTGTCTCTT	ATCTAAATTTG	3900
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	CGTTAAAAAT	ARGAGAAAA	CTTTAAATGT	CAAAATCTCA	CAACCCAGAT	ATATCATTTTC	4260
	TTTAAAGAAA	TTGTACTACA	AAATACCAT	CCATTATTTA	AAGTCATTCT	GACAGGAATC	4320
70	TGATGCTTTT	CCAGGAGTTT	CAGATCACAT	OGAGTTCAAC	ATGAATTCAC	TCAGTGAAGC	4380
	CAACACCAAG	TTCTATGTCG	ATCTGTTCCA	ACAGTTTACA	AAATCAAAAG	AGAAACAACAT	4440
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	CAACACTGCA	CAACAAATTA	GCAAGGTAGC	TATCAGCATC	ATTACGTTGT	CCTGTTGCGG	4560
	TTTTTCTCTG	GTTCCTGCGG	CTAGCAAGCA	GATGGTAATA	GATGTGGTGG	TCTGATGGGT	4620
75	AGCACAGGGG	GCTGTGCGAG	AATCCCATTA	ACTGTGAGAC	CAGTCACTTA	AACAGATCTT	4680
	TTGAGTAAAG	TTTTCTGTGC	CGGCTTCATG	TCTCTTCCAG	GTTCTTCACT	TTGATCAAGT	4740
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80	TTCAATGGCA	ATAATTTATTA	TTCTCTAATT	CTGGTTACT	AAAAGACAGT	CAGCACTGTA	4980
	CCTCAGAGCA	TAGTCTGGA	TCAGGATAGG	CTGGGTTTCA	ACTCCAGCTT	TGCTCTTCAC	5040
	AAATGATGAA	TAAAGACAGG	ACACAACTGC	TCCGAGTCCC	AGTGACCTCA	TCCAGAAAAA	5100
	CTAAGGGTAA	GAAAAAATCT	GACTCAATAC	ATGCAAAATAC	ATGCAAAATG	TTACAACAGT	5160
	GCCTTGCCCA	TAAAGTTCAT	AATAAATGTT	ATTATTAATTA	TAAAGTAGCT	ATAATTATAC	5220
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	GTTC AAAAT	TGGCACTTCT	AATTTATGTC	TCTATAAACA	GGGTTTTTTT	CCCCATTCTC	5460
5	TGAGCTTTCT	TGTGTTTATC	TGAATTGAAC	TAAAGACTTA	GAGTTACCCA	TGTAAAGTCC	5520
	TTAGCCATGG	ACCTGGCATA	CACCTCTTCT	ACGTGCAGAG	AATGACCATC	ATGAGGAAAG	5580
	AGCCACAGAT	CAGTCAATGT	GTCTTACAAG	ATAATAGCAC	CAACAGGTAT	AACAGGCTT	5640
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10	AACCCCTTAA	ACCAACAAGG	AGAAAATCTA	CTGGTAGACA	GCGCTGCATC	TTTAGTTCAG	5820
	AAGAGAAAAG	AATGCAGTAC	GTTAGAGCAA	GAAGAATTTT	CTGGAAGAAG	TCAAAATATA	5880
	GGTGAGTTT	GAAGGGTATT	TGAGGTGAAA	TACACCAATT	ATCAGGGAAT	AACATCAAG	5940
	GTCTCAATG	AGACTACCAG	CAITTAGGGA	CTGATCTAAC	AGACTTAGCA	TGGGTTTAGT	6000
	ATTACATTG	ATACAGCAAT	TGAATGATCT	CCTTTTTTGA	TGTTTGAAGG	TTGATAGGTC	6060
	AGGAAATGTT	CATCACCAGT	TTCAAAAGCT	TCTGACTGAA	TTCAACAAAT	CCACTGATGC	6120
15	ATATGAGCT	AATGTCGCGA	ACAAGCTCTT	CGGAGAAAAG	ACGTATCAAT	TTTTACAGGT	6180
	AAATTTCACT	GGCTTACCCA	CATTTCAATT	GCATCCTGAT	GTCTGTGCTC	CTGAGTGGCC	6240
	AAATGGAAAG	AGCAAGGCGA	GATGAGCCTG	GCCGACCCAG	GTGGAGAGCA	TTTACTCAGA	6300
	GTGCATTAGC	TCCATTTOCA	CAACTCTCCC	CCACTGGAGT	GTCCGAGACC	CCAACGATAC	6360
	ATCACTGAGG	TGTGATTFTA	GGGATAATCT	TGTGATAAAA	GAGGAGGTTG	TGTAAATAGAG	6420
20	TGAGTAAGAG	TAATAAGTAA	TAAGATACCA	TOGATAAACT	GGCACTGACT	CAGTCACATA	6480
	CGATACATCT	TGGTGGGAAA	TGTATGACTA	ATGGGATATT	ATTGGAATGG	GCAGGCTTGG	6540
	GTGAGTTCTT	GAGAATAGTT	GAGGAAGTAC	CAGGAAATAT	TGAATGCACA	GGATGAAAGA	6600
	CAAAAACAAA	GATCAGAAAC	ATCATGGTTA	AAATTACTGG	AGAGAAGTCT	GAGAAGCAAT	6660
	GAATCTCTCT	CAGGGAAGCC	TGCTCTGCAG	TTTGCAAAAC	ACAGCCTCTT	CTGCTTCTGC	6720
25	CTTTGGCCAA	GATGATATTG	ACCTTCAGTG	ACCTCTTTCT	TGTGCCAGCC	CACATTCCCC	6780
	TTTTGCATTG	CCTCATGAC	ACCTGTATAA	AAATATCCAT	GGACAGGAGA	TACTGCATCT	6840
	ATTCAAGGTC	TGGATTCAGC	TTACTGTTGT	TACAAATAAG	TAAGTTTGGT	AATATATAGT	6900
	TACATAAATT	ACTCTTAATT	CCTTCTATCT	CTTTCATATC	TCAAAAGGAA	ATTTAGATGC	6960
	CATCAGAAA	TTTTTACCAG	CCAGTGTGGA	ATCTACTGAT	TTTGCAATAG	CTCCAGAAAG	7020
30	AAGTCGAAG	AAGATTAACT	CCTGGGTGGA	AAGTCAAAG	AATGGTAGGA	GAGCCACCCA	7080
	TTATAGAAAC	ACCTTTGAGA	AACTATGCC	AGTGAGCCTT	GTGCTTGACA	CTGCATGGGG	7140
	GAACAGGTGT	GGGATTGAG	ATGGGTTTGC	AGGGAGGGCT	GAAGAGGGCA	CTCCAGATGA	7200
	AGGATTTGTC	CAATTAATA	TGAAGAGAGC	CTAGGGGAGC	CAAGGAGGAA	ATCACAGGAA	7260
	GCCAAATAGA	TGGAAACACA	CTTGAGAGAT	TATTTGCTTA	TGGCCCTGCA	TGACAAATAGC	7320
35	TTTGTGGATC	CCCTGTCTCC	GCTCAGACCT	ATTTTGAGAT	CATATCCTTT	ACTTTAAATC	7380
	AGACTCAAT	TTTTATGATG	AATATTTAAT	AGAAAACATT	AGAAAGCGTC	TCTCGTCTCC	7440
	TTTACTAATT	GGGAAACAG	CAGCTCTCTG	GTAATCACC	CTTTTGTCTC	TGAGCTGGAG	7500
	CTGCTTGCAT	CACATCTGTA	GCCAAATGTT	TCTGCAGGGA	TTATCAGAGC	TCTCTTCCCC	7560
	ATCAGGGGCA	AAGAGCTTGA	CAAGTCTCC	ATTTCTACAG	CATCTTCTT	ACCTCCCAAC	7620
40	TCTCATTACA	GGCCAAACTT	ACAGCAACTC	AACATGAGAG	TGAATAGGAA	GATACCCCGC	7680
	GAAGTAGTGT	TGCACAGCAC	AGGACATGCG	TTTCATATTA	CAGAGCTCAA	GTCACTCATC	7740
	CTAAAATGCA	ATCAGGGCCCT	CCTTCTCTTG	AATGGGGACC	CCGTAGTTAA	AAAAAATAA	7800
	AAGTAGGAAG	AGGAGGGAGG	GAGAAAGGAA	AGACACATGT	TGGAGAGGTA	GACAAAATCA	7860
45	GTTTATCAGT	ATTTCAAATC	AGATGATTGG	AGACATTCAT	ACACAGAGAA	CGTGAACCTC	7920
	TTCTCTATCA	CAAGAAGTGA	TGTCTCCATC	AAGGGTAACT	TTATACGACT	GGAGCCTTGA	7980
	AGAAAGCTGC	ATCTGGTGAA	CCACTGTGTA	GTGAGTCTAA	CAATTCAGAG	ATCAAACTCA	8040
	GTGAGTCTCA	AGCAGGGGAT	TGGGTCAATA	ATTAAAGATC	AGTCAAGAAC	ATTGCAAGAG	8100
	CATCTTCCAG	ACAGGCCATT	TGTAGCTTGT	GTAAAAGACT	CTTTTATCTT	TTCCCTTGCA	8160
50	GAAAAAATTA	AAAACTATT	TCTGATGGG	ACTATTGGCA	ATGATACGAC	ACTGTTCTCT	8220
	GTGAAGCCAA	TCTATTTCAA	AGGGCAGTGG	GAGAAATAAT	TTAAAAGAGA	AAACACTAAA	8280
	GAGGAAAAAT	TTTGGCCAAA	CAAGGTATTG	TCTATATTTT	ATTATATAG	TGTAATATGT	8340
	TAATACATGG	AATGTTAAAC	ATTTCTGATG	GAATGTAACA	TGATAAGTAA	AAAAATAAAA	8400
	TTGTTTATGT	CTGTTATTTT	GTTGTTTATC	TCTTATAACT	TTATTTAGTT	AGGAATACCT	8460
55	GAAAACTAT	TGTTTCTAAC	TCATGGAATT	CCTGGGTTAT	TTCTTAGAAG	AAGAAGGATG	8520
	TGTTGCTATC	TCAATTAATAT	TATCTTTTTT	GTCTTGTGTT	TCAGTGTTTA	TTTGTGGGAC	8580
	ACATTGATTT	TAGGGAATAT	ACATACAAAT	CTGTACAGAT	GATGAGGCAA	TACAATTCTT	8640
	TTAATTTTGC	CTTGCTGGAG	GATGTACAGG	CCAAGGTCCT	GGAAATACCA	TACAAAGGCA	8700
	AAGATCTAAG	CATGATTGTG	CTGCTGCCAA	ATGAAATGGA	TGGTCTGCAG	AAGGTAGGAA	8760
60	CTTGCACTTA	CAACTCTTCC	TTCTACTGCC	GGACATTTTT	CCAAAGATAC	CAAGTTTAAA	8820
	CAAGGTAAAA	GCTTATGACC	GAGTTGCTCT	AAAAATGATG	AAAATTCTAA	ATGAGGAATG	8880
	ATGACTCACC	TTCATATTAC	AAATATTGGA	GCATAGGGCC	TGACACAAAC	TGAAAGCTTA	8940
	GTTTGTGTTT	GTTTGTGTTT	TTTTATTATT	ATTATTATAA	TACTTTAAGC	TTTAGGGTAC	9000
	ATGTGCACAA	TGTGCAGGTT	AGTTACATAT	GTATACATGT	GCCATGCTGG	TGTGCTGCAC	9060
65	CCATTAACTC	ATCATTTAGC	GTTAGGTATA	TCTCCTAATG	CTATCCCTCC	CCCCCCCCC	9120
	CACCCACAAA	CAGTCTCTAG	AGTGTGATGT	TACCTTCTGT	TGTCCAGGTG	TTCTCATTTG	9180
	TCAATTCCCA	TCTATGATTT	AATTCATCT	ATGGCTTAGT	TAATGATTAA	TTTATTAGAG	9240
	TTACATGCAT	TGGATATCAA	TTTGATGATA	TTATTATGCA	GCAATTTAAA	CTTGACTGGG	9300
	AGAAATATAT	ACCAATGTGA	GGAAAGTTTA	CAAATAGGCC	GAGTAGAAAA	GGGAATACAA	9360
70	ATTTAGGAAT	TAGGGAATT	ACAAATTAAT	AATTGCAATG	TGTACTAAAT	AATGTATACA	9420
	GAAAAATATG	ATGAGCCTAT	TAAAAATTGA	CACATGTAGT	AGGCTGTGTT	CACAGGAAAT	9480
	AGTGATACAT	ACAGTTCATT	GTGTACAAAA	TAATGTAATC	ATATTTTACA	TGTGTATCAT	9540
	ACAGTTGTAT	ACATACATAT	GTACACATAT	ACATATACGT	AAAAACATGA	TTCTGTTTTT	9600
	ACATACATGT	ATATACATAT	ACACATATAA	CCCAATGTAT	TTATATATTC	AGGACTCATAT	9660
75	TTTTACTTAT	TAGATTAATA	ATGTCTATTA	AAGTGAAACT	TCTGTATTTT	ACATTTATTG	9720
	CCAAAATAAC	GAATCTCCAC	ATAGTCAATT	CATTGTTAAG	GTGTATTAGA	GATGACAGAT	9780
	TAGTCATATC	AGTTTCTTTT	TTCCATTGTT	ATAGCTTGAA	GAGAACTCA	CTGCTGAGAA	9840
	ATTGATGGAA	TGGACAAGTT	TGCAGAATAT	GAGAGAGACA	TGTGTGATTT	TACACTTACC	9900
	TGGGTTCAAA	ATGGGAAGAGA	GCTATGACCT	CAAGGACAGC	TTGAGAACCA	TGGGAATGGT	9960
80	GAATATCTCT	TAGGGGATG	CAGACCTCTC	AGGCATGACC	TGGAGCCACG	GTCTCTCAGT	10020
	ATCTAAAGTC	CTACACAAGG	CCTTTGTGGA	GGTCACTGAG	GAGGGAGTGG	AAGCTGCAGC	10080
	TGCCACGCGT	GTAGTAGTAG	TOGAATTATC	ATCTCCTTCA	ACTAATGAAAG	AGTTCTGTTG	10140
	TAATCACCCCT	TTCTTATTTT	TCATAAGGCA	AAATAAGACC	AACAGCATCC	TCTTCTATGG	10200
	CAGATTCTCA	TCCCATATGA	TGCAATTAGT	CTGTCACTCC	ATTAGAAAAA	TGTTCACTTA	10260
	GAGGTGTTCT	GGTAAACTGA	TTGCTGGCAA	CAACAGATTC	TCTTGGCTCA	TATTTCTTTT	10320

5 CTATCTCATC TTGATGATGA TAGTCATCAT CAAGAATTTA ATGATTAAAA TAGCATGCCT 10380
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 CTTGAGGAAA AATGTCGAAG ATAAGATGAA TCATTTAATA CCGTGTCTTC TAAATTTGAA 10500
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 ATTTAGCAAC CTAGAAACAC ACATTTCTTT GAATTTAGGT GATACCTAAA TCCTTCTTAT 10620
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 TTTTGTCTTA CCTGTTTTCT CTCTGGAAAG GGCAAGTGT CAGTTACACA TAGGAAAGAT 10740
 AATTTAGAGA TATATTAATC ATATATAAAG GAAATTTAAA AACAGAGTAG TTCATGATGA 10800
 10 GCCTGGAGTA GAAGGCATAT CCCAGAACAG GAGGAGCCTT GTAAACCACA TAGGAACCTC 10860
 CTATTTTATG CTAAGGGAT AAGAACTCA TTACAGGCTT TGATGGTTGT TTGTCAAAGA 10920
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 15 AGAAAGACAT CTAAGTTGCT GACCTATCTG ACTGGATGGA TGGAAGAATA TCTTGTCTCT 11160
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 TGATCTGAAG CTTAAATTT GTGATATTCA ATATAAATAC TTTAGAGTCA TTGGGATAAA 11340
 TATGTTAGTT GTAGCTAAAA GCAAAAATAA GATACTAGGG AGAAAGGATA AAGTTAGAAG 11400
 20 AAAGAGAAAT CTAGAATTGA CCTTGAAGTA TATCAGCATG TGTAAAGATC AGGAATTGAT 11460
 CATTTTTATT TTCCAGAAAG TAGCTTTTCT TAGGGTTCCA TATTACTCC CATAGATTCT 11520
 TCCC

25 A76 Protein sequence:
 Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
 Unigene number: Hs.227948
 Probeset Accession #: AB035089
 Protein Accession #: BAB21525
 30 Signal sequence: none found
 Transmembrane domains: none found
 Serine Proteinase Inhibitor domain: 13-390
 Cellular Localization: secreted

35 1 11 21 31 41 51
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 MNSLSEANTK FMFDLFQQFR KSKENNIFYS PISITSALGM VILGAKDNTA QQISKVLHFD 60
 QVTENTTEKA ATYHVDRSGN VHQFPQKLLT EFNKSTDAYE LKIANKLFGK KTYQFLQBYL 120
 40 DAIKKFYQTS VESDFANAP EESRKKINSW VESQTEKIK NLFPDGTIGN DTTLVLVNAI 180
 YPKQWENK KENTKREKF WFNKNTYKSV QMRQYNSFN FALLEDVQAK VLEIPYKGGK 240
 LSMIVLLPNE IDGLQKLEEK LTAELMEWT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300
 TMGMVNIENG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAAAATAV VVELSSPSTN 360
 EEFCNNHPL FPIRQNKTN ILFYGRFSSP

45 A77 DNA SEQUENCE
 Gene name: hypothetical protein FLJ13459
 Unigene number: none found
 Probeset Accession #: XM_047266
 50 Nucleic Acid Accession #: XM_047266
 Coding sequence: 485-1471 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 55 CTGACCTCAA GTGATCCACC CACCTCTGCC TCCCAAAGTG CTGGGATTAC AGGTGTGAGC 60
 CACCATGCCA GGCCCTCTTA ACCTCTTCAA GTCTGTTTTC TCATCTGCAA AACAGAGGTA 120
 ATAAGATCAG TATCTTCTTA ATGGAAGCAC CTGGACTACA TTTTTCAT TCATTGTTAT 180
 CATAAATGAG GACTAAACCTG TCTCCCGTTG GGAGTTTGA ACCTAGACCT CATGTCTTCA 240
 TGACGTATC ACTGCCCCAG GCCAGCTGT GTCCCTACAC CAGCCCCAGC TGACGATCT 300
 60 TCTTTTCTG CCTGTAGAGA TGGTTACAAT GCCTGGCGTG ATGCATTCTG GCCTTCGCAG 360
 ATCCTGGCGG GGCTGTGCCA AGCTGTGGC CTCCCTGCC CTGAATACCG AGCGGTGCT 420
 GTCAAGGTGG GCAGCAAGT CTTCCTGACA CCACCGGAGA CCTGCCCCC AGGGATCTCT 480
 TCACATGTGG ATTGACTCT TTCTCAAGA TGTGCTGCT CCACCCCGAG TTGACATCAA 540
 GCCTGGCAG CCAATCAGCT ATGAGCTCAG AGTTGTCTATC TGGAAACGGG AGGATGTGGT 600
 65 TCTGGATGAC GAGAATCCAC TCACCGGAGA GATGTGAGT GACATCTATG TGAAGAGCTG 660
 GGTGAAGGGG TTGGAGCATG ACAAGCAGGA GACAGACGTT CACTTCAACT CCTGACTGG 720
 GGAGGGGAAC TTCAATTGGC GCTTTGTGTT COGCTTTGAC TACCTGCCA CGGAGCGGGA 780
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 70 ATCCCTGGAG TTGCAGCTAC CAGACATGGT GCGTGGGGCC CGGGGCCCG AGCTCTGCTC 960
 TGTGCAGCTG GCCCGCAATG GGGCCGGGCC GAGGTGCAAT CTGTTTGGCT GCGCGCGCCT 1020
 GAGGGGCTGG TGGCCGGTAG TGAAGCTGAA GGAGGCAGAG GACGTGGAGC GGGAGGCGCA 1080
 GGAGGCTCAG GCTGCAAGA AGAAGCGAAA GCAGAGGAGG AGGAAGGGCC GGCAGAGA 1140
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 75 GTTGTAGCTG CTGACTGTGG AGGAGGCCGA GAAACGGCCA GTGGGGAAGG GCGGGAAGCA 1260
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 GCTGAAGAGC TTTGTCTTCT TCATCTGGCG CCGTACTGCG GCACCTCTGG TGCTGCTGCT 1380
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 CCAGGTATC TTCCGTCCCC TCACAAGTGG ACTCTGGCTG ACCTTGGACA CTCACCCAGG 1500
 80 GTGCCAACCC TTCAATGCCT GCTCCTGGAA GTCTTTCTTA CCATGTGAG CTACCCGAGA 1560
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A78 Protein sequence:
 Gene name: hypothetical protein FLJ13459

Unigene number: none found
 Probeset Accession #: XM_047266
 Protein Accession #: XP_047266
 Signal sequence: none found
 Transmembrane domains: 291-313
 C2 domain: 27-86
 Cellular Localization: plasma membrane / ER

1 11 21 31 41 51
 MWIDIFPDQV PAPPVVDIKP RQPISEYELRV VIWNTEDVVL DDENPLTGEM SSDIYVKSXWV 60
 KGLEHDKQET DVHFNLSLTGE GNFNWRPVFR FDYLPITEREV SVWRRSGPFA LEEAEFRQPA 120
 VLVLVQVWDYD RISANDFLGS LEIQLPDMVR GARGPELCSV QLARNAGAPR CNLPRCRRLR 180
 GWNFPVVKLKE AEDVEREAQE AQAGKKKRKQ RRRKGRPEDL EFTDMGNNVY ILTGKVEAEF 240
 ELLTVBEAEK RPYGKGRKQP EPLEKPSRPK TSNWNFVNPL KTFVFFIWR RYRVLVLLLL 300
 VLLTVFLLLV FYTIPGQISQ VIFRPLHK

20 A79 DNA SEQUENCE
 Gene name: Homo sapiens mRNA; cDNA DKFPz434K0322 (from clone DKFPz434K0322)
 Unigene number: Hs.161031
 Probeset Accession #: AL137708
 Nucleic Acid Accession #: AL137708
 25 Coding sequence: 1315-1791 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 30 GGCAITGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60
 GTGTGTGTGT GTCTGGAGTC ATGGCAGGGT CCTTTCTGT CTGTCTCCTT GCTCTGCCCC 120
 AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180
 ATGGCCTGGG CTGGGCCCTT GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCAGG 240
 CTCTTGTGGG CAAAGCAGGG GAGGCGCCAA TGTGGAGGAA CAGAGTCTCC TGGCTGGCTG 300
 35 CTGCTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCTTG 360
 GGGTACCGGT AGGCCCATG TAGCACCTGT GTTCCCTGTC CTGTAGGTGA CAGGAGCCAG 420
 CCCAGCCAGG TGTGCTCCCT CCCAGGCCC TAGGCAGGCG GGTACAGGGG CCAGCAGCTG 480
 CGCCCGCCCC ACCTTCTCTT CCACCCACAT GCGGAAGGGT GGCCAGGCAG GCAGGTGGAC 540
 GAGTCCAGGC AGCGGCTGAG TCAGTGTGTG TGGATGTTC TGGCCGCTCC CAGCTGCACC 600
 40 CTGCCCTCTG CTGCCACCAC CTCACCTTCA TCCTCAGGCG CTGCGGCCCT GAGCCCCTGC 660
 CAGGAATGCA CCTTTAGCCC AGGCTGTCTC AGTGAGCTCC GCCGACAGCC AGCCCTGTCT 720
 CTCCGCCCAT GACCTGTCAG ACCCTCTGCG GCTTCCAGT TCCTGGGGGC TGCAGTGAAC 780
 ATGCTCCACC TCATGCGCTG GCAAAACATG GTGGGCCCCA GCTGTGTGTC GTCTGGGGT 840
 45 AGAGGCAAGG AAGTGATGGG ACCGCAGAGA TGAGACCCCC AGGATGAGA TGGGACCCCC 900
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 55 GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCTCTACC 1500
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 65 CTCTGATGAG GCATGATGTC AGCAACCACT GCCCTTGTTC CCAACTCACT CCAGGTGCAA 2100
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 80 TGAAGCCCTT CTGTGCTGCC ACAGCCCGAG CAGGTGGGGG AGCTGTGCTT CTCTCTCGG 3000
 TACGTGCCCA GCTCAGGCCG GCTGACCGTG GTGGTGTCTG AGGCTGAGG CCTGGTCCA 3060
 GGACTTGCAG AGCCCTAAGT GAAGGTCCAG CTCATGCTGA ACCAGAGGAA GTGGAAGAAG 3120
 AGAAGAGCAG CACCAAAAAA GGGCACGGCG GCGCCCTACT TCAATGAGGC CTTCACCTTC 3180
 CTGGTGCCTT TCAGCCAGGT CCAGAAATGTG GACCTGGTGC TGGCTGTCTG GGAACGAGC 3240
 CTGCGCTCC GAACAGGACC CGTAGGCAAG GTGCACCTGG GTGCCCGGCG CTGGGGCAG 3300

CCOCTGCAGC ACTGGGCAGA CATGCTGGCC CACGCCCCGC GGCCCATTCG CCAGCGGCAC 3360
 CCOCTGCGGC CAGCCAGGGA GGTGGACGCG ATGCTGGCCC TGCAGCCCCG CCTTCGCGTG 3420
 CGCCTGCOCCT TGCCCCACTC CTGAATGCAC CACATGCCTC TGTCTCCCCG CTGAGCCACG 3480
 GCATTGCCCC AGGCGCGCCT GCAGGACCAC TGCAATAAAC GCCTTCTCCT GCC

A80 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFp434K0322 (from clone DKFp434K0322)
 Unigene number: Hs.161031
 Probeset Accession #: AL137708
 Protein Accession #: CAB70885
 Signal sequence: none found
 Transmembrane domains: 69-85
 Cellular Localization: plasma membrane

1 11 21 31 41 51
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 MGHPPVSPSA PAFAGTTAIP GLIPDLVAGT PCELWDSQEG CGDNPAKWGL QLSTDALSLA 60
 STPGPRWALI AGALAAGVLL VSCLLCAAC CRRHRKKPR DKESVLGSA RGTITTHLVR 120
 SGLLTQSRRE GLKSLRLQSPG QRGEFSPRDG LTPTEAGR

A81 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51
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 CGGAGCAGGA GCCCGGCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCTT GGGCAAGAGC 240
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 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC 420
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
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 TCTTTGGCCA CGCTGTGTGA GAGAATGGTG CCTCAGTGGG GAGACCCATG AACATCTCCA 660
 TCATCGTGAC CGACCAAGAT GACCAACAAG CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
 GTGTCTTAGA GGTGAGTCTA CCAGGTACTT CTGTGATGCA GGTGACAGCG ACAGATGAGG 780
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA 840
 AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
 CCAGTGGCCT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
 ACAATGCTCC CATGTTTGAC CCCAGAAAGT ACGAGGCCCA TGTGCTGAG AATGCACTGG 1080
 GCCATGAGGT CGAGAGGCTG ACGGTCACTG ATCTGACGCG CCCCAACTCA CCAGCGTGGC 1140
 GTGCCACCTA CCTTATCATG GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
 CTGAGAGCAA CCAGGGGATC CTGACAACCA GGAAGGGTTT GGATTTTGGG GCCAAAAACC 1260
 AGCACACCCCT GTACGTTGAA GTGACCAACG AGGCCCCCTT TGTGCTGAAG CTCCCAACCT 1320
 CCACAGCCAC CATAGTGGTC CAGGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
 CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACCTGG GGAGCCTGTG TGTGTCTACA 1440
 CTGCAGAAAG CCCTGACAAG GAGAATCAAA AGATCAGCTA CGCATCCTG AGAGACCCAG 1500
 CAGGCTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTGAC AGCTGTGGGC ACCCTCGACC 1560
 GTGAGGATGA GCACTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
 ATGGAAGCCC TCCACCAACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
 ACCATGGCCC AGTCCCTGAG CCCGTCAGA TCACCATCTG CAACCAAGAG CCTGTGCGCC 1740
 ACGTGTGTA CATCAAGGAC AAGGACCTGT CTCCCCACAC CTCCCTTTTC CAGGCCCAGC 1800
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTT TCTCTGTCTG 1920
 ACCATGGCAA CAAGAGCAG CTGACGGTGA TCAGGCGCAC TGTGTGCGAC TGCCATGGCC 1980
 ATGTGGAAC CTGCGCTGGA CCTGGAAAG GAGGTTTCAT CCTCCTGTG CTGGGGGCTG 2040
 TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100
 TCAAGGAGCC CCTCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
 AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
 AGGCGGCTAA CACGACCCCG ACAGCCCGCG CCTACGACAC CCTCTTGGTG TTGACATATG 2400
 AGGCGACGGG TCCGACGCGC GGTCCCTGA GTCCTCTCAC CTCTCCGCC TCGACCAAG 2460
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGGCTT CAAGAAGCTG GCAGACATGT 2520
 ACGTGTGGCG GGAGGACGAC TAGGCGGCTT GCCTGCAGGG CTGGGGACCA AAGTTCAGGC 2580
 CACAGAGCAT CTCCAGGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTCA 2640
 GGAAGTGGCC GTGACCACTT GCGGAGGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
 TCTTACCTCT TTAGGATGGG AGGAATGTGG CAGATTGAC TTGACACTG AAAACCTCTC 2760
 CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2820
 TGCTCAACCC TGTGTCCTGG GCCTGGGCTT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940
 TCAAAAGGTT AGAGAAAGTT CTTCAAAGT GCAGCCGAGA GCTGCTGGGC CCACTGGCCG 3000
 TCTGTCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GATGATGATCT CTGCGTTTTT 3060
 ATACTAGTGT TGCCTAGGTT GCCCTTATT TTTTATTTC CCGTGTGGGT TGCTATAGAT 3120
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAAGTTTTT TATTAAAGAA A

A82 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675 (second underlined sequence)

Cellular localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MGLPRGPLAS LLLQLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMCPCG 60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
KGPPFQRLNQ LKSNKDRDRTK IPYSITGPGA DSPPEGVPAV EKETGWLILN KPLDREBIAK 180
YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
DEDDAIYTYN GVVAYSIHSQ EPKDPEDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAEVPEP AVGHEVQRLT VTOLDAPNSP 360
AWRATYLMG GDDGDHPTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAEVVF VPFSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
DPAGWLANDP DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLLD 540
VNDHGPFVPE RQITICNQSP VRHVLNITDK DLSFHTSPFQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL 660
GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVYF YBEGGGGED QDYDITQLHR 720
GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN PDEIGNFIIIE NLKAANTDPT APPYDTLLVF 780
DYESGSDAA SLSSLTSSAS DQDQDYDYLN BWGSRFKILA DMYGGGEDD

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A83 DNA SEQUENCE

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Probeset Accession #: F07953
 Nucleic Acid Accession #: NM_016334
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
AGCACTCTGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCAGCGTGG CTGTGGCCTC 60
GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTTACACTTC GCCATGAGTT TCCTGATCGA 120
CTCCAGCATC ATGATTACCT CCACAAATCT ATTTTITGGA TTTGGGTGGC TTTTCTTCAT 180
GCGCCAATTG TTAAAGACTC ATGAGATAGC TCAATATGTT GTACAGGTGA TCTTCTCCGT 240
GACGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300
GAATAGCAGC TCCCGTTATT TTTCACTGAA AATGAACCTG TGCCTAATTC TGCTGATCCT 360
GGTTTTCATG GTGCCTTTT ACATTGGCTA TTTTATTGTG AGCAATATCC GACTACTGCA 420
TAAACAACGA CTGCTTTTCT CCTGTCTCTT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480
ACTAGGAGAT CCCTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
CATCAGCCGG GTTGGGTGTA TTGGAGTGAC TCTCATGGCT CTTCTTTCTG GATTGTGTGC 600
TGTCACATGC CCATACACTT ACATGTCTTA CTTCTCAGG AATGTGACTG ACACAGATAT 660
TCTAGCCCTG GAACGGCGAC TGCTGCAAA CATGGATATG ATCATAAGCA AAAAGAAAAG 720
GATGGCAATG GCACGGAGAA CAATGTTCCT GAAGGGGGAA GTGCATAACA AACCATCAGG 780
TTTCTGGGGA ATGATAAAAA GTGTTACCAC TTCAGCATCA GGAAGTGAAA ATCTTACTCT 840
TATTCAACAG GAAGTGGATG CTTTGGGAAGA ATTAAGCAGG CAGCTTTTTC TGGAAACAGC 900
TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAATATATT 960
TAATTTTCTT GGTATCTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020
CAATATTGTT TTTGATCGAG TTGGGAAAAC GGATCCTGTC ACAAGAGGCA TTGAGATCAC 1080
TGTGAATTAT CTGGGAATCC AATTGTATGT GAAAGTTTGG TCCCAACACA TTTCTTTCAT 1140
TCTTGTGGA ATAATCATCG TCACATCCAT CAGAGGATTT CTGATCACTC TTACCAAGTT 1200
CTTTATGCC ATCTCTAGCA GTAAGTCTC CAATGTCAAT GTCCTGCTAT TAGCAGATAT 1260
AATGGGCAAT TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTGAATA 1320
COGCACCATA ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACCTTCTAT ACGGTGTTG 1380
TGATGTGATC TTCTTGSTCA GCGCTCTCTC TAGCATACTC TTCTCTATT TGGCTCACAA 1440
ACAGGCCACCA GAGAAGCAAA TGGCACCTTG AACTTAAGCC TACTACAGAC TGTTAGAGGC 1500
CAGTGTGTTT AAAATTAGTA TATAAGAGGG GGGAAAAATG GAACCAAGGC CTGACATTTT 1560
ATAAACAAAC AAAATGCTAT GGTAGCATTT TTCACTTCA TAGCATACTC CTTCCCCCTC 1620
AGGTGATACT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAACCTCAG 1680
ACAATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG 1740
CAAAGAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGTTAGC 1800
TGAGCCAAAC ACGTAGGATT TCCGTTTAA GTTTCACATG GAAAAGGTTA TAGCTTTGCC 1860
TTGAGATTGA CTCATTAATA TCAGAGACTG T

```

A84 Protein sequence

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Protein Accession #: NP_057418.1
 Signal sequence: none found
 Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402,
 424-446
 Cellular Localization: plasma membrane

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1      11      21      31      41      51

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	MSFLIDSSIM	ITSQILFFPG	GWLFFMRQLF	KDYBIRQYV	QVIPSVTFAF	SCTMFELIIF	60
	EILGLVNSSS	RYFHWKNNLC	VILLILVFMV	PFIYGYFIVS	NIRLLHKQRL	LFSCLLWLT	120
5	MYFFKLGDP	FPILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGFGAVNCP	YTYMSYFLRN	180
	VTDTDLALAE	RRLQQTMDMI	ISKKKRMAMA	RRTMPQKGEV	HNKPSGFWGM	IKSVTTSASG	240
	SENLTLIQBE	VDALBELSRQ	LFLETADLYA	TKERIEYSKT	FKGKYFNFILG	YFFSIYCVWK	300
	IFMATINIVF	DRVGKTDVPT	RGIEITVNYL	GIQFDVKFWS	QHISFILVGI	IIVTSIRGLL	360
10	ITLTKFVFAI	SSSKSSNVIV	LLLAQIMGY	FVSSVLLIRM	SMPLEYRTII	TEVLGELQFN	420
	FYHRWFDVIF	LVSALSSILF	LYLAHQAPE	KQMAP			
	<u>A85 DNA SEQUENCE:</u>						
	Gene name:			TTK protein kinase			
	Unigene number:			Hs.169840			
15	Probeset Accession #:			M86699			
	Nucleic Acid Accession #:			NM_003318			
	Coding sequence:			1026-3551 (underlined sequences correspond to start and stop codons)			
20	1	11	21	31	41	51	
	GGAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACTC	TTGTTGGCCA	GGCTGGAGTG	60
	CAATGGCACA	ATCTCAGCTT	ACTGCAACCT	CCGCTCCCG	GGTTCACGCG	ATTCTCCTGC	120
	CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACATAATT	180
	CTTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	TGAACCTCTG	240
25	ACCTCAGGTG	ATCCACTTGC	CTTGGCCTCC	CAAAAGTGCTA	GGATTACAGC	CCTGAAACTG	300
	TGCTGGGTG	ATTCTTTTTT	TGTTGTGGA	TTTTTGAAAC	AGGGTCTCCC	TTGGTCGCCC	360
	AGGCTGGAGT	GCAGTGGTGC	GATCTGGCTC	CACATAAACC	TCCACCTCCT	GGTTTCAAGT	420
	GATCTCCCA	CTTTAGCTTC	CTGAGTAGCT	GTGATTACAG	GGGTGCACCA	CCACACCCGG	480
	CTAATTTTTG	TATTTTTTAT	AGAGACAGGG	TTTCACCATG	TTGGCCAGGC	TGTTCTCAAA	540
30	CTCCTGGACT	CAAGTAGTCC	GCCTGCCCTC	ACTTCCCAAG	GTCCCGAGAT	TACAGGTGTG	600
	AGTCACCATG	CCTGACCTTA	TAATCTTAA	GTCTTTTTTT	CTGTCCATT	TCTTCCTTAG	660
	GGTCTCTACA	ACAAATCTGC	ATTAGGCGGT	ACAATAATCC	TTAACTTCAT	GATTCACAAA	720
	AGGAAGATGA	AGTGATTCAT	GATTAGAAA	GGGGAAGTAG	TAAAGCCACT	GCACACTCCT	780
35	GGATGATGAT	CCTAAATCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
	TTTGGTTTAA	ATTAATTATC	TAAATATCTA	AAAACATTTT	TGGATACATT	GTTGATGTGA	900
	ATGTAAGACT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCATCTTTTC	ATTTCCCCAG	960
	TGCAGTTTTT	TGTAGAAATG	GAATCCGAGG	ATTTAAGTGG	CAGAGAATTG	ACAATTGATT	1020
	CCATAATGAA	CAAGTGAGA	GACATTAAAA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
40	AACTAAGCTT	GAATAAAAT	TCTGCTGATA	CTACAGATAA	CTCGGGAAGT	GTTAACCAAA	1140
	TTATGATGAT	GGCAACAAC	CCAGAGGACT	GGTTGAGTTT	GTTGCTCAAA	CTAGAGAAAA	1200
	ACAGTGTTC	GCTAAGTGAT	GCTCTTTTAA	ATAAATGTAT	TGGTCGTAC	AGTCAAGCAA	1260
	TTGAAGGCT	TCCCCAGAT	AAATATGGCC	AAATAGAGAG	TTTGTCTAGA	ATTCAAGTGA	1320
	GATTGTCTGA	ATTAAAGCT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAAAATG	1380
45	CCAGAGCAAA	CTGCAAGAAA	TTTGCTTTTG	TTTATATATC	TTTTCACAA	TTTGAAGTGT	1440
	CACAAGGTAA	TGTCTGAAA	AGTAAACAAC	TTCTTCAAAA	AGCTGTAGAA	CCTGGAGCAG	1500
	TACCACTAGA	AATGCTGGAA	ATTGCCCTGC	GGAATTTAAA	CCTCCAAAAA	AAGCAGCTGC	1560
	TTTCAGAGGA	GGAAAGAAAG	AATTTATCAG	CATCTACGGT	ATTAAGTCCC	CAAGAAATCAT	1620
	TTTCGGTTC	ACTTGGGCTT	TTACAGAATA	GGAACAACAG	TTGTGATTTC	AGAGGACAGA	1680
50	CTACTAAAGC	CAGGTTTTTA	TATGGAGAGA	ACATGCCACC	ACAAGATGCA	GAAATAGGTT	1740
	ACCGGAATTC	ATTGAGACAA	ACTAACAAAA	CTAACACGTC	ATGCCCATTT	GGAAGAGTCC	1800
	CAGTTAACT	TCTAAATAGC	CCAGATTGTG	ATGTGAAGAC	AGATGATTCA	GTTGTACTCT	1860
	GTTTTATGAA	AAGACAACCC	TCTAGATCAG	AATGCOGAGA	TTTGGTTGTG	CCTGGATCTA	1920
	AAACCAAGTG	AAATGATTCC	TGTGAATTAA	GAAATTTAAA	GTCTGTTCAA	AATAGTCATT	1980
55	TCAAGGAACC	TCTGGTGTCA	GATGAAAAGA	GTTCTGAACT	TATTATTACT	GATTCAATAA	2040
	CCCTGAAGAA	TAAACCGGAA	TCAAGTCTTC	TAGCTAAATT	AGAAGAAACT	AAAGAGTATC	2100
	AAGAAACAGA	GGTTCCAGAG	AGTAAACAGA	AACAGTGGCA	AGCTAAGAGA	AAGTCAGAGT	2160
	GTATTAAACA	GAATCCTGCT	GCACTCTCAA	ATCACTGGCA	GATTCGGGAG	TTAGCCCGAA	2220
	AAGTTAATAC	AGAGCAGAAA	CATACCACTT	TTGAGCAACC	TGCTTTTCA	GTTTCAAAAC	2280
60	AGTCAACACC	AATATCAACA	TCTAAATGGT	TTGACCCAAA	ATCTATTGTT	AAGACACCAA	2340
	GCAGCAATAC	CTTGATGAT	TACATGAGCT	GTTTGAAGAC	TCCAGTTGTA	AAGAATGACT	2400
	TTCCACCTGC	TTGTCAAGTG	TCAACACCTT	ATGGCCAACC	TGCTGTTTTC	CAGCAGCAAC	2460
	AGCATCAAT	ACTTGCCACT	CCACTTCAAA	ATTACAGGT	TTTAGCATCT	TCTTCAGCAA	2520
	ATGAATGCAT	TTGGTTTAAA	GGAAGAATTT	ATTCCATATT	AAAGCAGATA	GGAAGTGGAG	2580
65	GTTCAAGCAA	GGTATTTTCA	GTGTTAAATG	AAAAGAAACA	GATATATGCT	ATAAAATATG	2640
	TGAATTAAGT	AGAAGCAGAT	AACCAAACTC	TTGATAGTTA	CCGGAACGAA	ATAGCTTATT	2700
	TGAATAAACT	ACAACAACAC	AGTGATAAGA	TCATCCGACT	TTATGATTAT	GAAATCAAGG	2760
	ACCAATACAT	CTACATGGTA	ATGGAGTGTG	GAAATATTGA	TCTTAATAGT	TGGCTTAAAA	2820
	AGAAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTTACTG	GAAAAATATG	TTAGAGGCAG	2880
70	TTCAACAAT	CCATCAACAT	GGCATGTGTC	ACAGTGATCT	TAAACCAAGT	AACCTTCTGA	2940
	TAGTTGATGG	AATGCTAAAG	CTAATTGATT	TTGGGATTGC	AAACCAAAATG	CAACCAAGATA	3000
	CAACAAGTGT	TGTTAAAGAT	TCTCAGGTTG	GCACAGTTAA	TTATATGCOA	CCAGAAGCAA	3060
	TCAAGATAT	GTCTTCTCC	AGAGAGAAATG	GGAATCTTAA	GTCAAGATA	AGCCCAAAAA	3120
	GTGATGTTTG	GTCTTATGGA	TGTATTTTGT	ACTATATGAC	TTACGGGAAA	ACACCATTTT	3180
75	AGCAGATAAT	TACATCAGAT	TCTAAATTAC	ATGCCATAAT	TGATCCTAAT	CATGAAATTG	3240
	AATTTCCCGA	TATTCAGAG	AAAGATCTTC	AAAGTGTGTT	AAAGTGTGTT	TAAAAAAGGG	3300
	ACCCAACACA	GAGGATATCC	ATTCTGAGC	TCCTGGCTCA	TCATATGTT	CAAAATCAAA	3360
	CTCATCCAGT	TAAACCAATG	GCCAAGGGAA	CCAAGTGAAG	AATGAATAT	GTTCTGSGCC	3420
	AACCTGTTGG	TCTGAATTTCT	CCTAATCTCA	TTTTGAAAGC	TGCTAAAACT	TTATATGAAC	3480
80	ACTATAGTGG	TGGTGAAGT	CATAATTCTT	CATCCTCCAA	GACTTTTGA	AAAAAAGGG	3540
	GAAAAAATG	ATTGCAAGT	ATTGTAATG	TCAGATAGGA	GGTATAAAAT	ATATTGGAGT	3600
	GTATACTCT	TGATCCCTG	TGGAAATCTA	CAATTGAAGA	CAACATCAT	CTGAAGTGT	3660
	ATCAGCAAAA	AAAATTCAGT	GAGATTATCT	TTAAAAAGAA	ACTGTAAAAA	TAGCAACCCAC	3720
	TTATGGCACT	GTATATATTG	TAGACTTGTT	TTCTCTGTTT	TATGCTCTTG	TGTAATCTAC	3780
	TTGACATCAT	TTTACTCTTG	GAATAGTGGG	TGGATAGCAA	GTATATTCTA	AAAAACTTTG	3840

TAAATAAAGT TTTGTGGCTA AAATGA

A86 Protein sequence:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Protein Accession #: NP_003309
 Signal sequence: none found
 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

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1      11      21      31      41      51
|      |      |      |      |      |
15  MNKVRDIKVK FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLLKLEKNS 60
    VPLSDALLNK LIGRYSQAIE ALPPDKYQGN ESFARIQVRF AELKAIQEPD DARDYFQMAR 120
    ANCKKPAFVH ISFAQPELSQ GNVKKSQQLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS 180
    EEEKKNLSAS TVLTAQESFS GSLGHLQNRN NSCDSRGQTT KARPLYGENM PPQDAEIGYR 240
    NSLRQTNKTK QSCPFGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPGSKP 300
    SGNDSCLELN LKSVQNSHPK EPLVSEDEKS ELIITDSITL KNTKESSLLA KLEETKEYQE 360
    PEVPENQKQK WQAKRKSECI NQNPAASNNH WQIPELARKV NTEQKHITFE QPVFVSVKQS 420
    PPISTSKWFD PKSICKTPSS NTLDDYMSCF RTFVVKNDFF PACQLSTPYG QPACFQQQOH 480
    QILATPLQNL QVLASSANE CISVKGRIYS ILKQIGSGGS SKVPQVLNEK KQIYAIKYVN 540
    LERADNQTLD SYRNEIAYLN KLQGHSDKII RLYDYEITDQ YIYMVMECGN IDLNSWLKKK 600
    KSIDPWERKS YWKMLEAVH TIHQHGIHVS DLKPANPLIV DGMKLKIDFG IANQMOPDTT 660
    SVVKDSQVGT VNYMPPEAIK DMSSSRENGK SKSKISPKSD VWSLGCILYY MTYGTPTFPQ 720
    IINQISKLHA IIDPNHETEF PDIPEKDLQD VLKCKLRDP KQRISPELL AHPYVQIQTH 780
    PVNQMAKGT EEMKYVLGQL VGLNSPNSIL KAAKTYEHY SGGESHNSSS SKTFEKKRGK 840
    K
  
```

A87 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Nucleic Acid Accession #: NM_001719
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
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40  GGGGCGCAGG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CTGCCCCCT 60
    CTGCCACCTG GGGCGGTGGG GGCOCGSAGC CGGAGAGCCG GGTAGCGCGT AGAGCCGGCG 120
    CGATGCACTG GCGCTCACTG CGAGCTGCGG CGCGGCACAG CTTCGTGGCG CTCTGGGCAC 180
    CCTGTCTCTT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAAACAG GTGCACTCGA 240
    GCTTCATCCA CGCGCGCTCT GCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
    CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
    CCATGTTTAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGGG 420
    GCCAGGGCTT CTCTTACCCC TACAAGGCGG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
    GCGTCGAAGA TAGCCATTTT CTCACCGACG CGGACATGGT CATGAGCTTC GTCAACCTCG 540
    TGGAACATGA CAAGGAATTC TTCCAACCCA GCTACCACCA TGAGAGTTTC CGGTTTGATC 600
    TTTCCAGATG CCAGAAAGGG GAAGCTGTCA CGGCGAGCGA ATTCCGGATC TACAAGGACT 660
    ACATCGCGGA ACCTCTCGAC AATGAGACGT TCGGATCAG CGTTTATCAG GTGCTCCAGG 720
    AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CGTACCCCTC TGGGCTCGG 780
    AGGAGGGCTG GCTGTGTGTT GACATCAGC CCAACGACAA CCACTGGGTG GTCAATCCGC 840
    GGCACAACTT GGGCCTGCGG CTCTCGGTGG AGAOGCTGGA TGGGACAGC ATCAACCCCA 900
    AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960
    TCTTCAGGCG CAGCGAGGTC CACTTCCGCA GCATCGGTC CAGGGGGAGC AAACAGCGCA 1020
    GCCAGAACCG CTCCAAGACG CCCAAGAAC ACCAAGCCCT GGGGATGGCC AACGTGGCAG 1080
    AGAACAGCAG CAGCGACGAG AGGCAGGCGT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
    GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCTGAAGG CTACGCGGCC TACTACTGTG 1200
    AGGGGGAGTG TGCTTCCCT CTGAACCTCT ACATGAAOGC CACCAACACC GCCATCGTGC 1260
    AGACGCTGCT CCACTTCATC AACCCGGAAA CGGTGCCAA GCCCTGTGTG GCGCCACGCG 1320
    AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAAOGTCATC CTGAAGAAAT 1380
    ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GGCACAGCT OCTCGAGAA TTCAGACCTC 1440
    TTGGGGCCAA GTTTTCTCGG ATCTTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
    CTGCTTTTGG TGAGACCTTC CCTTCCCTAT CCCCACCTT AAAGGTGTGA GAGTATTAGG 1560
    AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
    TCTTCAAGC TGTGCAGGCA AAACCTAGCA GGAAAAAACA ACAACGCATA AAGAAAAATG 1680
    GCGGGGCCAG GTCATTGGCT GGGAACTCTC AGCCATGCAC GGAAGCTTT CCAGAGGTAA 1740
    TTATGAGCGC CTACAGGCCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAGGGGGT 1800
    GGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCGGGA AGTTCTCTGA ATAAATGTCA 1860
    CAATAAAACG AATGAATG
  
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A88 Protein sequence:

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Protein Accession #: NP_001710.1
 Signal sequence: 1-30
 Pfam domains: TGFb_propeptide [37-281]
 Transmembrane domains: none found
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
5  MHVRSRLRAA PHSFVALWAP LPLLRSALAD FSLDNEVHSS FIHRRRLRSQE RREMQREILS 60
   ILGLPHRPRP HLQGHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
   LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREFRFDL SKIPEGEAVT AAEFRYKYDY 180
   IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVDITA TSNHVVVNPR 240
   HNLGLQLSVE TLDGQSINPK LAGLGRHGP QNKQPFMVAE FRATEVHPRS IRSTGSKQRS 300
10  QNRSKTPKNQ BALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWDWIIA PEGYAAYYCE 360
   GECAFFLNSY MNATNHAIVQ TLVHPINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
   RNMVVRACGC H

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A89 DNA SEQUENCE:

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15  Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Nucleic Acid Accession #: AC012478
   Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

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20  1      11      21      31      41      51
   |      |      |      |      |      |
   ATGCGGCGCG TGCCTGCTGC CGCCCCGCTC CTGCGCTGCG TGCTGCTGCG GCTCCTGGCC 60
   GCTCCGCGCG CCCTGCTGCG CAGAGCCGAG TCCGCTCTCG CGCCCTGGCC CGAACCCGAG 120
25  CGCGAGTCCG GCGCACCGCC CGGCCCGGGG CCGCGGAACA CCACCGGTT TGGGCTGGG
   GCGGCGGGCG GCAGCGGCG CTCCAGCTCC AACAGCAGTG CGCAGCGCTT GGTGACCCGC 240
   ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAGGCAG CCGTGATCGT GCGGTTCCGC 300
   TTATCCACCC TCCTCATCGC CTGCTGCTG CTGCGGCTCT TCAGGTGCGG AAAGAGGTTA 360
   AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGGCCCA 420
30  CTAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG
   TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGCTGCC AGACGCTACT GACAGTTCCT 540
   GTGCCCCCAC CCTTCATCCT CGACATTGAC CTTCAGCAA GATGCAGTGG AAGGCTGTAT 600
   GGTGGAATCA GACCTGGTAA AACCTGTTTC CCAGCTGCTT GGCATCCTGT GGAAAGTTGG 660
   TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTGCGT CGGAGGTGTT 720
35  GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTC AGGCATCTGC
   TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCACCAAA TGGAGTTGCT TCTGCCACCC 840
   TTGGGCGATC CCTTTAAAGT GCCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTGCAG 900
   CTGAATCTCA TGGAAAAGCT GGATTCTCT GCCTTAAGCA GAAACACCGG GGCTCCATCT 960
40  GCCAGTGCTT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
   CCTTGTGTC ACTTCAGCGC CACAGGCTCT CCAATAAATA CCCTTTACAC ACAAAACCATG 1080
   AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCGGCGCAGC GGGGCACCTT TTGTGAAGAC 1140
   AGAGCAGTGA CTAAGGTTCT CCAGGCTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
   GCGCTAGAGA TCGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
45  ACCCATCTCG TCAGGTTGCG TCGTTGAGAT GCGCGGGGAC AAGCCAGCCT GACGCGGAGG 1320
   AGGGTGTGTT GCGCTGCGCG GCACTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380
   TGCCCTTTGG TTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTTCTACAAA 1440
   ATCTGTCTCC CCGTCTGTGC CGTGAACAC CTAAGGGAAG CCAAGAGAAG CTCAGTGACT 1500
   GTCTTGTGCT CATTTGAGCA GAGCCCAACA AAGGCAGCTG CTGCCCAAGG GGAGCCTGTC 1560
50  AAACGAGGGC CCGATGGGCA ATTGAACAGA CACATGATCC CTGGCTGGGG GATCACACAT 1620
   GCGAACCTCG AGACAATTCC AGATACCCAA GGCCAGGAAG GCCCAAGTGA GGATGTCACT 1680
   CACCCTGGAG GAGACTTGGA TGGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTTCCAG 1740
   GATGGCAGAT GCCAAGATG GGTCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
   TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCTCT 1860
   TCCCCCGGAC AGCCCTGTGT TCTGTCCAGG CCCTGA

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A90 Protein sequence:

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60  Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Protein Accession #: FGENESH predicted
   Signal sequence: 1-27
   Transmembrane domains: 94-115, 448-469
   Cellular Localization: not determined

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65  1      11      21      31      41      51
   |      |      |      |      |      |
   MRAVPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTRPGSG 60
   AAGSGSSSSS NSSGDALVTR ISILLRLDPT LKAAVIVAFV FTLLLIACLL LRVFRSGKRL 120
70  KKTRKYDIIT TPAERVMAP LNEDDEDED STVPDIKRV SLPAALRQL PGQTLTLP 180
   VPPFFILDID LPARCSGRPD GGIRPGKTCF PAWHPVESW SAATNGVKDW TWKPSCVGGV 240
   ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPP FGHPPKVPEPT STPHGFRQLQ 300
   LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAESDLFN FWWHFSATGS PIKTLTYQTM 360
   STLGLDVFCG AGQRTGFCED RAVTKVLQGS SPSKQLRWKP ALESGFPHHL RLLRECPPLS 420
75  THPVRLARSD ARGQASLTGR RVFRFRQSL HGGSGAGTAT CLLVLKILLR RHPHLDLPYK 480
   ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHGEPV KRGPQGLTR HTPGHWGITH 540
   ANLQTIPTDQ GQSGPREDDT HPGGDLGVA NPYLESEGFQ DGRQKQWLM SEDGPPSLTG 600
   CERLTGSHHF SSHSKSWFL SPRQPLFLSR P

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EWING**A91 DNA SEQUENCE**

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Gene name: G protein-coupled receptor 64
Unigene number: Hs.184942

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Probeset Accession #: AA435577
 Nucleic Acid Accession #: NM_005756
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5
 10
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1      11      21      31      41      51
|      |      |      |      |      |
AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTCTGAA 60
CTGCGGGTCA GGTATGTTTT CTCTGTGTCAG CAGTGTGGCC ATGTGGGCAG AACTGAAGAA 120
GTTTCTACTGA CGTTTCAAGAT ATTCTTGTCT ATCATTTGTC TTCATGTCGT TCTGGTAACA 180
TCCTCGGAAG AAGATACTGA TAAATCCAGT TTGTCAACAC CACCTGCTAA ATTATCTGTT 240
GTCAGTTTTG CCCCTCTCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300
AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAAAACA CTATAGTAAA AACCTTCAAT 360
GCTTCAGGCG TCAGAACCCA GAGAAATATC TGCAATTGT CATCTATTG CAATGACTCA 420
GCATTTTCTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAAT 480
CAACATATAA CGAATGGCAC CTAACTGGGA GTCTGTCTCT TAAGTGAATT AAAACGCTCA 540
GAGCTCAACA AACCCTGACA AACCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
GAGGCCCAAA GCACATTAAA TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA 660
TTGTCTGCAA TAGCCGCTTT GGAAAGAGTA AAGATTGAC CAATGGAACA CTGCTGCTGT 720
TCTGTGAGGA TCCCTGCCCA TTCTCTCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACGTGGCC CACCATTTTC TTCCAGCCAA 840
TCCATCCCAG TGGTGCCTCG GGCCTCTGTG CTTTCCAGG TCCCAAAAGC TACCTCTTTT 900
GCTGAGCCTC CAGATTATTC ACCGTGACAC CACAATGTTT CCTCTCCAAT AGGGGAGATT 960
CAACCCCTTT CACCCAGGCC TTCAGCTCCC ATAGCTTCCA GGCCTGCCAT TGACATGCCC 1020
CCACAGTCTG AAGCATCTCT TTCCCTATG CCCCCAACCC ATGTCTCCGG CACCCAGACT 1080
CCTGTGAAGC CCTCATTTTC CTCTCCACCC GTGTCTGCCC CTGCGAATGT CAACACTACC 1140
AGCGCACCTC CTGTCCAGAC AGACATCGTC AACACCAGCA GTATTTCTGA TCTTGAGAAC 1200
CAAGTGTTCG AGATGGAGAA GGCTCTGTTC TTGGGCAGCC TGGAGCCTAA CCTGCGAGGA 1260
GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTOCCCGC CTGACATGCT GGCCTCTCTG 1320
GCTCAAAGAT TGCTGAAGAT AGTGGATGAC ATTGGCCTAC AGCTGAACCT TTCAAACACG 1380
ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
TTCAACACAA CTACCTTTGT GGCCCAAGAC CTTGCAAAATC TTCAGGTTTC TCTGGAAACC 1500
CAAGCTCCTG AGAACAGTAT TGGCACAATT ACTCTTCTCT CATCGCTGAT GAATAATTTA 1560
CCAGCTCCTG ACATGGAGCT AGCTTCCAGG GTTCAAGTTA ATTTTTTTGA AACACCTGCT 1620
TTGTTTCAGG ATCCTTCCCT GGAGAACCTC TCTCTGATCA GCTACGTCAT ATCATCGAGT 1680
GTTGCAAAAC TGACCGTCAG GAACCTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740
AACCAGGACC AGGATGAGTT AACAGTGAGA TGTGTATTTT GGGACTTGGG CAGAAATGGT 1800
GGCAGGAGAG GCTGCTCAGA CAATGGCTGC TCTGTCAAAG ACAGGAGATT GAATGAAACC 1860
ATCTGTACCT GTAGCCATCT AACAGCTTC GCGTCTCTGC TGGACCTATC TAGGACATCT 1920
GTGCTGCTG CTCAAAATGAT GGCTCTGACG TTCATTACAT ATATTGGTTG TGGGCTTTCA 1980
TCAATTTTTC TGTCACTGAC TCTGTAAACC TACATAGCTT TTGAAAAGAT CCGGAGGGAT 2040
TACCTCTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TCTGCTGAAA CCTGGTCTTC 2100
CTCTCTCTAG CTGTGATTTG TCTGTATAAG ATGCAAGGCC TCTGCTATCT AGTGGCTGTA 2160
TTTCTTCAAT ATTTTCTCTT GGTCTCATTC ACATGGATGG GCTAGAAAGC ATTCCATATG 2220
TACCTGGCCC TTGTCAAAGT ATTTAATACT TACATCCGAA AATACATCCT TAAATCTGTC 2280
ATTGTGCGTT GGGGGGTACC AGCTGTGGTT GTGACCATCA TCTGACTAT ATCCCCAGAT 2340
AACTATGGGC TTGGATCCTA TGGGAAATTC CCCAATGGTT CACCGGATGA CTTCTGCTGG 2400
ATCAACAACA ATGCAGTATT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTGT 2460
CTGAACGTCA GCATGTTTCA TGTGCTCTCT GTTCAGCTCT GTGGAATTAA AAAGAAGAAG 2520
CAACTGGGAG CCCAGCGAAA AACCAATATT CAAGACCTCA GGAGTATCGC TGGCCTTACA 2580
TTTTACTTGG GAATAACTTG GGGCTTTGCC TTCTTTGCGT GGGGACCACT TAACGTGACC 2640
TTCACTGATC TGTGTTGCCAT CTTTAATACC TTACAAGGAT TTTTCAATAT CATCTTTTAC 2700
TGTGTGGCCA AAGAAATATG CAGGAAGCAA TGGAGGCGGT ATCTTTGTTG TGGAAAGTTA 2760
CGGCTGGCTG AAAATCTGTA CTGGAGTAAA ACTGCTACTA ATGTTTAAA GAAGCAGACT 2820
GTAARCCNAG GAGTGTCCAG CTCTTCAAAAT TCCTTACAGT CAAGCAGTAA CTCCACTAAC 2880
TCCACCAAC TGTCTAGTGA TAATGATTGC TCAGTACACG CAAGCGGAAA TGGAAATGCT 2940
TCTACAGAGA GGAATGGGCT CTCTTTTATG GTTCAGAAAT GAGATGTGTG CCTTCAAGAT 3000
TTCACTGATA AACAGCACAT GTTTAACGAG AAGGAAGATT CCTGCAATGG GAAAGGCGGT 3060
ATGGCTCTCA GAAGGACTTC AAAGCGGGA AGCTTACACT TTATTGAGCA AATGTGATTC 3120
CTTTCTCTTA AAATCAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACTCTTTA 3180
CACAATGTGA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT 3240
AAGCTAATTA AGGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300
TTTAGACATT TCTGATTTGG TTCTTATCT TCAATTTTAT AAGAAGGTTG GTTTTAAACA 3360
ATACACTAAG AATGACTCCT ATAAAGAAAA CAAAAAAGG TAGTGAACCT TCAGCTACCT 3420
TTTTAAGAGG CTAAGTTATC TTTGATAACA TCATATAAAG CAACTGTTGA CTTGAGCCTG 3480
TTGGTGAGTT TAGTTGTGCA TGCCCTTTGT GTATATAAGC TAAATCTAG TGACCCATGT 3540
GTCAAAATC TTACTCTTAC ATTTTCTGT ATTTATTTTC TACTGTGTAA ATGTATTCCT 3600
TTGTAGAATC ATGTTGTTTT TGTCTCACGT GATAATTCAG AAAATCCTTG CTCGTTCCGC 3660
AAATCTTAAA GCTCCTTTTG GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAAA 3720
TCAGAAATA ATGATCCGAG CCAGACTGAG AAAATGTAA GAGACAGTGC CACAGTTAGC 3780
TCATACAGG CCTTTGAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA 3840
TGGGTGATGG TTTGACAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG 3900
GTGCAGGACC TGTACAGCCA AACACAGCAT CCAATATGAA TACCCATCCC CTGACCGCAT 3960
CCCCAGTAGT CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020
AGAGGGATGA ACTGTCTACC AGACCATGTG TCAGGAAAT TGTGAACGTA GATGAGGTAC 4080
ATACACTGCC GCTTCTCAAA TCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTC 4140
CTTCTCTTAA AAAGGTACAT ATATATGGA AAAAATCATA TTGCCGTTCT TTAAGAGCA 4200
ACGCTATGTT ACATGTTTGA TTGTTATGAC TGGTACACTC TGGCCAGGCC AGAGCTATAA 4260
TTGTTTTTTA AATGTGCTTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA 4320
GGGAACGTGC CTACACTGCT ATTGTTGCTA CATGTATOGA GCCTTGATTG CTCCTAGTTA 4380
TATACAGGGT CTATCTGTCT TCCTACCTAC ATCTGCTTGA GCAGTGCTTC AAGTACATCC 4440
TTATTAGGAA CATTCTAAAC CCTTTTATG TAAGTCTTTC ACTAAGGTTT TCTTGATAT 4500
ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560
CTGACTGTCT TTTGCAATAT TTCTTTCTG ATTTATTATA TTTTCTTGTA TTTATATGTT 4620

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AAAATCAAAA ATGTTAAAT CAATGAAATA AATTGTCAGT TAAGA

A92 Protein sequence

Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942
 Protein Accession #: NP_005747.1
 Signal sequence: 1-38
 GPS domain: 564-615
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
15 MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSPF PAKLSVVSPA 60
PSSNEVETTS LNDVTLSELLP SNETERTKIT IVKTFNASGV KPQRNICNLS SICNDSAPFR 120
GEIMFQYDKE STVPQNHIT NGTLTGVLSL SELKRSELNK TLQTLSETYF IMCATAEAQS 180
TLNCTFTIKL NNTMNACAAI AALERVKIRP MEHCCSVRI PCPSSPEELG KLQCDLQDPI 240
VCLADHPRGP PFSSSQSIPV VPRATVLSQV PKATSPFAEPF DYSPVTHNVP SPIGEIQFLS 300
PQPSAPIASS PAIDMPQSE TISSPMPQTH VSGTTPPVKA SFSSPTVSAP ANVNTTSAPP 360
VQTDIVNTSS ISDLNQLVQ MEKALSLGSL EPNLAGEMIN QVSRLLHSPF DMLAPLAQRL 420
LKVVDDIGLQ LNFSTTTISL TSPSLALAVI RVNASSFNTT TFVAQDPANL QVSLETQAPE 480
NSIGTITLPS SLMMNLPAHD MELASRVQFN FFETPALFQD PSLENLSLIS YVSSSVANL 540
TVRNLTRNVT VTLKHINPSQ DELTVRCVFW DLGRNGGRGG WSDNGCSVKD RRLNETICTC 600
SHLTSFGVLL DLSRTSVLPA QMMALTFTY IGCGLSSIFL SVTLVTYIAF EKIRRDYPSK 660
ILIQLCALL LNLVFLDLS WIALYKMQGL CISVAVFLHY FLVSPFTWNG LEAFHMYLAL 720
VKVFNTYIRK YILKFCIVGW GVPVAVVTII LTISPNDYGL GSYGKPFNGS PDDFCWINNN 780
AVFYITVVGY FCVIFLLNVS MFIVVLVQLC RIKKKKQLGA QRKTSIQDLR SIAGLTFLLG 840
ITWGFAPFAN GPNVNTFMYL FAIFNTLQGF FIFIPYCVAK ENVRKQWRRY LCCGKRLRAE 900
NSDWSKTATN GLKKQTVNQG VSSSSNSLQS SSNSTNSTTL LVNNDSCVHA SGNGNASTER 960
NGVSFSVQNG DVCLHDFGK QHMFNEKEDS CNGKGRMALR RTSKRGSLHF IEQM

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Fibrosis

A93 DNA SEQUENCE

Gene name: BGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

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40      1      11      21      31      41      51
|      |      |      |      |      |
CGCGAGAGGA GCCTCGGCCA GGCTAGCCAG GCGGCCCCCA GCCCTCCCC AGGCGCGGAG 60
CGCCCTCGCC GCGGTGCGCT GCCTCCCTCC CCAGACTGCA GGGACAGCAC CCGGTAACGT 120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
GGGTCCGGCC GGGCGCCCTC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTCCGAGA 240
ATGCTCTGTC CCTGGAGCCT TCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
GGGAACGGCG CCACTGCAAG GCATCAGCGG TTGTTAGCAT CGGCACTGCA GCGTGGGTC 360
TGTCACATG GAACATAACT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC 480
AGATGCTTTC CAGGATACAC CGGAAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 540
AAACCCCGCG CAGTCCCAAC CAGATGTGTG AATACACAAG GAAGCTACAA GTGCTTTTGC 600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
ATAAATCTGC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
TCAGGACTCC GCTTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTCT 780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGAAG CTACTACTGC 840
AAATGTCACA TTGTTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
GGGTCCCTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTCTTGCT 1020
ATCCCTGAAA ATTCTGTGAA GGAAGTCCTC AGAGCACTG GTAACATCAA AGACAGAATC 1080
AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAGAAAG CAAAAATTAA AAATGTTACC 1140
CCGAACCCA CCAGGACTCC TACCCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA 1260
GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGOGA 1320
AGCCTCGGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCTGATT 1380
CTGGTCCAAA GGAAGCGCT AACTTCCAAA CTGGAACATA AAGATTAAAA TATCTCGGTT 1440
GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
TGGAACTCTG CTGATCGAGA TAATGCTATT GGCCTCTATA TGGCAGTTCC GGCCTTGGCA 1560
GGTCAACAAG AAGACATTGG CCGATTGAAA CTCTCCTAC CTGACCTGCA ACCCCAAAGC 1620
AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCGGAGACAA AAGTGGGAA ACTTGGAGTG 1680
TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCAAGAGTGA GGATGAAAAG 1740
TGGAAGACAG GGAATAATCA GTTGTATCAA GGAAGTATG CTACCAAAAG CATCATTTTT 1800
GAAGCAGAAC GTGCAAGGG CAARAACGGC GAAATGCGAG TGGATGGGCT CTGCTTGT 1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
TTGACTTTGT ATGTCAGTGT CCGTGGTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCTT 2040
TCTTGATATA GATATGCCAA TATTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAT GTCACTTTAT CTCCCCTCT 2160
CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TCTTAGAAAA 2220
TAGAAAAAAA AGCAGAGAGA AATGTTTAA TGTTTGACTC TTATGATACT TTTGGGAAAC 2280
TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT 2340
TGTATATTTA AATCTTTTGT AATAATAATA TCACATCAT CAAAAAATAA AAAAAAAA

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A94 Protein sequence:

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Protein Accession #: NP_056322.2
 Signal sequence: 1-21
 Transmembrane domains: none found
 MAM domain: 402-546
 EGF domain: 80-259
 Cellular Localization: secreted

1	11	21	31	41	51	
MPLPWSLALP	LLLSWVAGGF	GNAASARHFG	LLASARQPGV	CHYGTKLACC	YGWRRNSKGV	60
CEATCEPGCK	FGECVGFNKC	RCFPGYTGKT	CSQDVNECGM	KPRPCQHRCV	NTHGSYKCF	120
LSGHMLMPDA	TCVNSRTCAM	INCQYSCEDT	EEGPQCLCP	SGLRLAPNGR	DCLDIDECAS	180
GKVICPYNRR	CVNTFGSYIC	KCHIGFELQY	ISGRYDCIDI	NECTMDSHTC	SHHANCFTNQ	240
GSFKCKCKQG	YKGNGLRCSA	IPENSVKEVL	RAPGTIKDRI	KILLAHKNSM	KKKAKIKNVT	300
PEPTRTPTFK	VNLQPFNYBE	IVSRGGNSHG	GKKGNBEKMK	EGLEDEKREE	KALKNDIEER	360
SLRGDVFFPK	VNEAGEFGLI	LVQRKALTSK	LEHKDLNISV	DCSFNHGICD	WRQDREDDFD	420
WNPADRDNAI	GFYMAVPAFA	GHKKDIGRLK	LLLPDLQPOS	NFCLLFDYRL	AGDKVGKLRV	480
FVKNSNNALA	WEKTTSEDEK	WKTGKIQLYQ	GTDATKSIIF	EAERGKGTGT	EIAVDGVLLV	540
SGLCPSDLSL	VDD					

GLIOBLASTOMAA95 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1	11	21	31	41	51	
AGCAACGACG	COGGGCGAGC	GGAGCGGCGG	COGCGCCATG	TGGCTGTCTG	GGCGCTGTG	60
CCTGCTGCTG	AGCAGCGCGG	CGGAGAGCCA	GCTGCTCCCC	GGGAACAACT	TCACCAATGA	120
GTGCAACATA	CCAGGCAACT	TCATGTGCAG	CAATGGACGG	TGCATCCCGG	GCGCCTGGCA	180
GTGTGACGGG	CTGCCTGACT	GCTTCGACAA	GAGTGATGAG	AAGGAGTGCC	CCAAGGCTAA	240
GTOGAAATGT	GGCCCAACCT	TCTTCCCTCG	TGCCAGCGGC	ATCCATTGCA	TCATTGGTGG	300
CTTCGGGTGC	AATGGGTTTG	AGGACTGTCC	CGATGGCAGC	GATGAAGAGA	ACTGCACAGC	360
AAACCCCTCTG	CTTTGTCTCA	COGCGCGCTA	CCACTGCAG	AACGCGCTCT	GTATTGACAA	420
GAGCTTCATC	TGCGATGGAC	AGAATAACTG	TCAAGACAAC	AGTGATGAGG	AAAGCTGTGA	480
AAGTTCTCAA	GAACCCGGCA	GTGGGCAGGT	GTTTGTGACT	TCAGAGAACC	AACCTGTGTA	540
TTACCCGACG	ATCACCTATG	CCATCATCGG	CAGCTCCGTC	ATTTTGTGTC	TGGTGGTGGC	600
CCTGCTGGCA	CTGGTCTTGC	ACCACGAGCG	GAAGCGGAAC	AACCTCATGA	CGCTGCCCGT	660
GCACCGGCTG	CAGCACCTCT	TGCTGCTGTC	CGGCTGGTGG	GTCTGGGACC	ACCCGCCACCA	720
CTGCAACGTC	ACCTACACCG	TCAATAATGG	CATCCAGTAT	GTGGCCAGCC	AGGCGGAGCA	780
GAATGCGTGT	GAGTAGGGCT	CCCCACCTCT	CTACTCCGAG	GCTTGTCTGG	ACCAGAGGCC	840
TGCGTGGTAT	GACCTTCCTC	CACCGCCCTA	CTCTTCTGAC	ACGGAATCTC	TGAACCAAGC	900
CGACCTGGCC	CCCTACCGCT	CCCGGTCCGG	GAGTGCCAAC	AGTGCCAGCT	CCCAGGCAGC	960
CAGCAGCCTC	CTGAGCGTGG	AAGACACCAG	CCACAGCCCG	GGGCAGCGCT	GCCCCCAGGA	1020
GGGCACTGCT	GAGCCGAGGG	ACTCTGAGCC	CAGCCAGGGC	ACTGAAGAAG	TATAAGTCCC	1080
AGTTATTCCA	AAGTCCATAT	GGGTTAATCT	GCTCTGACTT	GTTGCCATTC	TAACAATTGG	1140
TGCTCATGGG	AAGCTCTTTA	AGCACCTGTA	AGGATGTCTC	AAGTTACAGT	TTGGGATATT	1200
AACATCTCTC	GCATTCCCTC	CCTCCCCCAG	ACTTCAGAGA	TGTTTTTCTG	GCGTCTCAGT	1260
TGACATGATC	TGTTGTGCGT	CTTTTCTGTC	AGGTCACTCT	TCOCTTGGGA	CCCGAGATCA	1320
CACCCCTCAT	TTTCACATTA	TTCTGTTTCT	GTTGGAGAGA	CAGCATATAA	AACAGTATTG	1380
AAATAGGCTG	GGAGAGAGCA	ATGTTTCTGT	GCTATATTGG	ATGCTCAGAA	GTGCAGGAGA	1440
CGCTGGACCC	AATCTCTCTC	GCTGGGTAGT	TACCTTATAG	CATTGTGGGA	TTTGGGTTAG	1500
ATGATCTAAC	CAGGAGGCCA	TCACTGGATG	GTACCCCCCC	CAAAAAAATT	CCATTGTAGC	1560
ATCAAAACCT	GCTTTGCACA	ATCCTATTTG	ATGCCCCGAG	TTGAGCAGAG	TCAGTGGCCA	1620
AAGAAACTTT	TGGACGTGAG	TAACACCCCT	CAGCAGTGGC	AACGTTATTT	TGGTTTGTG	1680
AAGGACTCTG	AAACCATCTA	CCCTGTATAA	ATTCTGGCTT	TAGAAATTGG	CCCAAGAAATG	1740
CTCATCTCTG	GAGCTTTCCT	CAGCAGCATA	TATCATCAGC	CTCATCTTAA	AATAGGCAGG	1800
GAGCCCTTCC	CATGAGTTTA	TCCAAGTTCT	CAGCTCTCTA	AATGCAGGCT	GCCAGAGACC	1860
TACACCTGCC	CTGGCTCTAC	AGCCACTTAC	CTGGTTTCTG	GACTGTCAAC	CTCCAGCTGT	1920
ACCTGCCCCG	AGCCAAGGAA	TGAGGAOCTA	ACTTGAGTTG	GCCCCAAGCT	TGACCTGGCT	1980
GTATGTCCCT	GTGGCCOACA	CCGAGCCTGT	CTTGCTCAIT	CATGCAGCTC	CAACACTGGC	2040
CTCCAAAGTT	CCCTTAACAC	TTGCAAGTCT	CTTTTACCTT	GTGCATTGAG	ACTTGAGGAC	2100
ACTGGTTTCT	ATCACAGGTG	AGAGCCATGT	TCAATACCTC	CAGCAAGCTC	TCCTGGCTCC	2160
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AGCTGTCTCT	TTTTTTGTTT	TTCTTTTAAC	AAGGTCCAAA	GAAAGATGCA	AAAGGAGATC	2460
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CCACTCCGGG	CAGCTGTAC	CCATTTCAGAA	CTTCTTCCG	CAGCTGAAGA	AATGTTCACT	2820
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5 TGATCCGTGT CTGTAGACTT TTCTTCTTT TTTTAACCAA ATCCAAAGGA TGTACAGAA 2940
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 CATTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTGTATGGGG CCCCTCTCTC 3180
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 10 TGATTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420
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 20 GAAACCTCTG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACCGCGCGGG 4020
 GGAAACCGCA GAGTGTTCGC TAAACCACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080
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25 A96 Protein sequence:
 Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AN043782
 Protein Accession #: none found
 30 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51
 MWLLGLPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD 60
 EKECPKAKSK CGPTFFPCAS GIHCIIGRFR CNGFEDCPDG SDEENTANP LLCSTARYHC 120
 40 KNGLCIDKSF ICDQNNQD NSDEBCESS QEPGSGQVFP TSENQLVYYP SITYAIIGSS 180
 VIFVLVALL ALVLAHQRR NNLMTLPVHR LQHPVLLSRL VLDHFHCN VTYNVNNGIQ 240
 YVASQABQNA SEVSGPPSYS BALDQRPAP YDLPPFPYSS DTESLNQADL PPYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PQQPGPQEGT AEPRDSEPSQ GTEEV

45 LUNG

50 A97 DNA SEQUENCE
 Gene name: putative GPCR, Weakly similar to dJ365012.1
 Unigene number: Hs.256897
 Probeset Accession #: BE001836
 Nucleic Acid Accession #: BE001836
 Coding sequence: 1-2955 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
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 GGTTAGGCC CACATAGCAC TAAAGTCTT CAACATGCAA TTAGAAGCTC AAATGTGTGAC 180
 60 GGAATATTG TCACTCTAA AAAAGATGTT TCTATTAGAA TTACTTACT CTTTCATGAA 240
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 GAGAAGTCAA ATTCTGACAC AATCCAGCAA GTAACATAA AACTGATGG CCCAGTCGAA 360
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 AATTTCTGA AGCTCTTGAA GCCTCCATTA TTATGGTCAC ATGGGCTAAT TAGAATTATC 480
 65 AGAGCAAAGG CTACCACAGA CTGCAACAGC CTGAATGGAG TCCTGCAGTG TACCTGTGAA 540
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 70 AAAGCATATG AAAGAATCA AGGTTTGTAG TCGGTTGAG TCACCCAATT TCGAAATGGA 840
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 75 TGTGATCCT CTGGGTGGCA GGTCACTAGG GAGACTTGTG TGCTCTCTCT GCTTGAAGAA 1140
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5 TCCACGGTTA TTCAAAACTA TTCCATAAAT GAAGTTTTC TATTTTTC CAAGATAGAG 1800
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 10 ACCTCCTTCT CCATATTGAT GTCACTTTT GTCCCTCTA CAATCTTCCC CGTTGTAAAA 1980
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 TACAAAAGGA AAGATGTGTG TTGGCTTAAC TGGTCCAATG GAAGCAAACC ACTCTGGCT 2460
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 20 ACAAAGCTCT GGAGGCCGAC TGTGGGGAA AGACTGAGTC GGGATGACAA GGCCACCATC 2580
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 TCATCAGATT TATCTGCCAA ACCCAAATTC TCAAGCCTT TCAACCCACT GCAAAACAAA 2880
 25 GGCCATTATG CATTTTCTCA TACTGGAGAT TCCTCCGACA ACATCATGCT AACTCAGTTT 2940
 GTCTCAAATG AATAA

A98 PROTEIN SEQUENCE

25 Gene name: putative GPCR, Weakly similar to dJ365012.1
 Unigene number: Hs.256897
 Protein Accession #: none found
 Signal sequence: 1-17
 Pfam domain: 7tm_2 [561-820]
 30 Transmembrane domains: 545-567, 571-593, 605-627, 641-663, 677-699, 721-743, 767-789
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51
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 MHALLLCFSV LINGASGLSL QSPVVEYQLL LQVYRDSKE KRDLRNFLKL LKPPILLWSHG 60
 LIRIIRAKAT TDCNSLNGVL QCTCEDSYTM FPPSCLDPNQ CYLHTAGALP SCECHLNLS 120
 QSVNFCERTK IWGTFKINER PTNDLLNSSS AIYSKYANGI EIQLKKAYER IQGFESVQVT 180
 QFRNGSIVAG YEVVGSSSAS ELLSAIEHVA EKAKTALHKL PFLDGGSPRV PGKAQCNDIV 240
 40 PFGSGKDEYV TLPCSSGYRG NITAKCESSG WQVIRETCVL SLLEBLNKNF SMIVGNATEA 300
 AVSSFVQMLS VIIRQNPSTT VGNLASVVS ILSNLSLSLA SHFRVSNSTM EDVISIADNI 360
 LNSASVTNWT VLLREEKYAS SRLLETLENI STLVPPTALP LNFSRKFIDW KGIPVNSQL 420
 KRGSYQIKM CPQNTSIPIR GRVLIGSDQF QRSLEPETIIS MASLTILGNL PVSXNGNAQV 480
 NGPVLSTVIQ NYSINEVFLF FSKIESNLQ FHCVPWDFSH LQWNDAGCHL VNETQDIVTC 540
 45 QCHLTFSFI LMSFPVPSTI FVVKWITYV GLGISIGSLI LCLIEALFW KQIKKQSTSH 600
 TRRIOMVNIA LSLLIADVNF IVGATVDTV NPSGVCTAAV PFTHFFYLSL FFWHLMLGIL 660
 LAYRIILVPH HMAQLHMAV GPCLGYGCP L IISVITIAVT QPSNTYKRD VCWLNWSNGS 720
 KPLLAFFVPA LAIVAVNFV VLLVLTKLWR PTVGERLSRD DKATIIRVGK SLLILTPLLG 780
 LTWGFIGITI VDSQNLAMHV IPALLNAFQV RTVTITYCIV K

A99 DNA SEQUENCE

55 Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Probeset Accession #: F07953
 Nucleic Acid Accession #: NM_016334
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
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 65 GCGCAATTG TTTAAAGACT ATGAGATAGC TCAGTATGTT GTACAGGTGA TCTTCTCCGT 240
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 70 ACTAGGAGAT CCTTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
 CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTCTCTTCTG GAITTGGTGC 600
 TGTCACTGCG CCATACACTT ACATGTCTTA CTCTCTCAGG AATGTGACTG ACACAGATAT 660
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 80 CAATATTGTT TTTGATCGAG TTGGGAAAAC GGATCCTGTC ACAAGAGGCA TTGAGATCAC 1080
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 CTTTATGACC ATCTCTAGCA GTAAGTCTCT CAATGTCAAT GTCTGCTAT TAGCAGAT 1260
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 CGCACCATTA ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACTTCTATC ACGTTGGTT 1380
 TGATGTGATC TTCTGGTCA GCGCTCTCTC TAGCATACTC TTCTCTATT TGGCTCACAA 1440

	ACAGGCACCA	GAGAAGCAAA	TGGCACCTTG	AACCTAAGCC	TACTACAGAC	TGTTAGAGGC	1500
	CAGTGGTTTC	AAAAATTTAGA	TATAAGAGGG	GGGAAAAATG	GAACCAGGGC	CTGACATTTT	1560
	ATAAACAAAC	AAAATGCTAT	GGTAGCATTT	TTCACTCTCA	TAGCATATCT	CTTCCCTCTC	1620
5	AGGTGATACT	ATGACCATGA	GTAGCATCAG	CCAGAACATG	AGAGGGAGAA	CTAACTCAAG	1680
	ACAATACTCA	GCAGAGAGCA	TCCCGTGTGG	ATATGAGGCT	GGTGTAGAGG	CGGAGAGGAG	1740
	CCAAGAACT	AAAGGTGAAA	AATACACTGG	AACCTCTGGG	CAAGACATGT	CTATGGTAGC	1800
	TGAGCCAAAC	ACGTAGGATT	TCCGTTTAA	GGTTCACATG	GAAAAGGTTA	TAGCTTTGCC	1860
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10	<u>A100 Protein sequence</u>						
	Gene name:	putative G-protein coupled receptor					
	Unigene number:	Hs.16085					
	Protein Accession #:	NP_057418.1					
	Signal sequence:	none found					
15	Transmembrane domains:	5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446					
	Cellular Localization:	plasma membrane					
20	1	11	21	31	41	51	
	MSFLIDSSIM	ITSQILFFGF	GWLFFMRQLP	KDYEIRQYVV	QVIFSVTFAP	SCTMPELIIP	60
	EILGVLNSSS	RYFHWKMNLC	VILLILVFMV	PFYIGYFIVS	NIRLLHKQRL	LFSCLLWLTP	120
	MYFFWLKGD	PFILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGFGAVNCP	YTYMSYPLRN	180
	VTDTDLALE	RRLQLTMDMI	ISKKKRMAMA	RRTMPQKGEV	HNKPSGFWCM	IKSVTTSASG	240
25	SENLTLLIQE	VDALKEELSRQ	LPLETADLYA	TKERIEYSKT	FKGKYFNFLG	YFYSIYCVNK	300
	IFMATINIVF	DRVGKTDPVT	RGIEITVNYL	GIQFDVKFWS	QHISFILVGI	IIVTSIRGLL	360
	ITLTKFFYAI	SSSKSSNVIV	LLLAQIMGY	FVSSVLLIRM	SMPLEYRTII	TEVLGELQFN	420
	FYHRWFDVIF	LVSALSSILF	LYLAHKQAPE	KQMAP			
30	<u>A101 DNA SEQUENCE</u>						
	Gene name:	ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]					
	Unigene number:	Hs.19322					
	Probeset Accession #:	AA088458					
	Nucleic Acid Accession #:	AA088458					
35	Coding sequence:	862-1995 (underlined sequences correspond to start and stop codons)					
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	CTGGGCGAGA	GCAGAGCCAG	CGCCGACTTT	GGGCTGTCAG	GGAGCCCCCG	CCCACTGGGG	240
	CGGCTACTGC	CCAAGGTACA	AGAGGTGGCC	CGGTGCTTGG	GGGAGCTGCT	GGCTGCAGCC	300
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	AGCCCTTCGA	GGGTGGGGCG	CCCATCGCAC	CCACCTCTCT	TGGCTGGAGA	CCCGCGGCAG	660
50	GCCGAGCAC	AGTCCCGGAG	TGGGCGCCTT	CCTGCGCGCC	TTGCCAGATG	GGCTCCCGAG	720
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	ACATGGGCTG	GGGCTCTCTT	TGAGTCCGCA	TAGTCCGCG	CTACTACTGG	CCGCTGTCAG	840
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	GGTCCCATCT	TCAGGGAAGG	GCACTGCCCA	CGCCAGGCTG	CACCTTCCAA	AACGGGCGAG	960
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	GTAAGCGGGG	GGTGCCTGCC	TGGCTGGGGA	GCCCCAGGGA	TAGCGGTGCG	ACTTCAGGTT	1140
	CTGGCCAGG	CTGAGGAGCC	CTGGCTGCAG	CGGATCGGCA	CGCGGGGTGG	GCGAGAGCTT	1200
	GGCTGTGATG	TGCCCTCCAC	AGACCCTGGG	GTGATGGCCT	TCCCCCTCTT	GGCGGGAGCG	1260
60	TTGCCCCACG	TTGAGTCCCA	CACAACATCC	TGTGAGCCTG	GCTCCCGAGG	AGGGCCCCCA	1320
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	CTGGGGTCTC	GCTCACCCCC	CTTTGCTCTC	ACGCCCCAGC	TGTCCCCAGG	TTTCACTGGG	1440
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	TGCTGCACCT	GGTCTGCAGG	GGTGTCCCAG	GACAGGCCCA	AGTCAGGCCA	GCATGCAGCT	1980
	GCCCTCTTAC	CTGAAGATG	GGAGTGGGCT	TTCCAGGGGA	CATAAGGATG	TCAGGCTGGG	2040
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80	CACGAGGGGA	GAATTTAAAG	GCCCCGGCTG	GCAGGGTCTA	GGTGGCTGGC	AGAGGCACAT	2520
	GCAGACCCCT	CCTGGAGCCT	GCCTTAGGAC	GCTGGGCGGG	TCACTCTCCG	TGCAGGATGT	2580
	GAGCAGCGTC	CTCGGGCTCT	ATCCGCGAGG	TGCCAGTAGC	GTGTGCAGGT	ACATACAGGT	2640
	GCGTGACAC	TGTGATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTG	TCCTTGGGGG	2700
	CAGAAAGTGC	CCCAAGTGAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GGCCTCAGGA	2760
	TTTGTGTGTT	ATCAAGTTCC	AAGGAAAAGG	AACATCTCAG	CCGGGCGTGG	TGGTTCACGC	2820

5 CTGGAATCCC AGCACTTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
 CCCCATCTCT ACARAAAAA AAAAAGAAAG AAAGAAATG AGAGATCCAG GTTTAAAAAT 2940
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
 TAGACCCGAG TACTAGAAAT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060
 AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

A102 DNA SEQUENCE

10 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

15 1 11 21 31 41 51
 | | | | | |
 ACCGGGCACC GGAAGGCTCG GGTACTTTGG TTCTTAATTA GGTTCATGCCC GTGTGAGCCA 60
 20 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACATGTGC CTACTATCTC TTCCGTGGTG 120
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCGGATGTC 180
 AGAGGTCCTG AATAGTGTAC CATGGGGGAA AATGATCCGC CTGCTGTGA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAATATA GTCCGTGTGC ACCAGATGCA 300
 GATGCTGTGG CTGCACAGAT CCTGTCACTG CTGCCAATGA AGTTTTTTCC AATCATCGTC 360
 25 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGAAGT ACAGATGTGG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACSCAAATGT TGCCTGTGCC CAACGGGTT TCCCAAGCTA TGTGAGTTCA 660
 30 GATAAECTCA GAGTGTGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCCCTCG GCCACGTGGT TACCTTCAG TGACAGCCT GTGTCATAG AAGGGGCTAC 840
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900
 CTTCACTTCC AGGGCTACCA CTTGTGCGGG GGCTCTGTCA TCACGCCCTC GTGGATCATC 960
 35 ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCCAAGT CATGGACCAT CCAGGTGGGT 1020
 CTAGTTTCCC TGTGTGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTAACCA 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCTTGCCCA ACTCTGAAGA GAACTTCCCC 1200
 GATGGAAGAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
 40 TCCCTGTGCC TGAACCAAGC GGCCTGCTCT TTGATTTCCA ACAAGATCTG CAACCAAGG 1320
 GAGTGTATCG GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGCGACCGC CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCCGTG TCACCTCCTT CTTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
 45 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA 1620
 TCCTCCCTCG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
 TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAAACCTT 1740
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800
 50 AGTGCAGTGG CGAATACCTT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860
 TTGCTCAGC TTCCCAAGTA GCTGGGACCA CAGGTGCCCG CACCAACACC CAACTAATTT 1920
 TTGTATTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
 CCTCAAATGA TGTGCTGCTC TCAGCCTCCC ACAGTGCTGG GATTACAGGC ATGGGCCACC 2040
 AOGCTTAGCC TCAGCTCCTT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGG AAAATTCCTG 2160
 55 ACGAGATAG CAGTTATGTG ACCTCAGGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
 GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCAGGTT TTCTCTCTA GGGACAGAAA 2280
 CCAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
 ATGACTCGTT TAAGGCCTAT TTTATGATT TCTTTGTAGC ATTGGTGCT TGACGTATTA 2400
 60 TTGTCCTTGG ATTCCAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAA

A103 Protein sequence:

65 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 70 Tryp_Spc domain: 216-444
 Cellular Localization: plasma membrane

75 1 11 21 31 41 51
 | | | | | |
 MGENDPPAVE APFSPFRSLFG LDDLKISFVA PDADAVAAQI LSLLPLKFPF IIVIGIIALI 60
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGNNAVLPVF 120
 TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
 80 VTALHHSVYV REGCASGEHV TLQCTACGHR RGYSSRIVGG NMSLLSQNFW QASIQFQGYH 240
 LCGGSVITPL WIIITAAHCYV DLYLPKSWTI QVGLVSLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QVCLFNSEE NFFDGRKVCWT SGWGATEDGA GDASPVLNHA 360
 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSQCGD SGGPLVQGER RLMLVVGATS 420
 PGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT

A104 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

10 | | | | |

ATGCACACCG TGGCTACGTC CGGACCCAAAC GCGTCCTGGG GGGCACCGGC CAAGCCCTCC 60

GGCTGCCCGG GCTGTGGGCG CAACGCCCTCG GACGGCCAG TCCTTCGCC GGGGCCCGTG 120

GACGCCTGGC TCGTGCCGCT CTCTCTCGCG GCGCTGATGC TGCTGGGCCT GGTGGGGAAC 180

TCGCTGGTCA TCTACGTCAT CTGCCGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC 240

15 ATGCCAACC TGGCGGCCAC GGACGTGACC TTCTCTCTGT GCTGCGTCCC CTTCACGGCC 300

CTGCTGTACC CGCTGCCCGG CTGGGTGCTG GCGGACTTCA TGTGCAAGTT GGTCAACTAC 360

ATCCAGCAG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC 420

TGGTACGTGA CCGTGTCTCC GTTGCGCGCC CTGCACCGCC GCACGCCCGC CCTGGCGCTG 480

CGTGTACGCC TCAGCATCTG GTTAGGCTCT GCGGCGGTGT CTGCGCGGT GCTCGCCCTG 540

20 CACCGCCTGT CACCGGGGCC GCGGCGCTAC TGCACTGAGG CCTTCCCGAG CCGCGCCCTG 600

GAGCGCGCCT TGCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCGCT GCTCGCCACC 660

TGCGCCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCGGG TCGCGGTGCG CCGCGCGCCC 720

GCGATAGCG CCTGTCAGGG GCAGGTGCTG GCAGAGCGCG CAGGCGCGGT GCGGGCCAAG 780

GTCTCGCGCG TGGTGGCGGG CGTGTCTCTG CTCTTCGCGG CTGCTGGGG CCGCATCCAG 840

25 CTGTTCTCTG TGGTCAAGCG CTGGGGCCCG GCGGGCTCTT GGCAACCAAG CAGCTACGCC 900

GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCTTACA GCAACTCCGC GCTGAACCGG 960

CTGCTCTACG CCTTCTCTGG CTCGCACTTC CGACAGCGCT TCGCGCGGT CTGCCCCCTG 1020

GCGCGCGGCC GCGCGCGCGG CCGGACCGCT CGGACCCGCG AGCCCCACAC 1080

30 CGCGAGCTGC ACCGCTGGG GTCCCAACCG GCGCGCGCA GGGCGCAGAA GCCAGGGAGC 1140

AGTGGGCTGG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA

A105 Protein sequence

Gene name:

Homo sapiens G protein-coupled receptor (HOT7T175), mRNA

Unigene number:

Hs.208229

Protein Accession #:

AI819198

Signal sequence:

none found

Pfam domains:

7tm_1 [59-323]

Transmembrane domains:

43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization:

plasma membrane

1 11 21 31 41 51

45 | | | | |

MHTVATSGPN ASWGAPANAS GCPGCGANAS DGPVPSRAV DAWLVPLFFA AIMLLGLVGN 60

SLVIYVICRH KPMRTVTNFI IANLAATDVT FLCCVPFTA LLYPLGWL GDFMCKPVNY 120

IQQVSVQATC ATLTAHSVDR WYVTVFPLRA LHRTTFLAL AVSLSIWVGS AAVSAFVLAL 180

HRLSPGPRAY CSEAFPPRAL ERAFALYNLL ALYLLPLLAT CACYAAMLR LGRVAVRPAP 240

ADSLQGVVL AERAGAVRAK VSRLVAHVVL LFAACWPIQ LFLVLQALGP AGSWHPRSYA 300

50 AYALKTNAHC MSYSNSALNP LLYAFLGSHF RQAFRRVPCP APRRRPRRR PGPSDPAAPH 360

AELHRLGSHF APARAQKPGS SGLAARGLCV LGEDNAPL

A106 DNA SEQUENCE

Gene name:

integrin, beta 8

Unigene number:

Hs.52620

Probeset Accession #:

AA479726

Nucleic Acid Accession #:

NM_002214

Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

60 | | | | |

CCCAGAGCCG CCTCCCGCTG TTGCTGGCAT CCGAGCTTC CTCCCTTGCC AGCCAGGACG 60

CTGCCGACTT GTCTTTGCCG GCTGCTCGCG AGACGGGGCT GCAAAGCTGC AACTAATGGT 120

GTTCGCCCTC CTGCCCACTT GTGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT 180

65 TCCCTCGAC CTGCGCGCGG TACCTCCCA CAGATCCAGC ATCACCAGT GAATGTATAC 240

TAGGGTGGTT TCCCCCCCAG CTGCGGCTT TGTTTGGGTT TGATTGTGT TGGCTCTTCG 300

CTAAGCTGAT TTATGCAGCA GAAGCCCGAC CGGCTGAGAG GAAACAAAAG CTCTTTCTTT 360

TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTGGC GCGGGGCCCT 420

TGGCCGTGCA AGGAGGTGCT TCTGCGGAG ACCGCGGAG CCGCGTGGC GAGCCGGGAG 480

70 GCGCGTAGGG GCGCTGAGAT GCGAGCGGT GCGCGGGGCC GCTTACCTGC ACCGCTTGCT 540

CCGAGCGCGG GGGTCCGCTT GCTAGGCTTG CGGAAAAGT OCTAGCGACA CTGCGCCGCG 600

GGGCGGGAGT TCGCCCGGGA GCGCGAGCCC GGTCCGGGAA GGCAGCCAGG CCGCGGGGCG 660

GGGCGGGAGT GTTTTGCAAT ATGTGCGGCT CCGCCCTGGC TTTTATAC GCTGCATTGG 720

TCTGCTGCA AAGGACCGG CGAGGTCCCG CCTGTTCT CTGCGCAGCC TGGGTGTTTT 780

75 CACTTGTCT TGGACTGGG CAAGGTGAAG ACAATAGATG TGCACTTCA AATGCAGCAT 840

CCTGTGCCAG GTGCTTGCG CTGGGTCCAG AATGTGATG GTGTGTTCA GAGGATTCA 900

TTTCAGGTG ATCAAGAGT GAACGTTGTG ATATTGTTTC CAATTATA AGCAAAGGCT 960

GCTCAGTTGA TTCAATAGAA TACCATCTG TGCACTTAT AATACCCACT GAAATGAAA 1020

TTAATACCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCGAAGCTA 1080

80 ATTTTATGCT GAAAGTTTCT CCTCTGAAGA AATATCCTGT GGATCTTAT TATCTGTGTT 1140

ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTTGGA AACGATTTAT 1200

CTAGAAAAAT GGCATTTTTC TCCCGTGAAT TTGCTCTTGG ATTGGCTCA TACGTTGATA 1260

AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATATATCA TGCACTGACT 1320

ACAATTATGA CTGATGCTCT CCGCATGGAT ACATCCATGT GCTGCTTTG ACAGAGAACA 1380

TCCTAGATT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440

5	AAGGAGGTTT	TGACGCCATG	CTTCAGGCAG	CTGTCTGTGA	AAGTCATATC	GGATGGCGAA	1500
	AAGAGGCTAA	AAGATTGCTG	CTGGTGATGA	CAGATCAGAC	GTCTCATCTC	GCTCTTGATA	1560
	GCAAAATTGGC	AGGCATAGTG	GTGCCCAATG	ACGGAAACTG	TCATCTGAAA	AACAACGTCT	1620
	ACGTCAAATC	GACAACCATG	GAACAACCCCT	CACCTAGGCCA	ACTTTCAGAG	AAATTAATAG	1680
	ACAACAACAT	TAATGTCATC	TTTGCACTTC	AAGGAAAACA	ATTTTCATGG	TATAAGGATC	1740
	TTCTACCCCT	CTTGCCAGGC	ACCATTGCTG	GTGAAATAGA	ATCAAAGGCT	GCAAACCTCA	1800
	ATAATTGCTG	AGTGGAGGCC	TATCAGAAAGC	TCATTTCAGA	AGTGAAAGTT	CAGGTGGAAA	1860
	ACCAGGTACA	AGGCATCTAT	TTTAACATTA	CGCCCATCTG	TCCAGATGGG	TCCAGAAAGC	1920
	CAGGCATGGA	AGGATGCAGA	AACGTGACGA	GCAATGATGA	AGTTCTTTTC	AATGTAACAG	1980
10	TTACAATGAA	AAAATGTGAT	GTACACAGGAG	GAAAAAACA	TGCAATAATC	AAACCTATTG	2040
	GTTTTAATGA	AACCGCTAAA	ATTTCATATC	ACAGAAACTG	CAGCTGTGAG	TGTGAGGACA	2100
	ACAGAGGACC	TAAAGGAAAG	TGTGTAGATG	AAACTTTTCT	AGATTCCAAG	TGTTTCCAGT	2160
	GTGATGAGAA	TAAATGTCAT	TTTGATGAAG	ATCAGTTTTC	TTCTGAGAGT	TGCAAGTCAC	2220
	ACAAGGATCA	GCTTGTTTGC	AGTGGTCCAG	GAGTTTGTGT	TTGTGGGAAA	TGTTTCATGTC	2280
15	ACAAATTTAA	GCTTGGAAAA	GTGTATGGAA	AATACTGTGA	AAAGGATGAC	TTTTCTTGTC	2340
	CATATCACC	TGGAATCTG	TGTGCTGGGC	ATGGAGAGTG	TGAAGCAGGC	AGATGCCAAT	2400
	GCTTCAGTGG	CTGGGAAGGT	GATCGATGCC	AGTGCCCTTC	AGCAGCAGCC	CAGCACTGTG	2460
	TCAATTCAAA	GGGCCAAGTG	TGCAGTGGAA	GAGGCACTGT	TGTGTGTGGA	AGGTGTGAGT	2520
	GCACCGATCC	CAGGAGCATC	GGCCGCTTCT	GTGAACACTG	CCCCACCTGT	TATACAGCCT	2580
20	GCAAGGAAAA	CTGGAATTGT	ATGCAATGCC	TTCACTCTCA	CAATTGTGCT	CAGGCTATAC	2640
	TTGATCAGTG	CAAAACCTCA	TGTGCTCTCA	TGGAACAACA	GCATTATGTC	GACCAAACTT	2700
	CAGAATGTTT	CTCCAGCCCA	AGCTACTTGA	GAATATTTTT	CATCATTTTC	ATAGTTACAT	2760
	TCTTGATTGG	GTTCCTTAAA	GTCCCTGATCA	TTAGACAGGT	GATACTACAA	TGGAATAGTA	2820
25	ATAAAATTAA	GTCTCATCAT	GATTACAGAG	TGTCAGCCTC	AAAAAAGGAT	AAGTTGATTC	2880
	TGCAAAAGTGT	TTGCACAAGA	GCAGTCACCT	ACCGACGTGA	GAAGCCTGAA	GAATAAAAAA	2940
	TGGATATCAG	CAAAATTAAT	GCTCATGAAA	CTTTCAGGTG	CAACTTCTAA	AAAAAGATTT	3000
	TTAAACACTT	AATGGGAAAC	TGGAATTTGT	AATAATTGCT	CCTAAAGATT	ATAATTTTAA	3060
	AAGTCACAGG	AGGAGACAAA	TTGCTCAOGG	TCATGCCAGT	TGCTGGTTGT	ACACTCGAAC	3120
30	GAAGACTGAC	AAGTATCCTC	ATCATGATGT	GACTCACATA	GCTGCTGACT	TTTTCAGAGA	3180
	AAAATGTGTC	TTACTACTGT	TTGAGACTAG	TGTGTTGTA	GCACITTTACT	GTAATATATA	3240
	ACTTATTTAG	ATCAGCATAG	AATGTAGATC	CTCTGAAGAG	CACCTGATTAC	ACTTTACAGG	3300
	TACCTGTTAT	CCCTACGCTT	CCCAGAGAGA	ACAATGCTGT	GAGAGAGTTT	AGCATTGTGT	3360
	CACCTACAAGG	GTACAGTAAT	CCCTGCACCTG	GACATGTGAG	GAATAAATA	ATCTGGCAAG	3420
35	TATATTCTAA	GGTGTCCAAA	CACCTCAACA	GTGTGTTGTT	GAATAGACAA	GAACAGCTAG	3480
	ATGAATTAAT	GATTGTGTTT	TCACCTTTTC	AAGAGGTGAA	CAGATACAA	CTTAATCTTA	3540
	AAAGATTATT	GCTTTTAA	GTGTGTAGTT	TTATGCATGT	GTGTTTATGG	TTTGCTTATT	3600
	TTTGCAAGAT	GGATACTAAT	TCCAGCATTC	TCTCTCTTTT	GCCTTTATGT	TTTGTTTTCT	3660
	TTTTTACAGG	ATAAGTTTAT	GTATGTACCA	GATGACTGGA	TTAATTAAGT	GCTAAGTTAC	3720
40	TACTGCCATA	AAAAACTAAT	AATACAATGT	CACCTTTATCA	GAATACTAGT	TTTAAAGCT	3780
	GAATGTAA						

A107 Protein sequence:

45	Gene name:	Integrin, beta 8
	Unigene number:	Hs.52620
	Probeset Accession #:	AA479726
	Protein Accession #:	NP_002205.1
	Signal sequence:	1-39
50	Transmembrane domains:	682-704
	BGF domain:	552-584
	INB domain:	54-469
	Cellular Localization:	plasma membrane

55	1	11	21	31	41	51	
	MCQSALAFFT	AAFVCLQNDR	RGFASFLWAA	WVPSLVGLG	QGEDNRCASS	NAASCARCLA	60
60	LGPECGWCQV	EDFISGGSRS	ERCDIVSNLI	SKGCSVDSIE	YPSVHVIIPT	ENEINTQVTP	120
	GEVSIQLRPG	AEANFMLKVR	PLKKYPVDLY	YLVVDSASMH	NNIEKLNSVG	NDLSRKMAFP	180
	SRDFRLGFGS	YVDKTVSPYI	SIHPERIHNQ	CSDYNLDCMP	PHGYIHVLSL	TENITEFEKA	240
	VHRKQISGNI	DTPEGGFDAM	LQAAVCESHI	GWRKEARRLL	LVMTDQTSHL	ALDSKLAGIV	300
	VPNDGNCHLK	NNVYVKSTTM	EHPSLQQLSE	KLIDNNINVI	FAVQKQKPHW	YKDLLPLLP	360
65	TIAGEIESKA	ANLNLVVEA	YQKLISEVKV	QVENQVQGIY	FNITAICPDG	SRKPGMEGCR	420
	NVTNDEVLFL	NVTVTMKKCD	VTGGKNYAI	KPIGFNETAK	IIHNRNCSQ	CEDNRGPRGK	480
	CVDETFLDSK	CFQCDENKCH	FDQDQSSSES	CKSHKQPVPC	SGRGVCVCGK	CSCHKIKLKG	540
	VYGYKCEKDD	FSCPYHHGNL	CAGHGECEAG	RQCFPSGNEG	DRQCPSAAA	QHCVNSKGQV	600
	CSGRGTCVCG	RCECTDPRSI	GRFCEHCPTC	YTACKENWNC	MQCLHFNLS	QAILDQCKTS	660
70	CALMEQOHYV	DQTSECFSSP	SYLRIFFIIF	IVTFILIGLLK	VLIRQVILQ	WNSNKKSSS	720
	DYRVASASKD	KLILQSVCTR	AVTYRREKPE	EIKMDISKLN	AHETPRCNF		

A108 DNA sequence

75	Gene name:	ESTs
	Unigene number:	Hs.128899
	Probeset Accession #:	AA983251
	Nucleic Acid Accession #:	AA983251
	Coding sequence:	1-1749 (underlined sequences correspond to start and stop codons)

80	1	11	21	31	41	51	
	ATGCTGTCTG	GCTTCTTGAT	GAGTCCCACT	ACCCAGCACA	GAGCACAGTA	CACCTCCCGGA	60
	GGAAAGAAAC	TTCCGTGGGA	GGCTTCCATC	GGTGCACACA	CCTCCGAGGG	GCGAGGCAGC	120
	GACCGGAGAG	GGGAGAGCCG	GCGGAGGCT	GCGGGGCTCC	TGTGGGACCG	CGCTGCAGCC	180
	GGGGAGGCGG	AGAAGGGGAA	CCGGGGCGAG	CCGCCGCCT	GGATCCGCGC	CCAGCAGCAG	240

5	CGCGGGCCGC	CGCCAGCTGG	GCAGGCTCCC	GGGACTGCGG	CTGGGGGCGC	GCAGGACCCCT	300
	CGCCTGCGTC	CTGGAGCTTC	CGGGGGGAGG	GTCCGGTTGC	CAGTGAAACC	TCCAGAGGCT	360
	TCCGAGCGAC	AGCCCCGGGG	GCCTTCTGAC	TGCATCCOGA	GATTTCATC	AGCGAGTGCA	420
	ACTCATAAAG	CAGTCCCTAA	GGGACCCGGG	CCACCGGCTG	AGGACGGGGA	TGGCTTAGGA	480
	GCTCCTGGAC	CTAGGGCCCG	GGTGGTGGC	CTCCTGGGCG	TGCGGCGAGA	GGGGAGTGGC	540
	CGCGCGGAA	AGCGCGCGG	GACAGTCAGT	GACGAGGCC	GGGGTGGCC	GGGGCCACGA	600
	CTTCTCGGAG	ACGCTCTGCG	GCTCTCTGGA	GACGCGCTGT	CGCGGCCAG	GGTGGTGCCA	660
	TGTTGGGGCG	TGCGCGCTCG	TCCGTCTCT	CATCCTGGAA	CGCGGCTTGG	CTCCTGCAGC	720
10	TGCTGCTGGC	TGCGCTGCTG	GCGCGGGGG	CGAGGGGCCA	GCGGCGAGTA	CTGCCACGGC	780
	TGGCTGGACG	CGCAGGGCGT	CTGGCGCATC	GGCTTCCAGT	GTCCGAGCG	CTTCGACGGC	840
	GGGACGCGCA	CCATCTGCTG	CGGCGCTGCG	GCCTTGGCGT	ACTGCTGCTC	CAGCGCCGAG	900
	GCGCGCCTGG	ACCAGGGCGG	CTGCGACAAT	GACGCGCAGC	AGGGCGCTGG	CGAGCCTGGC	960
	CGGGCGGACA	AAGACGGGCC	CGGACGGCTC	GGCAGGGCTT	CATGCTTAG	GGGTACCCAA	1020
15	GGAGACGGCG	AGGGTGCGCC	CCCACCCGTG	AGGGCTTGGC	AGCGGTGCTC	CCCTGAAGGC	1080
	TCCCGGAAAG	GAAGGCAGCT	CCTCAGGGCT	TTCCCGGGGC	TGCTGCCCGG	TGCCAGACGC	1140
	CGCGGATTCC	CATCTTCTCC	ACGCGCGCGC	CCCTCTCCCC	TGCAGCGGCC	CGCCTTGCCC	1200
	ATCTACGTGC	CGTTCTCTCAT	TGTTGGCTCC	GTGTTTGTGG	CCTTATCAT	CTTGGGGTCC	1260
	CTGGTGGCAG	CTGTGTGCTG	CAGATGTCTC	CGGCCTAAGC	AGGATCCCCA	GCAGAGCCGA	1320
20	GCCCCAGGGG	GTAACCGCTT	GATGGAGACC	ATCCCATGTA	TCCCCAGTGC	CAGCACTCTC	1380
	CGGGGGTGGT	CCTCAGCGCA	GTCCAGCACA	GCTGCCAGTT	CCAGCTCCAG	CGCCAACTCC	1440
	GGGGCCCCGG	CGCCCCCAAC	AAGGTACAG	ACCAACTGTT	GCTTGCCTGA	AGGGACCATG	1500
	AACAACGGTG	ATGTCAACAT	GCCACGGAAT	TTCTCTGTGC	TGAACGTGTA	GCAGGCCACG	1560
	CAGATTGTGC	CACATCAAGG	GCAGTATCTG	CATCCCCCAT	ACGTGGGGTA	CACGGTGCAG	1620
25	CACGACTCTG	TGCCCCATGAC	AGCTGTGCCA	CCTTTTCATG	ACGGCTTGA	GCCTGGCTAC	1680
	AGGCAGATTG	AGTCCCCCTT	CCCTCACACC	AACAGTGAAC	AGAAGATGTA	CCGAGCGGTG	1740
	ACTGTATTAAC	CGAGAGTCA	TGGTGGGTTT	CTTTACTGAA	GGGAGACGAA	GGCAGGGGTG	1800
	GATTCTCGAG	TGGGAAGTCC	GCACATGTGG	GTGGTAITTA	TGGCAGGATT	CCTTTGGATG	1860
	GCTTCATTTC	CCCCCAGACT	GTATGAAAAC	ATCTCCGAAT	TAGCATTTCT	GGATATGTTT	1920
30	CATCCAGGGT	ATCATTTGAT	TATGATGGAA	AACCGGCTCT	AGCTGGAGAT	GACTGTGATG	1980
	TGCTGATGG	GTGTATAAACA	AATGCTTGAG	TCCGAAGTGC	CCTTGAGATA	TGGTTGACGA	2040
	AAGAATTTTA	TAAACGTGATA	AATTAAGGAT	TTTTATTATG	TGTTATTAT	TATTTCTTTT	2100
	TGTTGTGTTGA	CTGCACAGGA	TCAAAATGCC	TGTTATCTCC	CTTTACTGG	GACTTTTTTT	2160
	TTTTTTTTTT	TTTTTTTTTA	TCAGACAGGG	TCTTGCTCTG	TGCCCCAGGC	TGGAGTGCAG	2220
35	TGTTGGGATC	TGCGCTCACT	GCAACTTCAG	CCTCCTGGAT	TCAGGCAACA	CTCCTGCTCT	2280
	AGCTCCCAAC	GTGGCTGGGA	TTACAGGTGC	CTGCCCCCAT	GGCTAATTTT	TGTTATTTTT	2340
	TGTAGAGATG	GGGTTTCACC	ATGTTGGCTG	GGCTGGTCTC	ACTCTCTGTA	CCTCAAGCAA	2400
	TCGSCCTGTC	TCAGCCTCCC	AAAGTGCTGG	GATTACAGGC	GTGAGCCACC	GCCCCAGGCC	2460
	TGAGCCTTTT	TTTTTTTCTA	ATGCATCCAA	GGTTAAGGGG	AAGACGCAAA	TAACAGGACT	2520
40	ATTTCTAAAG	GAAACCTGTT	TGAACTCTGT	GAGATCAGTC	ATCAGTCTCA	GTATTCCACA	2580
	GGCACACCTT	AAITTTCAITG	TAAAAAGATA	TATATATTTT	GTCTATTTTT	GTGCTTTTGG	2640
	GGGCTATTTT	TGTCCTTTTT	TACCTTATGT	AGAGATCTTA	TTACAAAGTG	ATTTTCTACA	2700
	TTAAAAAGAG	ACTGAAATAA	ATTGTATAGT	TACTTAACTA	ATGAAGACAT	TTGAGAACTC	2760
	TGGGATGATT	TGAATCTTGA	AGTAGTAGGT	GGTATAGTCA	TAAACCAATT	CATCCCCCTC	2820
45	TTGATTGTAT	CTTAATTTTC	TGGCTTTAAG	GTGACATCTG	AGAGGTAATG	CATCTTTTTT	2880
	TATATTGAAA	TCATAAACTA	TCACCGCTG	CTTCTCTGAG	TTACTTTTAA	TTTTGCCTTG	2940
	TGGTTATGGT	TTGGCGTTTC	CTTCTGTTTG	GTTTTCAGAG	CCCCATGTCT	ATATAGTCTT	3000
	GAGTGCAAGT	AATTACTATA	CTGTGAAATG	AAGATCAGTA	TTTCTGCTTA	GATCTGATAA	3060
	AAAAATTTAT	TTTCTTTAGT	TATAAAAAAT	CAAGAAATG	TGTTACAAAG	ATACTTAGTA	3120
50	TAGCTCCTCA	GCCATTAACCT	GAGACTTGGG	ATGAAATTTA	AACAGATAC	GATTTACTTT	3180
	GCAGATCATA	AGGCTTTTTA	TACTCTTGT	ATCAAAATGG	CTTATTTTTC	AGGCACTAAG	3240
	GATTGTTAAG	AGAAAAGCTT	TTCAACGAAG	GATTGCTTTT	CTTCTCCAC	ACTGTTCTTG	3300
	ATTTCTCTCT	TCPTTCAGGC	CTCAACAGGC	ACTGTATCTA	TTGCCAATGT	TCCAAATAT	3360
	CAAAATCARR	RGPSGEYCHG	WLDAGQVWRI	GFQCFERFDG	GDATICOGSC	ALRYCCSSAE	3420
55	ATGTGCAAGT	ACATTTCCAA	CTGCTAGCAC	AACCAATATT	TGTAATTAAT	ACAAATCGCT	3480
	GTATGATATG	GTCTTCTACA	CATTTATGTC	TATAGATATC	TATGATCAT	CTTCTATTC	3540
	TGTTTCTAGA	CTGAATAATG	TAAACCAAGT	GTTGGCAATT	GATATCATCA	ATGATACTCA	3600
	TTTTTTAATA	ACCAAGGCA	GGGAAAAATC	ATTTTACTTA	TTAATAAATA	TTTTATGATG	3660
60	TGAAAAAAA	AAAAAAA	AAAAAAA				

A109 Protein sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular Localization: not determined

70	1	11	21	31	41	51	
	MLSGFLMSPS	TOHRAQYTPG	GKKLPWEASI	GAHTRSRGRS	DRERESRPEA	AGLLWDRAAA	60
	GEAEKGNRGE	PPAWIRAQQQ	FRPPFPAGQAP	GTAAGGAQDP	RLRPGRSRGR	VRFPVKPPEA	120
75	SGRQRPSPSD	CIPRFPSSASA	THKAVPKGTG	PPAEDGDGLG	APGPRARRRR	LLGVAAEGSG	180
	PRGKRRTVS	DEARGSPGPR	LLGDRPALSG	DALSAPRVVP	CGALAAARPS	HPGTPLRSCS	240
	CCWLRCWRRG	RGPSGEYCHG	WLDAGQVWRI	GFQCFERFDG	GDATICOGSC	ALRYCCSSAE	300
	ARLDQGGCND	DRQQGAGEPG	RADKDGPRRL	GRASCLRGTO	GDGEGAPPVV	RAWQRCSPEG	360
	SPKGRQLLRA	PPGLLPARRR	RGFPSSPRGG	PSPLQRPALP	IYVPLIVGS	VFVAFIILGS	420
80	LVAACCCRCL	RPKQDPQQR	APGGNRLMET	IPMIPSASTS	RGSSSRQSST	AASSSSSANS	480
	GARAPPTRSQ	TNCCLPBEGTH	BNVYVNMPTN	FSVLNCCQAT	QIVPHQGGYL	HPFYVGYTVQ	540
	HDSVPMTAVP	PFMDGLQPGY	RQIQSPFPHT	NSEQNMYPV	TV		

A110 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JB0350 Anterior gradient-2 [H.sapiens]

Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

5

```

1      11      21      31      41      51
|      |      |      |      |      |
10 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60
   CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGCTCACAG TTTCTTCCAA CCTTGCCATT 120
   GCAATAAAAA AGGAAAAGAG GCCTCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
   ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTATGCTC AAAAAAGTAA GAAGCCATTA 240
   ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
   CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
   GAAACCACCTG ATAAGAATT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
   GACCCCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
   TATGAGCCTC GGGATTTACC CCTATTGATA GAAAAACATG AGAAAGCATT AAGACTTATT 540
   CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTAT 600
   GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
20 TTACTATTTA GTTTTITTTAA TGIGTTTGCA ATAGTCTTAT TAAAAATAAT GTTTTITTTAA 720
   TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

```

25 All1 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

30

```

35 1      11      21      31      41      51
   |      |      |      |      |      |
   MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEB GLFYAQKSKK 60
   PLMVIHLED CQYSQALKKV PAQNBEIQEM AQNKFIIMNL MHETTDKNLS PDGQYVPRIM 120
   FVDFPSLTVA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

```

40 All12 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

45

```

1      11      21      31      41      51
|      |      |      |      |      |
50 ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TGGATGTCAA ACCCTGCGC 60
   AAAACCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
   CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCTCATCA AGGTGATTCT GGATAAATAC 180
   TACTTCTCT GGGGCGAGCC TCTCCACTTC ATCCGAGGA AGCAGCTGTG TGACGGAGAG 240
   CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGCGCT 300
   GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTGGGCCACA 360
   GGGAACTGGT TCTCTGCTG TTTCGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
   AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
   GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTGCGATGCG GAACTCAAGT 540
   GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
   AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
   AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGAGCC CCACTGGGTC 720
   CTCACGGCAG CCACTGCTT CAGGAAACAT ACOGATGTGT TCAACTGGAA GGTGCGGGCA 780
   GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
   TTCAACCCCA TGTACCCCAA AGACAATGAC ATGCGCCTCA TGAAGCTGCA GTTCCCACTC 900
   ACTTCTCTAG GCACAGTCAG GOCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
   GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
   GACATACGTC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
   GGTACCAGG GGGAAAGTCA CAGAAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG 1140
   GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
70 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCGAGG AGTATACACC 1260
   AAGGTCTCAG CTAATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

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75 All13 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLa domain: 54-94
 Tryp_SPC domain: 204-429
 Cellular Localization: plasma membrane/ER

80

1	11	21	31	41	51	
MLQDPDSQDP	LNSLDVKPLR	KPRIPMETFR	KVGIPILIAL	LSLASIIIVV	VLIKVILDKY	60
YFLCGQPLHF	IPRKQLCDGE	LDCPLGEDEE	HCVKSFPEGP	AVAVRLSKDR	STLQVLDSAT	120
GNWFSACFDN	FTEALAEATC	RQMGYSSKPT	FRABEIGPDQ	DLDDVEITEN	SQSLMRMNSS	180
GPCLSGSLVS	LHCLACGKSL	KTPRVVGGEE	ASVDSWPNQV	SIQYDKQHVC	GGSIIDPHWV	240
LTAAHCFRKH	TDVFNWVKRA	GSDKLGSPFS	LAVAKIIIE	FNPMYFKDND	IALMKLQFPL	300
TFSGTVRPIC	LPFFDEELTP	ATPLWIIIGW	FTKQNGGKMS	DILLQASVQV	IDSTRCNADD	360
AYQGEVTEIM	MCAGIEGGV	DTCQGDSSGP	LMYQSDQHWV	VGIVSWGYGC	GGPSTPGVYT	420
KVSAYLWNWY	NVWKAEI					

A114 DNA SEQUENCE:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Nucleic Acid Accession #: NM_003318
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
GGAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACCT	TTGTTGGCCA	GGCTGGAGTG	60
CAATGGCACA	ATCTCAGCCT	ACTGCAACCT	CGCCTCCCG	GGTCAAGGCG	ATTCTCCTGC	120
CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACTAATTT	180
CTTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	TGAACCTCTG	240
ACCTCAGGTG	ATCCACTTGC	CTTGCCCTCC	CAAAGTGCTA	GGATTACAGC	CGTGAACCTG	300
TGCTCGGTCT	ATTCCTTTTT	TGTTGTTGGA	TTTTTGAAAC	AGGGTCTCCC	TTGGTCCGCC	360
AGGCTGGAGT	GCAGTGGTGC	GATCTTGGCT	CACATATAAC	TCCACCTCCT	GGTTTCAAGT	420
GATCCTCCCA	CTTTAGCCTC	CTGAGTAGCT	GTGATTACAG	CGTGCACCA	CCACACCCGG	480
CTAATTTTTG	TATTTTTTAT	AGAGACAGGG	TTTCAACATG	TTGGCCAGGC	TGTTCTCAAA	540
CTCCTGGACT	CAAGGGATCC	GCTTGCCTCC	ACTTCCCAAA	GTCCCGAGAT	TACAGGTGTG	600
AGTCACCATG	CCGACCTTA	TAATTCCTAA	GTCAATTTTT	CTGGTCCATT	TCTTCTCTAG	660
GGTCTCTACA	ACAAATCTGC	ATTAGGCGGT	ACAATTAATC	TAACTTCAT	GATTACACAA	720
AGGAAGATGA	AGTTAGTTCAT	GATTTAGAAA	GGGGAAGTAG	TAAGCCCACT	GCACACTCCT	780
GGATGATGAT	CCTAATATCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
TTTGGTTTAA	ATTAATATAT	TAAATATCTA	AAAACATTTT	TGGATACATT	GTTGATGTGA	900
ATGTAAGACT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCATCTTTTC	ATTTCCCCAG	960
TGCAGTTTTT	TGTAGAAATG	GAATCCGAGG	ATTTAAGTGG	CAGAGAATTG	ACAATTGTAT	1020
CCATAATGAA	CAAAGTGAGA	GACATTAAAA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
AACTAAGCTT	GAATAAAAT	TCTGCTGATA	CTACAGATAA	CTCGGAAACT	GTTAAACAAA	1140
TTATGATGAT	GGCAAAACAC	CCAGAGGACT	GGTTGAGTTT	GTTGCTCAAA	CTAGAGAAAA	1200
ACAGTGTTC	GCTAAGTGAT	GCTCTTTTAA	ATAAATTGAT	TGGTGGTTAC	AGTCAAGCAA	1260
TTGAAGCGCT	TCCCCAGAT	AAATATGGCC	AAATGAGAG	TTTGTCTAGA	ATTCAAGTGA	1320
GATTTGCTCA	ATTAAAGCT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAAATGG	1380
CCAGAGCAAA	CTGCAAGAAA	TTTGTCTTTG	TTTATATATC	TTTTGCACAA	TTTGAAGTGT	1440
CACAAGGTAA	TGTCAAAAAA	AGTAAACAAC	TTCTTCRAAA	AGCTGTAGAA	CGTGAGCAG	1500
TACCACCTAGA	AATGCTGGAA	ATTGCCCTGC	GGAATTTAAA	CCTCCAAAAA	AAGCAGCTGC	1560
TTTCAGAGGA	GGAAAGAAAG	AATTTATCAG	CATCTACGGT	ATTAACCTGC	CAAGAAATCAT	1620
TTTCCGGTTC	ACTTGGGCAT	TTACAGAATA	GGAAACAAC	TGTGTATTCC	AGAGGACAGA	1680
CTACTAAAGC	CAGGTTTTTA	TATGAGAGGA	ACATGCCACC	ACAAGATGCA	GAAATAGGTT	1740
ACCGGAATTC	ATTGAGACAA	ACTAACAAAA	CTAACACATC	ATGCCCATTT	GGAGAGTCC	1800
CAGTTAACTT	TCTAAATAGC	CCAGATTGTG	ATGTGAAGAC	AGATGATTCA	GTTGTACCTT	1860
GTTTTATGAA	AAGACAAACC	TCTAGATCAG	AATGCCGAGA	TTTGGTTGTG	CCTGGATCTA	1920
AACCAAGTGG	AAATGATTCC	TGTGAATTAA	GAAATTTAAA	GTCTGTTCAA	AATAGTCATT	1980
TCAAGGAACC	TCTGGTGTCA	GATGAAAAGA	GTTCTGAACT	TATTATTACT	GATTCAATAA	2040
CCCTGAAGAA	TAAACCGGAA	TCAAGTCTTC	TAGCTAAATT	AGAAGAAACT	AAAGAGTATC	2100
AAGAACCAGA	GGTTCCAGAG	AGTAAACCAGA	AACAGTGGCA	AGCTAAGAGA	AAGTCAGAGT	2160
GTATTAAACA	GAATCCTGCT	GCACTCTCAA	ATCACTGGCA	GATTCCGGAG	TTAGCCCGAA	2220
AAGTTAATAC	AGAGCAGAAA	CATACCCTT	TTGAGCAACC	TGCTTTTCCA	GTTTCAAAAC	2280
AGTCACCACC	AATATCAACA	TCTAAATGGT	TTGACCCAAA	ATCTATTGTT	AAGACACCAA	2340
GCAGCAATAC	CTTGGATGAT	TACATGAGCT	GTTTTAGAAC	TCCAGTTGTA	AAGAATGACT	2400
TTCCACCTGC	TGTTCAGTTG	TCAACACCTT	ATGGCCAACC	TGCTGTGTTT	CAGCAGCAAC	2460
AGCATCAAA	ACTTGCCACT	CCACTTCAAA	ATTTACAGGT	TTTAGCATCT	TCTTCAGCAA	2520
ATGAATGCA	TTCGGTTAAA	GGAAGAAATT	ATTCATATT	AAAGCAGATA	GGAAGTGGAG	2580
GTTCAAGCAA	GGTATTTTCA	GTGTTAATAT	AAAAGAAACA	GATATATGCT	ATAAAATATG	2640
TGAATTAAGA	AGAAGCAGAT	AACCAAACTC	TTGATAGTTA	COGGAACGAA	ATAGCTTATT	2700
TGAATAAACT	ACAAACAAC	AGTGATAAGA	TCATCCGACT	TTATGATTAT	GAAATCACGG	2760
ACCAATACAT	CTACATGGTA	ATGGAGTGTG	GAAATATTGA	TCTTAATAGT	TGGCTTAAAA	2820
AGAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTTACTG	GAAAAATATG	TTAGAGGCGA	2880
TTACACAAT	CCATCAACAT	GGCATTTGTT	ACAGTGATCT	TAAACCAAGT	AACTTTCTGA	2940
TAGTTGATGG	AATGCTAAAG	CTAATTGATT	TTGGGATGTC	AAACCAATG	CAACCAAGTA	3000
CAACAAGTGT	TGTTAAAGAT	TCTCAGTTG	GCACGTTAA	TTATATGCCA	CCAGAAGCAA	3060
TCAAAGATAT	GTCTTCCTCC	AGAGAGAAAT	GGAATCTTAA	GTCAAAGATA	AGCCCCAAAA	3120
GTGATGTTTG	GTCTTTAGGA	TGTATTTTGT	ACTATATGAC	TTACGGGAAA	ACACCAATTTC	3180
AGCAGATAAT	TCTAAATTAC	ATGCCATAAT	TGATCTTAAT	CATGAAATTG		3240
AAITTCOCGA	TATTCAGAG	AAAGATCTTC	AAAGTGTGTT	AAAGTGTGTT	TTAAAAAGGG	3300
ACCCAAAAACA	GAGGATATCC	ATTCCTGAGC	TCTCGCTCA	TCCATATGTT	CAAAATCAAA	3360
CTCATCCAGT	TAACCAAAAT	GCCAGGGGAA	CCACTGAAGA	AATGAAATAT	GTCTTGGGCC	3420
AACTTGTGTT	TCTGAATTTCT	CCTAACTCCA	TTTTGAAAGC	TGCTAAAACT	TTATATGAAC	3480
ACTATAGTGG	TGGTGAAGAT	CATAATTCTT	CATCCTCCAA	GACTTTTGAA	AAAAAAGGG	3540
GAAAAAAATG	ATTTGCAAGT	ATTCGTAATG	TCAGATAGGA	GGTATAAAAT	ATATTGGACT	3600
GTTACTACTCT	TGAATCCCTG	TGGAATCTTA	CATTTGAAGA	CAACATCACT	CTGAAGTGTG	3660
ATCAGCAAAA	AAAATTCAGT	GAGATTATCT	TTAAAGAGAA	ACTGTAAAAA	TAGCAACAC	3720

TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAATCTAC 3780
 TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAACTTGG 3840
 TAAATAAAGT TTTGTGGCTA AATAGA

A115 Protein sequence:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Protein Accession #: NP_003309
 Signal sequence: none found
 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

1	11	21	31	41	51	
MNKVRDIKKN	PKNEDLTDEL	SLNKISADTT	DNSGTVNQIM	MMANNPEDWL	LLLLKLEKNS	60
VPLSDALLNK	LIGRYSQAIE	ALPPDKYQON	ESFARIQVRF	AELKAIQEPD	DARDYFQMAR	120
ANCKKFAFVH	ISPAQFELSQ	GNVKKSKQLL	QKAVERGAVP	LEMLEIALRN	LNLQKKQLLS	180
EEEKKRLSAS	TVLTAQESFS	GSLGHLQNRN	NSCDSRGQTT	KARPLYGENM	PPQDAEIGYR	240
NSLRQTNKTK	QSCPFGRVPV	NLLNSPDCDV	KTDDSVVPCF	MKRQTSRSEC	RDLVVPGSKP	300
SGNDSCELRN	LKSVQNSHPK	EPLVSEKSS	ELIITDSITL	KNKTESSLLA	KLEETKQYQE	360
PEVPESNQKQ	WQAKRKSECI	NQNPAASSNH	WQIPELARKV	NTEQKHTTPE	QPVFVSQKQS	420
PPISTSKWFD	PKSICKTPSS	NTLDDYMSCF	RTFVVKNDFP	PACQLSTPYG	QPACFQQQOH	480
QILATPLQNL	QVLASSANE	CISVKGRIS	ILKQIGSGGS	SKVFQVLNEK	KQIYAIFYVN	540
LEEADNQITLD	SYRNEIAYLN	KLQQHSKII	RLYDYEITDQ	YIYMVMCEGN	IDLNSWLKKK	600
KSIDPWERKS	YWKMLEAVH	TIHQHGIVHS	DLKPANFLIV	DGMLKLIDFG	IANQMOPDTT	660
SVVKDSQVGT	VNYMPPFAIK	DMSSSRENGK	SKSKISPKSD	VWSLGCILYY	MTYGRTPFPQ	720
IINQISKLHA	IIDFNHEIEF	PDIPEKDLQD	VLKCCLEKRP	KQRISTPELL	AHPYVQIQTH	780
PVNMMAKGT	EEMKYVLGQL	VGLNSPNSIL	KAATLYEHY	SGGESHNSSS	SKTFEKKRCK	840
K						

OVARIAN

A116 DNA SEQUENCE

Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Nucleic Acid Accession #: NM_001508
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
<u>ATGGCTTCAC</u>	CCAGCCTCCC	GGGCAGTGAC	TGCTCCCAAA	TCATTGATCA	CAGTCATGTC	60
CCGAGTTTGG	AGGTGGCCAC	CTGGATCAAA	ATCACCCCTTA	TTCTGGTGTGA	CCTGATCATC	120
TTGGTGTATGG	GCCTTCTGGG	GAACAGCGCC	ACCATTGGGG	TCACCCAGGT	GCTGCAGAAG	180
AAAGGATACT	TGCAGAAGGA	GGTGACAGAC	CACATGGTGA	GTTTGGCTTG	CTCGGACATC	240
TTGGTGTTC	TCATCGGCAT	GCCCATGGAG	TTCTACAGCA	TCATCTGGAA	TCCCTTGACC	300
ACGTCCAGCT	ACACCTGTCT	CTGCAAGCTG	CACACTTTCC	TCTTCGAGGC	CTGCAGCTAC	360
GCTACGCTGC	TGCACGTGCT	GACACTCAGC	TTTGAGCGCT	ACATCGCCAT	CTGTCACCCC	420
TTCAGGTACA	AGGCTGTGTC	GGGACCTTGC	CAGGTGAAGC	TGCTGATTGG	CTTCGTCTGG	480
GTCACCTCOG	CCCTGGTGGC	ACTGCCCTTG	CTGTTTGCCA	TGGGTACTGA	GTACCCCTTG	540
GTGAAGCTGC	CCAGCCACCG	GGGTCTCACT	TGCAACCGCT	CCAGCACCGG	CCACCACGAG	600
CAGCCCGAGA	CCTCCAAATAT	GTCCATCTGT	ACCAACCTCT	CCAGCCGCTG	GACCGTGTTC	660
CAGTCCAGCA	TCTTCGGCGC	CTTCGTGGTC	TACCTGTGGG	TCTGCTCTC	CGTAGCCTTC	720
ATGTGCTGGA	ACATGATGCA	GGTGCTCATG	AAAAGCCAGA	AGGGCTCGCT	GGCCGGGGGC	780
ACGCGCCTTC	CGCAGCTGAG	GAAAGTCGAG	AGCGAAGAGA	GCAGGACCGC	CAGGAGGCAG	840
ACCATCATCT	TCTTCGAGCT	GATTGTGTGT	ACATTTGGCG	TATGCTGGAT	GCCCAACGAG	900
ATTGCGAGGA	TCATGGCTGC	GGCCAAACCC	AAGCACGACT	GGACGAGGTC	CTACTTCGGG	960
GCGTACATGA	TCCTCTCTCC	CTTCGCGGAG	ACGTTTTTCT	ACCTCAGCTC	GGTCATCAAC	1020
CGCTCCTGT	ACACGGTGTCT	CTCGCAGCAG	TTTCGGCGGG	TGTTGCTGCA	GGTGTCTGTC	1080
TGCGCGCTGT	CGCTGCAGCA	CGCCAACCA	GAGAAGCGCC	TGCGGTGACA	TGCGCACTCC	1140
ACCACGACGA	GCGCCGCTT	TGTGCAGCGC	CGTTGTCTCT	TGCGTCCCG	GCGCCAGTCC	1200
TCTGCAAGGA	GAACGTAGAA	GATTTTCTTA	AGCACTTTTC	AGAGCGAGGC	CGAGCCCGAG	1260
TCTAAGTCCC	AGTCATTGAG	TCTCGAGTCA	CTAGAGCCCA	ACTCAGGCGC	GAAACCAGCC	1320
AATTCTGCTG	CAGAGAATGG	TTTTCAGGAG	CATGAAGTTT	<u>GA</u>		

A117 Protein sequence:

Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Protein Accession #: NM_001508, NP_001409
 Signal sequence: none found
 Pfam domains: 7tm_1 [72-172, 224-344]
 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
NASPSLPGSD	CSQIIDHSHV	PEFEVATWIK	ITLILVYLII	FVMGLLGNSA	TIRVTQVLQK	60

- 5 KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIWNPLT TSSYTLSCKL HTPLFEACSY 120
 ATLLHLVLTLS FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LPAMGTEYPL 180
 MCVNMMQVILT CNRSSTRHHE QPETSNNMSIC TNLSSRWTVF QSSIFGAPVV YLVVLLSVAF 240
 IRRIMAAAKP KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC 300
 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPO 360
 SKSQSLSLES LEPNSGAKPA NSAAENGFOE HEV 420
- 10 A118 DNA sequence
 Gene name: bone morphogenetic protein receptor IB (ALK-6)
 Unigene number: Hs.87223
 Probeset Accession #: AA250737
 Nucleic Acid Accession #: NM_001203
 Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

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 50

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1      11      21      31      41      51
|      |      |      |      |      |
CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGACGCGGGC AGTGC GGAGAG CCGCGGGCGCT 60
GAGGACGCGG GAGCGGGGAG CGCAGCGCGG GGGTGGAGTT CAGCCTACTC TTCTCTAGAT 120
GTGAAAGGAA AGGAAGATCA TTTCATGCCT TGTGTATAAA GGTTCAGACT TCTGCTGATT 180
CATAAACCAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
TGCCATAAGT GAGAAGCAAA CTTCTTGAT AACATGCTTT TGCGAAGTGC AGGAAATTA 300
AATGTGGGCA CCAAGAAAGA GGATGCTGAG AGTACAGCCC CCACCCCCCG TCCAAAGGTC 360
TTGCGTGTGA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGACGACA 420
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCCTGTG GGTCACTTCT 480
GGTTCCTTAG GACTAGAAGG CTCAGATTTT CAGTGTGCGG ACACCTCCAT TCCTCATCAA 540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCCCTACA 600
CTGCTCTCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660
ATATCTGTGA CTGTCTGTAG TTGCTCTTGG GTCCCTATCA TATTATTTTG TTAATCTCCG 720
TATAAAGAAC AAGAAACACG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC 780
ATTCTCTCTG GAGAAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAAGTGA 840
TCAGGCTCTC CTCTGCTGGT CCAAAGGACT ATAGCTAAGC AGATTCAGAT GGTGAAACAG 900
ATTGAAAAGG GTGCTATGAG GGAAGTTTGG ATGGGAAAGT GCGTGGGCGA AAAGGTAGCT 960
GTGAAAGTGT TCCTTACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGACA 1080
GGGTCTTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
TATCTGAAGT CCACCAACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200
AGTGGCTTAT GTCATTTTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260
CATCGAGATC TGAAAGATGA AAACATTTCT GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320
GACCTGGGCC TGGCTGTATA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
ACTCGAGTTG GCACCAAAACG CTATATGCCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA 1440
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500
GTGCTAGAGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC 1560
CTAGTCCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620
CGCCCTCAT TCCCAAACCG GTGGAGCAGT GATGAGTGTG TAAGGCAGAT GGGAAACTC 1680
ATGACAGAAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA 1740
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TAAGCATCCA CAGTACAAAG CTTGAACATC GTCTGCTTCC CAGTGGGTT CAGACCTCAC 1920
CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
TCTGTTTGTA GCGCGAGAAA COGTGGGTA ACTTGTTCAT GATATGATGC AT

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- 55 A119 Protein sequence
 Gene name: bone morphogenetic protein receptor IB (ALK-6)
 Unigene number: Hs.72472 / Hs.87223
 Probeset Accession #: AA250737 / U89326
 Protein Accession #: NP_001194
 Signal sequence: 1-13
 Transmembrane domains: 128-144
 PFAM domains: activin_receptor [30-111], protein kinase [204-491]
 Cellular Localization: plasma membrane

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 70
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1      11      21      31      41      51
|      |      |      |      |      |
MLLSRAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHCPE DSVNNICSTD GYCFTMIED 60
DSGLFVVTSQ CLGLEGSDFO CRDTPIPHQR RSIEOCTERN ECKDLHPTL PPLKNRDFVD 120
GPIHRRALLI SVTVCSLLLV LIILPCYPRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180
EQSQSSSGSG GLPLLVRTI AKQIQMVQKI GKGRYGEVWM GKWRGEKVAV KVFPTEBAS 240
WPRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
MLKLAYSSVS GLCHLETEIF STQKPAIAH RDLKSNILV KKNGTCCIA LGLAVKPID 360
TNEVDIPNT RVGTRKYMPP EVLDESINRN HPQSYIMADM YSPGLILWEV ARRCVSGGIV 420
EBYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMKLM TECWAHPAS 480
RLTALRVKKT LAKMESQDI KL

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- 80 A120 DNA SEQUENCE
 Gene name: LIV-1 protein, estrogen regulated
 Unigene number: Hs.79136
 Probeset Accession #: U41060
 Nucleic Acid Accession #: NM_012319.2
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

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CTCGTGCGCA ATTCCGACAG AGACCGCGTG TTCGCGCGCT GTAGAGATTT CTCGAAGACA 60
 CCACTGGGCC CGTGTGGAAAC CAAACCTGCG CGCGTGGCCG GGCGGTGGGA CAACGAGGCC 120
 GCGGAGACGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTGTGCTCTG ACCTTTTGCC 180
 TCTCTGTAC AAATCCCTTT CATGAACATA AAGCAGCTGC TTTCCCCAG ACCACTGAGA 240
 AAATTAAGTCC GAATTTGGGA TCTGGCATTG ATGTTGACTT GGCAATTTCC ACACGGCAAT 300
 ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTTCTTTGCA GTTGAAGGGT 360
 TCAGAAAATT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420
 ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480
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 CTGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCAGA CCATGACTCA GATAGTTTCA 600
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 GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAAACATG 720
 TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAATCTTTCC 780
 CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCAATC AAAGAGCCGG GTGAGCCGGC 840
 TGGCTGGTAG GAAACAAAT GAATCTGTGA GTGAGCCCG AAAAGGGCTT ATGTATTCCA 900
 GAAACACAA TGAATTCCT CAGGAGTGT TCAATGCATC AAAGCTACTG ACATCTCATG 960
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 TCAACCAAT TGATGCTAGA TCTTGTCTGA TTCAATCAAG TGAAGGAAG CCGTGAATCC 1080
 CTCCAAGAC CTATTCATTA CAATAGCTT GGGTTGGTGG TTTTATAGCC ATTTCCATCA 1140
 TCAGTTTCTT GTCTCTGCTG GGGTTTATCT TAGTGCTCTT CATGAATCCG GTGTTTTTCA 1200
 AATTTCTCTT GAGTTTCTTT GTGGCAGTGG CGTTTGGGAC TTTGAGTGGT GATGCTTTTT 1260
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 TTCACCAACA TCATGACTAC CATCATATTC TCCATCATCA CCACCAACAA AACCCACATC 1860
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 TTTTCAAGAA CTAACACAGT TATTCCTATA CTGGATTTTA GGTCTCTGAA GAAGTCTGCTG 2760
 TGTTTAGGAA TAAGAATGTG CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA 2820
 AGCAAGAGAA TAAAGGAGAA AAGAGAAGAA TCTGAGAATT GGGGAGGCAT AGATTCTTAT 2880
 AAAAATCACA AAATTTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAG TATAAAAGG 2940
 CAGAAATTAG AGAGTAGTAA TTCAATTAAC AITTTTGTCA AGATTATTTT CCGTAAAAAC 3000
 GTAGTAGACA CTCTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT 3060
 AAATATATT AATGAATTC AGCAATATAC ACTTGACCAA GAAATGGAA TTTCAAAATG 3120
 TCTGTCGGG TTATATACCA GATGAGTACA GTGAGTAGTT TATGATCAC CAGACTGGGT 3180
 TATTGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTCTGAGT ACCTGGTTTA 3240
 CAAATATTAT CAGAGTAGTAA AACTTTGATA TATATGAGGA TATTAAACT ACATAAGTA 3300
 TCATTTGATT CCAATCAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCATTTG 3360
 GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCGTCTCTGT GCATTCTCTA 3420
 GATGTTTCTT TTTTACAAA TAAATTCCTT ATATCAGCTT G

A121 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
 Unigene number: Hs.79136
 Protein Accession #: NP_036451
 Signal sequence: 1-21
 Pfam domain: Zip[591-743]
 Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745
 Cellular Localization: plasma membrane

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 75
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1 11 21 31 41 51
 MARKLSVILI LTFALSVTNP LHELKAAFP QTTEKISPFW ESGINVDLAI STRQYHLQQL 60
 FYRYGENNSL SVEGPKLLQ NIGIDKIKRI HIHHDHDSHS DHEHSDHER HSDHEHSDH 120
 EHSDDHDSHS HNHAAAGKN KRALCPDHD SDSSGKDPFN SQKGARHPE HASGRNRVKD 180
 SVSASEVTST VYNTVSEGT FLETITPRP GKLPFKDVSS STPPSVTSKS RVSRLAGRKT 240
 NESVSEPRRG FMYSRNTNEN PQECFNASKL LTHSGMGIQV PLNATEPNYL CPAIINQIDA 300
 RSLCLHTSEK KAIIPPKTYS LQIAWVGFP AISIISFLSL LGVILVPLMN RVFPKFLLSF 360
 LVALAVGTLG GDAFLHLPLH SHASHHSHS HEPPAMEMKR GLPFSHLSSQ NIEBSAYFDS 420
 TWKGLTALGG LYPMFLVEHV LTLIKQPKDK KKKQKKPEN DDDVEIKQL SKYESQLSTN 480
 EERKVDITDRT EGYLRADSQ PSHFDSQPPA VLESEVMIA HAHPEVYNE YVPRGCKNKC 540
 HSHFPHDQGT SDDLHSHHD YHHLHSHHS QNHHPHSHSQ RYSREELKDA GVATLAWMVI 600
 MGDGLNPFSD GLAIGAAFTS GLSSGLSTSV AVFCHLPHE LGDFAVLLKA GMTVKQAVLY 660
 NALSANLAYL GMATGFIGH YAEVNSWIF ALTAGLFMYV ALVDMVPEML HNDASDRGCS 720

RWGYFFLQNA GMLLGFGIML LISIFERKIV PRINF

5 A122 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

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CGCCCCCTGCC	GCGGTGCCTG	GCCTCCCTC	CCAGACTGCA	GGGACAGCAC	CCGGTAACTG	120
CGAGTGGAGC	GGAGGACCCG	AGCGGCTGAG	GAGAGAGGAG	GCGGCGGCTT	AGCTGCTACG	180
GGGTCCGGCC	GGCGCCCTCC	CGAGGGG3GC	TCAGGAGGAG	GAAGGAGGAC	CCGTGCGAGA	240
<u>ATGCTCTTCG</u>	<u>CCTGGAGCCT</u>	<u>TGCGCTCCCG</u>	<u>CTGCTGCTCT</u>	<u>CCTGGGTGGC</u>	<u>AGGTGGTTTC</u>	300
GGGAACGCGG	CCAGTGCAAG	GCATCACGGG	TTGTTAGCAT	CGGCAOGTCA	GCCTGGGGTC	360
TGTCACTATG	GAACTAAACT	GGCTGCTGTC	TACGGCTGGA	GAAGAAACAG	CAAGGGAGTC	420
TGTGAAGCTA	CATGCGAACC	TGGATGTAAG	TTTGGTGAGT	GCGTGGGACC	AAACAAATGC	480
AGATGCTTTC	CAGGATACAC	CGGAAAAACC	TGCAGTCAAG	ATGTGAATGA	GTGTGGAATG	540
AAACCCCGGC	CATGCCAACA	CAGATGTGTG	AATACACAG	GAAGCTACAA	GTGCTTTTGC	600
CTCAGTGCC	ACATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATG	660
ATAAATCTGC	AGTACAGCTG	TGAAGACACA	GAAGAAGGCG	CACAGTGCCT	GTGTCCATCC	720
TCAGGACTCC	GCCTGGCCCC	AAATGGAAGA	GACTGTCTAG	ATATTGATGA	ATGTGCCTCT	780
GGTAAAGTCA	TCTGTCCCTA	CAATCGAAGA	TGTGTGAACA	CATTGTGAAG	CTACTACTGC	840
AAATGTCACA	TTGGTTTCGA	ACTGCAATAT	ATCAGTGGAC	GATATGACTG	TATAGATATA	900
AATGAATGTA	CTATGGATAG	CCATACGTGC	AGCCACCATG	CCAATTGCTT	CAATACCCAA	960
GGGTCTTCA	AGTGTAAATG	CAAGCAGGGA	TATAAAGGCA	ATGGAATTCG	GTGTTCTGCT	1020
ATCCCTGAAA	ATTCTGTGAA	GGAAGTCTC	AGAGCACTG	GTACCATCAA	AGACAGATC	1080
AGAAAGTTGC	TTGCTCACAA	AAACAGCATG	AAAAAGAAGG	CAAAAATTAA	AAATGTTACC	1140
CCAGAACCCA	CCAGGACTCC	TACCCCTAAG	GTGAACTTGC	AGCCCTTCAA	CTATGAAGAG	1200
ATAGTTTCCA	GAGGCGGGAA	CTCTCATGGA	GGTAAAAAAG	GGAATGAAGA	GAAAATGAAA	1260
GAGGGCTTG	AGGATGAGAA	AAGAGAAGAG	AAAGCCCTGA	AGAATGACAT	AGAGGAGCGA	1320
AGCCTGCGAG	GAGATGTGTT	TTTCCCTAAG	GTGAATGAAG	CAGGTGAATT	CGGCTTGATT	1380
CTGGTCCAAA	GGAAGCGCGT	AACCTTCCAA	CTGGAACATA	AAGATTATAA	TATCTGGGTT	1440
GACTGCAGCT	TCAATCATGG	GATCTGTGAC	TGGAAACAGG	ATAGAGAAGA	TGATTTTGAC	1500
TGGAATCTCG	CTGATCAGAG	TAATGCTATT	GGCTTCTATA	TGGCAGTTCC	GGCCTTGGCA	1560
GGTCACAAGA	AAGACATTGG	CCGATTGAAA	CTTCTCTAC	CTGACCTGCA	ACCCCAAAGC	1620
AACCTCTGTT	TGCTCTTTGA	TTACCGGCTG	GCGGAGAGCA	AAGTCGGGAA	ACTTCGAGTG	1680
TTTGTGAAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAAGA	CCACGAGTGA	GGATGAAAAG	1740
TGGAAGACAG	GGAAATTCAC	GTTGTATCAA	GGAACGTATG	CTACCAAAG	CATCAITTTT	1800
GAAGCAGAAC	GTGGCAAGGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGTT	1860
TCAGGCTTAT	GTCCAGATAG	CCTTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
TTGACTTTGT	ATGTCAGTTC	CCTGGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCATT	1980
TTAGAATTAC	TAGCTGAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGCCCTT	2040
TCITGTATAA	GATATGCCAA	TATTTGCTTT	AAATATCATA	TCACGTATAT	TTCTCAGTCA	2100
TTTCTGAATC	TTTCCACATT	ATATTATATA	ATATGGAAAT	GTCACTTTAT	CTCCCTCTCT	2160
CAGTATATCT	GATTTGTATA	AGTAAGTTGA	TGAGCTTCTC	TCTACACACT	TTCTAGAAAA	2220
TAGAAAAAAA	AGCACAGAGA	AATGTTTAAC	TGTTTGACTC	TTATGATAC	TCTTGGAAC	2280
TATGACATCA	AAGATAGACT	TTTGCCTAAG	TGGCTTAGCT	GGGTCTTCA	TAGCCAAACT	2340
TGTATATTTA	AATTCCTTGT	AATAATAATA	TCCAAATCAT	CAAAAAAAA	AAAAAAA	

55 A123 Protein sequence:

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Protein Accession #: NP_056322.2
 Signal sequence: 1-21
 Transmembrane domains: none found
 MAM domain: 402-546
 EGF domain: 80-259
 Cellular Localization: secreted

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1	11	21	31	41	51	
MPLPWSLALP	LLLSVWAGGF	GNAASARHHG	LLASARQPGV	CHYGTKLACC	YGWRRNSKGV	60
CEATCEPGCK	FGECVGFNKC	RCFPGYTGKT	CSQDVNECGM	KRPQCQHRV	NTHGSYKFC	120
LSGHMLMADA	TCVNSRTCAM	INQYSCEDT	EEGPQCLCPG	SGLRLAPNGR	DCLDIDECAS	180
GKVICPYNRR	CVNTPGSYYC	KCHIGFELQY	ISGRYDCIDI	NECTMDSETC	SHHANCFTNQ	240
GSFKCKCKQG	YKGNGLRCSA	IPENSVKEVL	RAPGTIKDRI	KKLLAHNSM	KKAKIKNVT	300
PEPTTPTPK	VNLQPFNYEE	IVSRGGNSHG	GKKGNEEKMK	BGLEDEKREB	KALKNDIEER	360
SLRGDVFPFK	VNEAGFGLI	LVQRKALTSK	LEHKDLNISV	DCSPNHGICD	WKQDREDDFD	420
WNPADRDNAI	GFMVAVPALA	GHKDIDGLRK	LLLPDLQPGS	NFCLLPDYRL	AGDKVKGKLRV	480
FVKNSNNALA	WEKTTSEDEK	WTKGIQLYQ	GTDATEKSIIF	EAERGKGTG	EIAVDGVLLV	540
SGLCPSLLS	VDD					

80 A124 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Nucleic Acid Accession #: NM_001719

Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

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  CGATGCACTG GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC 180
  CCCTGTTCTT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
10 GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGGGGGA GATGCAGCGC GAGATCCTCT 300
  CCATTTTGGG CTGCCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
  CCATGTTTCA CTGGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
  GCCAGGGGCT CTCTACCCCG TACAAGGCCG TCTTCAGTAC CCAGGGCCCG CCTCTGGCCA 480
  GCCTGCAAGA TAGCCATTTC CTCACCGAGC CCGACATGGT CATGAGCTTC GTCAACCTCG 540
15 TGGAAACATGA CAAGGAATTTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
  TTTCCAAGAT CCCAGAAAGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT 660
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  GGCACAACCT GGGCTGTCAG CTCTCGGTGG AGACGCTGGA TGGGAGAGC ATCAACCCCA 900
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  TCTTCAAGGC CACGAGGTC CACTTCCGCA GCATCCGTC CACGGGAGC AAACAGCGCA 1020
  GCCAGAACCG CTCCAAGACG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACCTGGCAG 1080
  AGAACAGCAG CAGCGACGAG AGGCAGGCTT GTPAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
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  ACAGAAACAT GGTGTGTCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440
30 TTGGGGCCAA GTTTTTCGAG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
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  AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAAG 1620
  TCTTACAAGC TGTGACGGCA AAACCTAGCA GGAAAAAATA ACAACGCATA AAGAAAAATG 1680
  GCGGGGCGAG GTCATTTGGT GGGGAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
35 TTATAGCGC CTACCAAGCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
  GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
  CAATAAAACG AATGAATG

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40 **Al25 Protein sequence:**
 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Protein Accession #: NP_001710.1
 Signal sequence: 1-30
 Pfam domains: TGFb_propeptide [37-281]
 Transmembrane domains: none found
 Cellular Localization: secreted

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50  1      11      21      31      41      51
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  ILGLPHRPRP HLQKHNKSNP MFMLDLNLYM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
  LQDSHPLTDA DMVMSFVNLV EHDKEFPFPR YHREPRFDL SKIPEGEAVT AAEFRYKDY 180
  IRERFDNETP RISVYVLQVE HLGRESLFL LDRSLWASE EGMLVFDITA TSNHVVNPR 240
  HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
  QNRSKTPKNQ EALRMANVAE NSSSDQRCAC KKHLYVSFR DLGWDWIIA PBGYAAYYCE 360
  GECAFPINSY MNATNHAIVQ TLVHPINPET VPKPCAPTQ LNAISVLVFD DSSNVILKKY 420
  RNMVVRACGC H

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65 **Al26 DNA SEQUENCE**
 Gene name: integrin, beta 8
 Unigene number: Hs.52620
 Probeset Accession #: AA479726
 Nucleic Acid Accession #: NM_002214
 Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

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70  1      11      21      31      41      51
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  TCCCTCGAC CTGCGCGGCG TACCTTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
  TAGGGTGGTT TCCCCCCCAG CTTGCGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300
  CTAAGCTGAT TTATGCAGCA GAAGCCCGAC CGGCTGGAGA GAAACAAAG CTCTTTTCTT 360
  TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCGGGCCCT 420
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  CCGAGCGCGG GGGTCCGCTT GCTAGGCTTG CGGAAAGGCT CAGAGCGACA CTGCGCCGCG 600
  GGGCCCGGAG TCGCGCGGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGGCGC 660
  GGGCGGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGCG TTTTTCACG GCTGCATTTC 720
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	CACCTGTTCT	TGGACTGGGC	CAAGGTGAAG	ACAATAGATG	TGCATCTTCA	AATGCAGCAT	840
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	TTTCAGGTGG	ATCAAGAAGT	GAACGTTGTG	ATATTGTTTC	CAATTTAATA	AGCAAAGGCT	960
5	GCTCAGTTGA	TTCAATAGAA	TACCCATCTG	TGCATGTTAT	AATACCCACT	GAAAATGAAA	1020
	TTAATACCCA	GGTGACACCA	GGAGAAGTGT	CTATCCAGCT	GGGTCCAGGA	GCGGAAGCTA	1080
	ATTTTATGCT	GAAGTTTCAT	CCTCTGAAGA	AATATCCTGT	GGATCTTTAT	TATCTTGTGG	1140
	ATGTCCTCAGC	ATCAATGCAC	AATAATATAG	AAAAATTAAA	TTCGTTTGA	AACGATTAT	1200
	CTAGAAAAAT	GGCATTTC	TCCCGTGACT	TTCGTTTGG	ATTTGGCTCA	TACGTTGATA	1260
10	AAACAGTTTC	ACCATACATT	AGCATCCACC	CCGAAAGGAT	TCATAATCAA	TGCAGTGACT	1320
	ACAAATTAGA	CTGCATGCCT	CCCCATGGAT	ACATCCATGT	GCTGCTTTG	ACAGAGAACA	1380
	TCAGTGAGTT	TGAGAAAGCA	GTTCCATAGAC	AGAAGATCTC	TGGAAACATA	GATACACCAG	1440
	AAGGAGGTTT	TGACGCCATG	CTTCAGGCAG	CTGTCTGTGA	AAGTCATATC	GGATGGCGAA	1500
	AAGAGGCTAA	AAGATTGCTG	CTGGTGATGA	CAGATCAGAC	GTCCTATCTC	GCTCTTGATA	1560
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	ACGTCAAATC	GACAACCATG	GAACACCCCT	CACTAGGCCA	ACTTTCAGAG	AAATTAATAG	1680
	ACAACAACAT	TAATGTCATC	TTTGTCAGTT	AAGGAAACA	ATTTTCATTG	TATAAGGATC	1740
	TTCTACCCCT	CTTGCCAGGC	ACCATGCTG	GTGAAATAGA	ATCAAAGGCT	GCAACCTCA	1800
	ATAATTGCT	AGTGAAGCC	TATCAGAAAG	TCATTTTCAA	AGTGAAAGTT	CAGGTGGAAA	1860
20	ACCAGGTACA	AGGCATCTAT	TTTAAACATTA	CCGCCATCTG	TCCAGATGGG	TCCAGAAAGC	1920
	CAGGCATGGA	AGGATGCAGA	AACGTGACGA	GCAATGATGA	AGTTCTTTTC	AATGTAACAG	1980
	TTACAAATGAA	AAAATGTGAT	GTCACAGGAG	GAAGAACTA	TGCAATAATC	AAACCTATTG	2040
	GTTTTAATGA	AACCGCTAAA	ATTCATATAC	ACAGAACTG	CAGCTGTGAG	TGTGAGGACA	2100
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25	GTGATGAGAA	TAAATGTCAT	TTTGATGAAG	ATCAGTTTTT	TTCTGAGAGT	TGCAAGTCAC	2220
	ACAGAGATCA	GCTGTGTTGC	AGTGGTGGAG	GAGTTTGTGT	TTGTGGGAAA	TGTTCTATGC	2280
	ACAAAATTAA	GCTTGGAAAA	GTGTATGAAA	AATACTGTGA	AAAGGATGAC	TTTTCTGTG	2340
	CATATCACC	TGGAAATCTG	TGTGCTGGGC	ATGGAGAGTG	TGAAGCAGGC	AGATGCCAAT	2400
	GCTTCAGTGG	CTGGGAAGGT	GATCGATGCC	AGTGCCCTTC	AGCAGCAGCC	CAGCACTGTG	2460
30	TCAATTCAAA	GGGCCAAAGT	TGCAGTGGAA	GAGGCACGTG	TGTGTGTGGA	AGGTGTGAGT	2520
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	GCAAGAAAA	CTGGAATTGT	ATGCAATGCC	TTACCCCTCA	CAATTTGTCT	CAGGCTATAC	2640
	TTGATCAGTG	CAAAACCTCA	TGTGCTCTCA	TGGAACACCA	GCAATTATGTC	GACCAAACTT	2700
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50	TTTTTACAGG	ATAAGTTTAT	GTATGTCACA	GATGACTGGA	TTAATTAAGT	GCTAAGTTAC	3720
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55	A127 Protein sequence:	
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	Unigene number:	Hs.52620
	Probeset Accession #:	AA479726
	Protein Accession #:	NP_002205.1
60	Signal sequence:	1-39
	Transmembrane domains:	682-704
	EGF domain:	552-584
	INB domain:	54-469
65	Cellular Localization:	plasma membrane

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	SRDFRLGFGS	YVDKTVSPYI	SIHPERIHNO	CSYDNLDCMP	PHGYIHVLSL	TENITEFEKA	240
	VHRQKISGNI	DTFEGGPDAM	LQAAVCESHI	GWRKEAKRL	LVMTDQTSHL	ALDSKLAGIV	300
75	VPNDGNCHLK	NNVYVKSTTM	EHPSLGQLSE	KLIDNNINVI	FAVQGRQFHW	YKDLLPLLP	360
	TIAGEIESKA	ANLNLVVEA	YQKLISEVKV	QVENQVQGIY	FNITAICPDG	SRKPGMEGCR	420
	NVTSNDEVLP	NVTVMKSCA	VTGGKRYALI	KPIGPNETAK	IHIHNCSCQ	CEDNRGPKGK	480
	CVDETFDLDSK	CFQCDENKCH	FDDEQFSSSE	CKSHKDQVPC	SGRGVCVCGK	CSCHKIKLKG	540
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	CALMEQQHYV	DQTSCEFSFP	SYLRIFFIIP	IVTFLIGLLK	VLIIRQVILQ	WNSNKIKSSS	720
	DYRVASAKKD	KILQSVCTR	AVTYRREKPE	EIKMDISKLN	AHETFRCNF		

A128 DNA SEQUENCE

Gene name: G protein-coupled receptor 64

Unigene number: Hs.184942
 Probeset Accession #: AA435577
 Nucleic Acid Accession #: NM_005756
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

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5 A129 Protein sequence
 Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942
 Protein Accession #: NP_005747.1
 Signal sequence: 1-38
 GPS domain: 564-615
 10 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
 Cellular Localization: plasma membrane

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35 A130 DNA SEQUENCE
 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 ProbeSet Accession #: AA460530
 Nucleic Acid Accession #: NM_003667
 40 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

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 GTCTCAATCC CCTTCTCTAC ATCTTGTTC AATCTCACT TAAGGAGGAT CTGGTGAGCC 2700
 TGAGAAAGCA AACCTACGTC TGGACAAGAT CAAAACACCC AAGCTTGATG TCAATTAACT 2760
 CTGATGATGT CGAAAAACAG TCCTGTGACT CAACTCAAGC CTTGGTAACC TTTACCAAGT 2820
 CCAGCATCAC TTATGACCTG CCTCCAGTT CCGTGCCATC ACCAGCTTAT CCAGTGACTG 2880
 AGAGCTGCCA TCTTCTCTCT GTGGCATTGT TCCCATGTCT CTAATTAATA TGTGAAGGAA 2940
 AATGTTTCA AAGGTTGAGA ACCTGAAAT GTGAGATTGA GTATATCAGA CGAGTAATTA 3000
 ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA

A131 Protein sequence

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Protein Accession #: NP_003658.1
 Signal sequence: 1-22
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825
 Cellular Localization: plasma membrane

25
30
35
40

1 11 21 31 41 51
 MDTSLRGVLL SLFVLQLLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
 PSNLVFTSY LDLSMNINISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120
 LQNLQLRHVP TEALQNLRLSL QSLRLDANHI SYVPPSCFSG LHSRLHLWLD DNALTEIPVQ 180
 AFRSLALQQA MTLALNKIHH IPDYAFGNLS SLVVLHLNN RIHSLGKKCF DGLHSLRLTD 240
 LNNYNNLDEFP TAIRTLNLSK ELGPHSNIR SIPEKAFVGN PSLITIHFPD NPIQFVGRSA 300
 FQHLPELRTL TIAGASQITE FPDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNLQVLDLS 360
 YNLLLEDLPFSV SVQCLQKID LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI AIHFNAPST 420
 LPSLKLKDL SMLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFFELKV IEMPYAYQCC 480
 AFGVCENAYK ISNQWNKGDN SSMDDLHKKD AGMFAQDER DLEDPLDPE EDLKALHSVQ 540
 CSPSPGPFKP CEHLLDGWLII RIGVWTIAVL ALTCNALVTS TVFRSPLYIS PIKLLIGVIA 600
 AVNMLTGVSS AVLAGVDAFT FGSPARHGAW WENGVGCHVI GFLSIFASES SVFLLTLAAL 660
 ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLFPFGE 720
 STMGYMVALI LLNSLCFLAM TIATYTKLYCN LDKGDLENIN DCSMKHIAL LLFTNCILNC 780
 PVAFLSPSSL INLTPISEPV IKFILLVVVP LPACLNPLLY ILFNPHFKED LVSLRKQTYV 840
 WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS 900
 VAFVPC

A132 DNA SEQUENCE

Gene name: parathyroid hormone receptor 2
 Unigene number: Hs.159499
 Probeset Accession #: U25128
 Nucleic Acid Accession #: NM_005048
 Coding sequence: 143-1795 (underlined sequences correspond to start and stop codons)

50
55
60
65
70
75
80

1 11 21 31 41 51
 GGCCGGTGGC CGGGGCCCGA CCACCCAGC TGGCGTGTGT TACTGGCCAC AAGTTTGCTC 60
 TGGGCGAGCC AAGTTGGCAA CTTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120
 TCTTCTCTACA GCGGTTCCGG GCATGGCCGG GCTGGGGGGG TCGCTCCAGC TCTGGGGTTG 180
 GCTAATGCTC GGCAGCTGCC TCTGGCCAG AGCCAGCTG GATTCTGATG GCACCATTA 240
 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300
 AGCTCAACTC CAGAGGGGAG AAGGTAATTG TTTCCTGAA TGGGATGGAC TCATTGTGTG 360
 GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGC CCTCTTATA TTTATGACTT 420
 CAACCATAAA GAGATTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480
 CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTCTGCG AGCCAGATAT 540
 CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600
 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCAT GGTACTTCA GAGGATGCA 660
 TTGCACTAGG AACTATATCC ACATGCACTT ATTGTGTCT TTTATGCTGA GAGCTACAAG 720
 CATCTTTGTC AAGACACAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780
 AATAATGCAG GATGACCCAC AAAATTCAT TGAGGCACT TCTGTGGACA AATCACAATA 840
 TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG 900
 GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTTCT TTTCCGACAC 960
 CAAATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTGTCAGC 1020
 ATGGGCTGTG GCACGAGCAA CTCTGGCTGA TGGAGGTGTC TGGGAACCTA GTGCTGGAGA 1080
 CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140
 TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1200
 CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCTCGGTCC TAGTCTTTGG 1260
 AGTGCAATAC ATCGTGTTCG TATGCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320
 CCGCATGCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGCT TTCTTTGTGT CTATCATCTA 1380
 CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAG AGTGTGAGTC GGTGGAATCT 1440
 CTCGGTGGAC GTTAAAGGGA CACCGCCATG TGGCAGCCGC AGATGGGGCT CAGTGCTCAC 1500
 CACCGTGAAG CACAGCACA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560
 TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACCTTACC 1620
 TGGCTATGTC TGGAGTAAT CAGAGCAGGA CTGCTGCCA CACTCTTTCC ACGAGGATAC 1680
 CAAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740
 GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAACT GAGGATGTTT TCTGAATGGA 1800
 CATTGTGGC TGACTTTTCT GGGCTGGTCC AATGCTGCTG TGTGTGAGAG GGCTTGGCTG 1860
 ATACTCTTAT GCTTGAGTTC AAAGGCTGAA AATTCAAGTA AGGTGTTTACT TAATAATAGT 1920
 TTTTAGGCTC CATGAATTGG TCTCTGATAA TACTAACGAC ATGAAATATC AAGTGTCAAT 1980

5 GGAGTAGTATT ATTACCTTCT ATTGGCATCA AGTTTTCTCT TAAATTAATG TATGGTATTT 2040
 GCTCTGTGAT TGTTCATTTT TTTCTGCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100
 GCTGTAGCTT TCTCTCATAT ATATCACCTT AAATATAATG AAGATCTTTT AGTGTGTATC 2160
 ATTTTCCITT TAGAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC 2220
 ATTTATTTTG CCTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280
 GATCTAAGAA CAAGTACTTG CTGGAAAAAT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340
 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAG AATATTTTAC 2400
 ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCATCTTTTC 2460
 10 TTCTTTGTAA ACCATGTCAT GTGGAAAGAT TTCCTCAGTT AGTGAGCTTG TGTCTGCAAA 2520
 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTTCTTG 2580
 TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAATAATTT GTTTTAAAAA 2640
 T

15 A133 PROTEIN SEQUENCE

Gene name: parathyroid hormone receptor 2
 Unigene number: Hs.159499
 Protein Accession #: NP_005039.1
 Signal sequence: 1-25
 Pfam domain: 7tm_2 [141-420]
 20 Transmembrane domains: 177-197, 228-250, 253-275, 280-302, 320-342, 363-385, 398-419
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51
 | | | | |
 MAGLGASLHV WGLMLGSLC LARAQLDSGD TITIEEQIVL VLKAKVQCEL NITAOQLEGE 60
 GNCFPEDWGL ICMFPRGTGK ISAVPCFPYI YDFNHKGVAF RHCNPNGTWD FMHSLNKTWA 120
 NYSDCLRPLQ FDISIGKQEF FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYYIH 180
 30 MHLFVSFMLR ATSIPIKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240
 VMFIYFLATN YYNIIIVGLY LBNLIIVAFV SDTKYLWGP LIGWGPFAAF VAAWAVARAT 300
 LADARCWELS AGDIKWIYQA PILAAIGLNF ILFLNTVRVL ATKIWETNAV GHDTRKQYRK 360
 LAKSTLIVLV VFGVHVIVFV CLPHSPTGLG WEIRMHCELF FNSPQGFVFS IYCYCNGEV 420
 QAÉVKQWWSR WNLSVDWKRT PPGSRRCGS VLTTVTHTST SQSQVAASTR MVLISGKAAK 480
 35 IASRQPDSDH TLPGVVWSNS EQDCLPHSFH EETKEDSGRQ GDDILMEKPS RFMESNPDTRE 540
 GCQGETEDVL

40 A134 DNA sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251.
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 | | | | |
 ATGCTGTCTG GCTTCTTGAT GAGTCCCACT ACCCAGCACA GAGCAGAGTA CACTCCCGGA 60
 GGAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGGGCACA CCTCCGAGG GCGAGGCAGC 120
 GACCGGAGGA GCGAGAGCCG GCGGAGGCTT GCGGGGCTCC TGTGGGACCG CGCTGCAGCC 180
 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240
 50 CCGCGCGCGC GCGCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCCCT 300
 CGCCTGCGTC CTGAGCCTTC CCGGGGGAGG GTCCGCTTGC CAGTGAAACC TCCAGAGGCT 360
 TCCGAGCAGC AGCCCGCGGG GCCTTCTGAC TGCACTCCGA GATTTCCATC AGCGAGTGCA 420
 ACTCATAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGCGTTAGGA 480
 55 GCTCCTGGAC CTAGGGCCCG GCGTCGTGCG CTCTCGGCGC TCGCGGCAGA GGGGAGTGGC 540
 CCGCGCGGAA AGCGCGCGGG GACAGTCACT GACGAGGCCG GGGGGTCCGC GGGGCCACGA 600
 CTTCTCGGAG ACCGTCTCTG GCTCTCTGGA GAOCGCTGTG CCGCGCCAG GGTGGTGCCA 660
 TGTGGGGCGC TCGCGGCTCG TCCGTCTCCT CATCTCTGAA CGCGGCTTCG CTCCTGCAGC 720
 TGTCTGTGCG TCGCTGCTCG GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780
 60 TGGCTGGACG CGCAGGGGCT CTGGGSCATC GGCTTCCAGT GTCCCGAGCG CTTGACGGC 840
 GGCAGCGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
 GCGGCGCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGGCTGG CGAGCCTGGC 960
 CGGGCGGACA AAGACGGGCC CCGACGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020
 GGAGACGCGG AGGGTGGGCC CCCACCGGTG AGGGCTGGC AGCGGTGCTC CCCTGAAGGC 1080
 65 TCCCGAAGAG GAAGGCAGCT CCTCAGGGCT TTCCGGGGG TGCTGCCCGG TGCCAGAGCG 1140
 CGCGGATTCC CATCTTCTCC AGCGGGCGGC CCTCTCTCCC TGCAAGCGCC CGCCTTGCCC 1200
 ATCTAGCTGC GTTCTCTCAT TGTGGCTTCC GTGTTGTGCG CCTTTATCAT CTTGGGGTCC 1260
 CTGGTGGCAG CCTGTGCTG CAGATGTCTC CGGCTTAAGC AGGATCCCCA GCAGAGCCGA 1320
 GCGCCAGGGG GTAACCGCTT GATGGAGACC ATCCCATGA TCCCAAGTGC CAGCACTTCC 1380
 70 CGGGGGTGGT CCTCAGCCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG GCGCAACTCC 1440
 GGGGCGCGGG CGCCCCAAC AAGGTCACAG ACCAACTGTT GCTTGCCGGA AGGGAACATG 1500
 AACAAAGTGT ATGTCAACAT GCCCAAGAA TTTCTGTGCG TGAAGTGTCA GCAGGCCACC 1560
 CAGATTGTGC CACATCAAGG CAGATATCTG CATCCCCCAT ACGTGGGGTA CAGGTGACAG 1620
 CACGACTCTG TGCCTATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCTC GCCTGCTAC 1680
 75 AGGCAGATTG AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740
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 GATTCTGAGT GTGGAAAGTC GCACATGTGG GTGGTATTTA TGGCACGATT CCTTGGATG 1860
 GCTTCATTTG CCCCAGACT GTATGAAAC ATCTCCGAAT TAGCAATTCT GGATATGTTT 1920
 CATCCAGGGT ATCATTTGATT TATGATGAA AACCGGCTC AGCTGAGAT GACTGTGATG 1980
 80 TTGCTGATGG GTGTATAACA AATGCTTGAG TCGAAGTGC CTTGAGATA TGGTTGACGA 2040
 AAGAAATTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTCTTTT 2100
 TTGTTGTGTA CTGCACAGGA TCAAAATGCC TGTATCTGCC CTTTACTGCG GACTTTTTT 2160
 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTGTCTCTG TTGCCAGGC TGGAGTGACG 2220
 TGGTGGGATC TCGGCTCACT GCAACTTCAG CTCCTCTGAT TCAGGCAACA CTCCTGCCCT 2280
 AGCCTCCACG TTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGATTTTT 2340

5 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400
 TCTGCTGTCT TCAGCTCTCC AAAGTGTCTG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
 TGAGCCTTTT TTTTCTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAA TAACAGGACT 2520
 ATTCTAAAG GAAACCTGTT TGAACCTCTG GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
 GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTT GTGCTTTTGG 2640
 GGGCCTATTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700
 TTAAAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACCTA ATGAAGACAT TTCAGAACTC 2760
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAATT CATCCCCCTC 2820
 10 TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCTTTT 2880
 TATATTGAAA TCATAAATA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940
 TGGTTATGTT TTTGCGTTTC CTTCTGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCTT 3000
 GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060
 AAAAAATTTT TGTCTTAGT TATAAAATT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
 TAGCTCTCTA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTTT 3180
 15 GCAGATCATA AGGCTTTTTA TACTCTTGT ATCAAAATGG CTTATTTTTC AGGCCTAAG 3240
 GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCCTTT CTTCTCCAC ACTGTTCTTG 3300
 ATTTCTCTCT TCTTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360
 CAAATCAAG TGAATTATAT TGTGTGTCTT TACTTATAT AAAAAAGAT AACTTTAAGG 3420
 20 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTA ACAATCGCT 3480
 GTATGTTATG GTCTTCTACA CATTATGTCT TATAGATATC TATCGATCAT CTTCTATTCT 3540
 TGTTCATGA CTGAATAATG TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600
 TTTTAAATA ACCAAGGCA GGGGAAATC ATTTTACTTA TTAATAATA TTTATGATG 3660
 TGAATAAAAA AAAAAAATA AAAAAAATA

25 **Al35 Protein sequence**
 Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 30 Transmembrane domains: 402-424
 Cellular Localization: not determined

35 1 11 21 31 41 51
 | | | | |
 MLSGFLMSPS TQHRAQYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
 GEAEKGNRGE PPAWIRAQQQ PRPPPAQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPPEA 120
 SGRQPRGSPD CIPRPPSASA THKAVFKGTG PPAEDGDGLG APGPRARRRR LLGVAEAGSG 180
 PRGRRRTVS DEARGSPGPR LLGDRPALSG DALSAAPRVV CGALAAPSP HPGTPLRSCS 240
 40 CCNLRCHRRG RGPSEYCHG WLDQAQVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300
 ARLDQGGCDN DRQQAGEPG RADKDGPRRL GRASCLRGTO GDGEGAPPV RANQRCSPG 360
 SPKGRQLLRA FPGLLPRARR RGPSPSPRGG FSPQLRPLP IYVFFLIVGS VFVAFIILGS 420
 LVAACCCRCL RPKQDPQOSR APGNRLMET IPMIPASSTS RGSRRQSST AASSSSSANS 480
 45 GARAPPTRSQ TNCCLPBGTM NNYYVNMPTN FSVLNCQQAT QIVPHQGGYL HPPYVGYTVQ 540
 RDSVPMATAV PFMGLQPGY RQIQSPFPHT NSBQKMPAV TV

Al36 DNA SEQUENCE
 Gene name: selectin E (endothelial adhesion molecule 1)
 50 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 | | | | |
 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGG 60
 GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
 CAGCAAAAGT ACACACACCT GGTTCGAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180
 60 TCATATTGA GCTATTACCC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAAGTG GGTCCAGGT 300
 GAACCCAACA ATAGGCAAAA AGATGAGGAC TGCGTGGAGA TCTACATCAA GAGAGAAAAA 360
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
 GCTGCCTGTA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
 65 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAACCTG 540
 ACAGCCCTGG AATCCCTGGA GCATGGAAGC CTGCTTTGCA GTCACCCACT GGGAAACTTC 600
 AGCTACAATT CTCTCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
 ACCATGCAAT GTATGCTCTC TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GSGTTCTGTG AATGTTTCCA AAACCTTGGA 780
 70 AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTGGA ACTAATGGGA 840
 GCCCAGAGCC TTAGGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900
 GCTGTGACAT GCAAGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
 CCGTCTGGAG AGTTCACTCT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
 TTGCAGGAC CAGCCAGGT TGAATGCACC ACTCAAGGCC AGTGGACACA GCAATCCCA 1080
 75 GTTTGTGAAG CTTTCCAGT CACAGCCTTG TCCAAACCCG AGCGAGGCTA CATGAATTGT 1140
 CTTCCTAGTG CTCTCTGGAG TTTCCGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200
 GGTTTTGTGT TGAAGGGCTC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260
 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
 GTGAGGTGTG CTATTCCCC TATTGGAGAA TTCACCTACA AGTCTCTTGT TGCCTTCAGC 1380
 80 TGTGAGGAGG GATTGGAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440
 TGGACAGAAC AGGTTCTCTC CTGCCAAGTG GTAAAAATGT CAAGCCTGGC AGTTCGGGA 1500
 AAGATCAACA TAGCTGTGAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCGCTGTG 1560
 CCTGAAGGAT GAGCGCTCAA TGGCTCTGCA GCTGGACAT GTGGAGCCAC AGGACACTGG 1620
 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCTCT GTAGCTGGA 1680
 CTTCTGCTG CTGACACTCT TTAGCACCAT TTCTCTCTG GCTTGGGAAA 1740

TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

5

A137 Protein sequence:

Gene name: Selectin B (endothelial adhesion molecule 1)
Unigene number: Hs.89546
Probeset Accession #: M24736
Protein Accession #: NP_000441
Signal sequence: 1-22
Transmembrane domains: 555-573
C-lectin domain: 23-139
Cellular Localization: plasma membrane

10

15

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1      11      21      31      41      51
|      |      |      |      |      |
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRYTHLVAI QNKKEIEYLN 60
SILSYSPSYW WIGIRKVMNV WVMVGTQKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120
DVGWMDNERC SKKKLALCYT AACINTSCSG HGECVETINN YTCKCDPGFS GLKCEQIVNC 180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
ECDAVINPAN GFVECFQNPQ SFPWNTTCTF DCEEGFELMG AQSLQCTSSG NWDNEKPTCK 300
AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEGFM LQGPQVBECT TQGWTTQIIP 360
VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN 420
EKPTCAVRVC DAVHQPPKGL VRCASPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480
WTEEVPSQCV VKCSSLAVPG KINMSCSGEP VPGTVCKFAC PEGWTINGSA ARTCGATGHW 540
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAFPLLWLRL CLRKAKKFVP ASSCQSLESD 600
GSYQKPSYIL

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30

A138 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Nucleic Acid Accession #: AA487468
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

35

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1      11      21      31      41      51
|      |      |      |      |      |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60
CTACACTCAG CTTGGGTCTT CTGCTCTCTA CTGTCACAG TTTCTTCCAA CCTTGCCATT 120
GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
ATGGTTATTC ATCACCCTGA GGAATTGTCA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAAATT ATCACCTGAT GGGCAATATG TGCTAGAAAT CATGTTTGTA 420
GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
TATGAGCCTC GGGATTATCC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTCAT 600
GAGAGAAACC TCTGGCAGAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAATA 660
TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720
TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

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55

A139 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Protein Accession #: none found
Signal sequence: 1-23
Transmembrane domains: none found
Cellular Localization: secreted

60

65

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1      11      21      31      41      51
|      |      |      |      |      |
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQSKSK 60
PLMVIHLED CQSQALKKV PAQNEBIQEM AQNKFIIMNL MHETTDKNLS PDGQYVPRIM 120
FVDPSTLTRA DIAGRYNRL YTYEPRDLPL LIENMKKALR LIQSEL

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70

A140 DNA SEQUENCE

Gene name: TMPS33a
Unigene number: Hs.298241
Probeset Accession #: AI538613
Nucleic Acid Accession #: AB038157
Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

75

80

```

1      11      21      31      41      51
|      |      |      |      |      |
ACGGGGCACC GGAOGGCTCG GGTACTTTCG TTCTTAATTA GGTCAATGCC GTGTGAGCCA 60
GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACCTGTGC TACTATCTCT TTCGTGGTGT 120
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGATGTCT 180
AGAGGTCTCT AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240

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5 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAATATA GTCTGTGTC ACCAGATGCA 300
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGAAAGT ACAGATGTGG CTCACTCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CCGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCGGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
 AAGGGTCACT AGCAAAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAAGTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 10 TGTGCTCTG GCCACGTGGT TACCTTGAGC TGCAACGCT GTGTCATAG AAGGGGTAC 840
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900
 CTTAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCT GTGGATCATC 960
 ACTGCTGCAC ACTGTGTTTA TGAATTGTAT CTCCCAAGT CATGGACCAT CCAGTGGGT 1020
 CTAGTTTCCC TGTGGAACA TCCAGCCCA TCCCACTGG TGGAGAAGAT TGTCTACCAC 1080
 15 AGCAAGTACA AGCAAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCOCGGCCA 1140
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCC ACTCTGAAGA GAACTTCCCC 1200
 GATGGAAAAG TGTGCTGGAC GTCAAGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
 TCCCTGTGCC TGAACCAAGC GGCCTGCTCT TTGATTTCAC ACAAGATCTG CAACCAAGC 1320
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 20 GTGGACAGCT GCCAGGGGGA CAGCGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGCGACAGC CTTTGGCATC GGCTCGCAG AGGTGAACAA GCCTGGGGTG 1500
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 25 TTCCGGCACC AGTAGCAGGC CGGAAAGAG CACCTTCCA TCTGATTCCA GCACAACCTT 1740
 CAAGCTGCTT TTGTTTITTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTG CCCAGGCTGG 1800
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCGCTT CCCTGGTTCA AGCGATTCTC 1860
 TTGCTCTAGC TTCCCACTG GCTGGGACCA CAGGTGCCCC CCACCACACC CAACTAATTT 1920
 30 TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
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 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160
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 GCACCAGCCC AGAAGTGCAG AACTGCAGTC ACTGCAGTT TTCATCTCTA GGGACCAGAA 2280
 35 CCAAAACCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
 ATGACTCGTT TAAGGCTAT TTTCTATGAT TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400
 TTGCTCTTG ATTCCAAATA ATATGTTTCC TTCCCTCAA AAAAAAAA AAAAAAAA 2460
 AAAAAA

40 A141 Protein sequence:
 Gene name: TMPSR33a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 45 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 Tryp_Spc domain: 216-444
 Cellular Localization: plasma membrane

50
 1 11 21 31 41 51
 | | | | |
 MGENDPPAVE APPSFRSLFG LDDLKISPVA PDADAVAQI LSLPLKFPF IIVIGIILI 60
 LALAIGLGIH FDCSGKYRCR SSPKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVQLQVF 120
 55 TAASWMTMCS DDMKRGHYANV ACAQLGFPSY VSDNLRVSS LBGQFREEFV SIDHLLPDDK 180
 VTALHSHVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240
 LOGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEB NFPDGKVCWT SGWGATEDGA GDASPVNLHA 360
 60 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSQGD SGGPLVCQER RLWKLVGATS 420
 FGIGCAEVNK PGVITRVTSP LDWIEQMER DLKT

65 A142 DNA SEQUENCE
 Gene name: BSTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Nucleic Acid Accession #: none found
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

70
 1 11 21 31 41 51
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 CCAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
 CTGAGATCCT TGCAGTACT ACATCTCTAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
 75 CGGCTGCTCC TATTGCTGAG CTGCTGGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180
 AGACCCAGCT GTGCTCCTGG ATGCTTTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG 240
 AAGCTGAGGA ACTGCTCTGA TGGGAGCTC GAGTGTGAGT CTTACGGAAA CGGAGCCAC 300
 CTGCAATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
 CAGAGAAGCC AGCCGATATG GATTGGCCTG CAGAACCCAC AGAAGAGGCA GCAGTGGCAG 420
 TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGCTCTG GCAAGTCCAT GGGTGGGAAC 480
 80 AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTAA CTTGGAGCAG CAACGAATGC 540
 AACAGGCGCC AACACTCTCT GTGCAAGTAC CGACCATAGA GCAAGAAATCA AGATTCTGCT 600
 AACTCTTGCA CCAGCCCGCT CTCTCTCTTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660
 TTCAGAGGGG AACCTAGACA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTTTA 720

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GGCTTAGAGA CAGAAACTTT AGCAITGGGC CCAGTAGTGG CTTCTAGCTC TAAATGTTTG 780
CCCCGCCATC CCTTTCCACA GTATCCTTCT TCCCTCCTCC CTTGTCTCTG GCTGTCTCGA 840
GCAGTCTAGA AGAGTGCAATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT 900
AAAGATTGGA AGACAGAAGG AAGAAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
ACACCCCTCT GCCCTCTCTC CATTCCTGTC ACCCCACCCC AGCCACTCAA CTCTCGCTTG 1020
TTTTTCCTTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTGG ATGTGGGCCA 1080
TACATTCTTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA

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A143 Protein sequence:

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Protein Accession #: none found
 Signal sequence: 1-22
 Transmembrane domains: none found
 C-type lectin domain: 47-156
 Cellular Localization: secreted

1 11 21 31 41 51
 MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWPHYKSN CYGYPRKLBN WSDAELEQCS 60
 YNGNAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLRSWSWG 120
 KSMGNGKHCA EMSSNNNPLT WSSNECNKRO HFLCKYRP

A144 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

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GGGGAACACC GGCCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
TCCCTCTGTG ACCTCTCGCG GTCTCTCTCC TTCTCCAGGT TTGCTGGCTG CAGTGCGCCG 120
CCTTCGAGGC GTGCGGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
CGGAGCAGGA GCGCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
AAGACACAAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC 420
CCTTCCCCCA GGAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
ACAGCATCAC GGGGCGGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540
AGACAGGCTG GTTGTGTGTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660
TCATCGTAGC CGACCAAGAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCGGAGGGA 720
GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCATAGC CAAGAACCAA 840
AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
CCAGTGCCCT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
ACAAATGCTCC CATGTTTGAC CCCCAGAAAT ACGAGGCCCA TGTGCTGAG AATGCAGTGG 1080
GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGACGC CCCCACCTCA CCAGCGTGGC 1140
GTGCCACCTA CCTTATCATG GCGGTGAGG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
CTGAGAGCAA CCGTGCAGAT CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
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CCACAGCCAC CATAGTGGTC CAGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
CCTCCAAAGT CGTTGAGGTC CAGGAGGSCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
CTGCAGAAAG CCGTGCAGAG GAGAATCAAA AGATCAGCTA CGCATCCTG AGAGACCCAG 1500
CAGGTTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTGACC 1560
GTGAGGATGA GCACTTTGTG AGGAACAACA TCTATGAAGT CATGCTCTG GCCATGGACA 1620
ATGGAAGCCC TCCCAACACT GGCACGGGAA CCTTCTGCT AACACTGATT GATGTCAACG 1680
ACCATGGCCC AGTCCCTGAG CCGGTGAGA TCACCATCTG CAACCAAGC CCGTGTGCGC 1740
ACGTGCTGAA CATCACGGAC AAGGACCTGT CTCCCCACAC CTCCCCTTTC CAGGCCCAGC 1800
TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTT TCTCTGTCTG 1920
ACCATGGCAA CAAAGAGCAC CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
ATGTCGAAAC CTGCCCTGGA CCCTGGAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
TCCTGGCTCT GCTGTTCTCT CTGCTGTGTC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100
TCAGAGAGCT CCTCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160
AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGTCCAC CGAGGTCTGG 2220
AGGCCAGGCC GGAGGTGGTT TCCCGCAATG ACGTGGCAC AACCATCATC CCGACACCCA 2280
TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATGGGCAA CTTTATAATT GAGAACCCTGA 2340
AGGCGGCTAA CACAGACCCC ACAGCCCCGC CTAACGACAC CCTCTTGGTG TTGACTATG 2400
AGGCGAGGCT CTCGAGCGCC GGTCTCCCTG GCTCCCTCAC CTCTCCGCG TCGACCAAG 2460
ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGCTT CAAGAAGCTG GCAGACATGT 2520
ACGGTGGGCG GGAGGAGGAG TAGGCGGCCT GCCTGCAGGG CTGGGGACCA AAGCTCAGG 2580
CACAGAGCAT TCCCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTGG GAGCTTTGTC 2640
GGAAAGTGCC GTAGCAACTT GCGGAGAGCA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
TCCTTAGGCT TTAGAGTGG AGGAATGTGG GCACTTTGAC TTCAGCACTG AAAACCTCTC 2760
CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAA 2820
TGCTCAACCC TGTGCTCTGG GCTGGGGCT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
CTGGAATGGA ACCTTCTTAG GCCTCCTGCT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940

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TCAAAAAGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCAAG GCTGCTGGGC CCACTGGCCG 3000
 TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGGGTTTTT 3060
 ATACTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTTC CCTGTGCGT TGCTATAGAT 3120
 GAAGGGTGAG GACAACTGTG TATATGTACT AGAACITTTT TATTAAGAA A

Al45 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675

Cellular localization: plasma membrane

1 11 21 31 41 51
 MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV PREAEVTLEA GGAQEPEGQA LGKVFMGCPG 60
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
 KGPPFPRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLN KPLDREBIK 180
 YELFGHAVSE NGASVEDPMN ISIIITDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIITYN GVVAYSIHSQ EPKDPHLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TDMGDGSTT TAVAVVEILD ANDNAPMFDP QKYBAHVPEV AVGHEVQRLT VTDLDAFNSP 360
 AWRATYLLIM GDDGDHFTIT THPESNQIL TTRKGLDPEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLAMP DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540
 VNDHGPVPEP RQITTCNQSP VRHVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKFL KQPTYDVHLS LSDHGNKEQL TVIRATVCDQ HGHVETCPGP WKGGFIFLVL 660
 GAVLALLFL LVLLLVRKK RKIKEPLLLP EDDTRDNVY YGEEGGSEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTII PTPMYRPRPAN PDEIGNFIE NLKAAINTDPT APPYDTLLVF 780
 DYEAGSGDAA SLSSLTSSAS DQDQDYDVLN EWGSRFKKLA DMYGGGEDD

Al46 DNA SEQUENCE:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Nucleic Acid Accession #: NM_003318
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 CTCAGCCTCT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT 180
 CTTTCTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACCTCCTG 240
 ACCTCAGGTG ATCCACTTGC CTGGCCTCC CAAAGTGCTA GGATTACAGC CGTGAAACTG 300
 TGCCCTGGCTG ATCTTTTTT TGTGTGTGGA TTTTGAAGAC AGGGTCTCCC TTGGTCGCC 360
 AGGCTGGAGT GCATGGTGC GATCTTGGCT CACTATAACC TCCACTCTCA GGTTCAGT 420
 GATCCTCCCA CTTAGCCTC CTGAGTAGCT GTGATTACAG CGCTGCACCA CCACACCCCG 480
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 CTCTCGGACT CAAGGATGCC GCCTGCCCTCC ACTTCCCAAA GTCCCGAGAT TACAGGTGTG 600
 AGTCACCATG CCTGACCTTA TAATCTTAA GTCAATTTTT CTGGTCCATT TCTCTCTTAG 660
 GGTCCCTACA ACAATCTGCG ATTAGGCGGT ACAATAATCT TTAACCTCAT GATTACAAAA 720
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 GGATGATGAT CCTAAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAAA 840
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 ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCCCCAG 960
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 AACTAAGCTT GAATAAAAT TCTGCTGATA CTACAGATAA CTGGGAACT GTTAACCAAA 1140
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 ACAGTGTCC GCTAAGTGAT GCTCTTTTAA ATAAATTGAT TGGTGTGTAC AGTCAAGCAA 1260
 TTGAAGCGCT TCCCCAGAT AAATATGGCC AAAATGAGAG TTTTGCTAGA ATTCAAGTGA 1320
 GATTGTCTGA ATTAAGAGCT ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAATGG 1380
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5 GCAGCAATAC CTTCAGTAT TACATGAGCT GTTTTAGAAC TCCAGTTGTA AAGAATGACT 2400
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 10 TTCAACAAT CCATCAACAT GGCATTGTTT ACAGTGATCT TAAACCAGCT AACTTTCTGA 2940
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 TCAAGATAT GTCTTCTCC AGAGAGAAATG GGAATCTAA GTCAAAGATA AGCCCCAAAA 3120
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 15 AGCAGATAAT TAATCAGATT TCTAAATTAC ATGCCATAAT TGATCCTAAT CATGAAATG 3240
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 ACCCAAAACA GAGGATATCC ATTCCTGAGC TCCTGGCTCA TCCATATGTT CAAATTCAAA 3360
 CTCATCCAGT TAACCAAAATG GCCAAGGGAA CCACTGAAGA AATGAATAT GTTCGGGCC 3420
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 20 ACTATAGTGG TGGTGAAGT CATAATTCTT CATCTCCAA GACTTTTGAA AAAAAAGGG 3540
 GAAAAAATG ATTTGAGATT ATTCGTAATG TCAGATAGGA GGTATAAAT ATATTGGACT 3600
 GTTATACTCT TGAATCCCTG TGGAAATCTA CATTGAAGA CAACATCACT CTGAAGTGT 3660
 ATCAGCAAAA AAAATTCAGT GAGATTATCT TTAAGAGAAA ACTGTAAAA TAGCAACCAC 3720
 25 TTATGGCACT GTATATATG TAGACTTGT TTCTCTGTTT TATGCTCTTG TGAATCTAC 3780
 TTGACATCAT TTACTCTTG GAATAGTGGG TGGATAGCAA GTATATCTA AAAAACTTG 3840
 TAAATAAAGT TTGTGGCTA AAATGA

30 A147 Protein sequence:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Protein Accession #: NP_003309
 35 Signal sequence: none found
 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

40 1 11 21 31 41 51
 MNKVRDIKKNK FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDNL SLLKLEKNS 60
 VPLSDALLNK LIGRYSQAI ELPDDKYQN ESPARIQVR AELKAIQEPD DARDYFQMAR 120
 ANCKKPAFVH ISFAQFELSQ GNVKSKQLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS 180
 45 EEEKKNLSAS TVLTAAQSEFS GSLGHLQNRN NSCDRSGQTT KARFLYGENM PPQDAEIGYR 240
 NSLRQNTNKK QSCPPGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVGSKP 300
 SGNDSCLELRN LKSVQNSHEK EPLVSDKES ELIITDSITL KNTBESSLLA KLEETKEYQE 360
 FEVPESNQKQ WQAKRSECI NQNPASSENH WQIPELARKV NTEQKHTTFE QPVFVSKQS 420
 PPISTSKWFD PKSICKTPSS NTLDDYMSCF RTPVVKNDPF PACQLSTPYG QPACFQQQOH 480
 50 QILATPLQNL QVLASSANE CTSVKGRIYS ILKQIGSGGS SKVFOVLENEK KQIYAIKYVN 540
 LEEADNQTL DSYRNEIAYLN KLQHSKDKII RLYDYBITDQ YIYVMECCN IDLNSWLKKN 600
 KSIDPWERKS YWKNMLEAVH TIHQHGVHS DLKPNANFLIV DGMKLIDFG IANQMOPDIT 660
 SVVKSQVGT VNYMPPFAIK DMSSSRENGK SKSKI SPKSD VMSLGCLLY MTYKTPFQ 720
 IINQSKLHA IIDPNHEIEF PDPEKDLQD VLKCCLEKRP KQRISIPELL AHPYVQIQTH 780
 55 PVNQMAKGT BEMKVLVQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTPEKRGK 840
 K

60 A148 DNA SEQUENCE

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
 Unigene number: Hs.258583
 Probeset Accession #: NM_012152
 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 CTTCCTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
 GACAAGCACA TGGACTTTT TTATAATAGG AGCAACACTG ATACTGTGTA TGACTGGACA 120
 70 GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTT TCTGCCTGTT TATTTTCTAT 180
 TCTAATCTTC TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCAATT CCCTTCTCAT 240
 TAOCCTGTGG CTAATTAGC TGCTGCCGAT TTCTTGGCTG GAATGCGCTA TGTATCTCTG 300
 ATGTTTAAACA CAGGCCCACT TTCAAAAATC TTGACTGTCA ACOGCTGGTT TCTCCGTCAG 360
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCGGTGGAG 420
 75 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480
 CTGCTCATTT TGCTTGTCTG GGCCATCGCC ATTTTATATG GGGCGGTCCC CACACTGGGC 540
 TGGAAITGCC TCTGCAACAT CTCTGCTGCG TCTTCCCTGG CCCCATTTA CAGCAGGAGT 600
 TACCTTGTGTT TCTGGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGTT TGTGGGTATC 660
 CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAACGTCT TGCTCCGCA TACAAGTGGG 720
 80 TCCATCAGCC CCGCGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780
 GCGTTTGTGG TATGCTGGAC CCGGGGCTG GTGGTTCTGC TCCTCGACGG CCTGAACATG 840
 AGGCAGTGG TGTGAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900
 GTCGTGAACC CCATCATCTA CTCTACAAG GACGAGGACA TGTATGCGAC CATGAAGAAG 960
 ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGCGTC CTTCTCGCAT CCCTCCACA 1020
 GTCCTCAGCA GGAGTGACAG AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080

GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGCCACCCCA GGTGATGACT 1140
GTCCTAGG

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A149 Protein sequence:

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
Unigene number: Hs.258583
Probeset Accession #: NM_012152
Protein Accession #: NP_036284
Signal sequence: none found
Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295
Cellular Localization: plasma membrane

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1	11	21	31	41	51	
MNECHYDKHM	DFFYNRSNTD	TVDDWTGTXL	VIVLCVGTFF	CLFIPFNSNL	VIAAVIKNRK	60
FHFFPYLLA	NLAAADFFAG	IAYVPLMFNT	GPVSKTLTVN	RWFLRQGLLD	SSLTASLTNL	120
LVIIVERHMS	IMRMVHSNL	TKKRVTLIL	LVNAIAIFNG	AVPTLGWNCL	CNISACSSLA	180
PIYSRSYLVF	WTVSNLMAFL	IMVVVYLRIY	VYVKRKTINV	SPHTSGSISR	RRTPMKIMKT	240
VMTVLGAFVV	CWTPGLVLL	LDGLNCRQCG	VQHVKNRFL	LALLNSVVP	IYYSYKDEDM	300
YGTMKRMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK	STS	

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ProstateA150 DNA SEQUENCE

Gene name: ESTs
Unigene number: Hs.293616
Probeset Accession #: AW043782
Nucleic Acid Accession #: none found
Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

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1	11	21	31	41	51	
AGCAACGACG	CGGGGACGCG	GGAGCGGCGG	CGCGGCCATG	TGGCTGCTGG	GGCCGCTGTG	60
CCTGCTGCTG	AGCAGCGCGG	CGGAGAGCCA	GCTGCTCCCG	GGGAACAAC	TCACCAATGA	120
GTGCAACATA	CCAGGCAACT	TCATGTGCAG	CAATGGACGG	TGCATCCCGG	GCGCTGGCA	180
GTGTGACGGG	CTGCCTGACT	GCTTCGACAA	GAGTGTAGAG	AAGGAGTGCC	CCAGGCTAA	240
GTGGAATGT	GGCCCAACCT	TCCTCCCTCG	TGCCAGCGCG	ATCCATTGCA	TCATTGGTCG	300
CTTCGGTGC	AATGGGTTTG	AGGACTGTCC	CGATGGCAGC	GATGAAGAGA	ACTGCACAGC	360
AAACCCCTCG	TCCTGCTCCA	CGCCCGCTA	CCACTGCAG	AAACGGCTCT	GTATTGACAA	420
GAGCTTCATC	GTCGATGGAC	AGAATAACTG	TCAAGACAAC	AGTGATGAGG	AAAGCTGTGA	480
AAGTTCTCAA	GAACCCGGCA	GTGGGCGAGT	GTTTGTGACT	TCAGAGAACC	AACTTGTGTA	540
TACCCGAGC	ATCACTATG	CCATCATCGG	CAGCTCCGTC	ATTTTGTGTC	TGGTGGTGGC	600
CCTGCTGGCA	CTGGTCTTGC	ACCACGAGCG	GAAGCGGAAC	AACTCATGA	CGCTGCCCGT	660
GCACCGGCTG	CAGCACCCCTG	TGCTGCTGTC	CGGCTGGTGG	GTCTTGAGCC	ACCCCAACCA	720
CTGCAACGTC	ACCTACAAAG	TCAATAATGG	CATCCAGTAT	GTGGCCAGCC	AGGCGGAGCA	780
GAATGCGTGG	GAAGTAGGCT	CCCAACCTTC	CTACTCCGAG	GCCTTGCTGG	ACCAGAGGCC	840
TGCGTGGTAT	GACCTTCTTC	CACCGCCCTA	CTCTTCTGAC	ACGGAATCTC	TGAACCAAGC	900
CGACCTGCCC	CCCTACCGCT	CCCGTCCCGG	GAGTGCCAAC	AGTGCCAGCT	CCCAGGCAGC	960
CAGCAGCCTC	CTGAGCGTGG	AAGACACCCG	CCACAGCCCG	GGGCAGCCCTG	GCCCCCAGGA	1020
GGGCACTGCT	GAGCCACAGG	ACTCTGAGCC	CAGCCAGGGC	ACTGAAGAAG	TATAAGTCCC	1080
AGTTATTCCA	AAGTCCATAT	GGGTTAATCT	GCTCTGACTT	GTTGCCATTC	TAACAATTTC	1140
TGCTCATGGG	AGGCTCTTTA	AGCACCTGTA	AGGATGCTCT	AAGTTACAGT	TTGGGATATT	1200
AACTATCTCT	GCATTCCCTT	CCCTCCCGAG	ACTTCAGAGA	TGTTTTCTG	GOGTCTCAGT	1260
TGACATGATC	TGTTGTGCGT	CTTTCTGTCT	AGGTCACTCT	TCCCTTGGGA	CCCGAGATCA	1320
CACCCCTCAT	TTTCACTTA	TTCTGTTTCT	GTTGGAGAGA	CAGCATATAA	AACAGTATTG	1380
AAATAGGCTG	GGAGAGAGCA	ATGTTTCTGT	GCTATATTGG	ATGCTCAGAA	GTGCAGGAGA	1440
CGCTGGACCC	AATTCTCTCT	GCTGGGTAGT	TACCTTATAG	CATTTGGGGA	TTTGGGTTAG	1500
ATGATCTAAC	CAGGAGGCCA	TCATGAGATG	GTCAACCCCG	CAAAAAAATT	CCATTGAGC	1560
ATCAAAACCT	GCTTTGACCA	ATCCTATTTC	ATGCCCCGAG	TTCAAGCAGG	TCAGTGCCCA	1620
AAGAAAACCT	TGGACGTGAG	TAACACCCCT	CAGCAGTCGC	AACGTTATTT	TGGTTTGTG	1680
AAGGACTCTG	AAACCATCTA	CCCTGTATAA	ATTCTGGGCT	TAGAAATTTC	CCCAAGAATG	1740
CTCATCTCTG	GAGCTTTCTT	CAGCAGCATA	TATCATCAGC	CTCATCTTAA	AATAGGCAGG	1800
GAGCCCTCTC	CATGAGTTTA	TCCAAGTTCT	CAGCTCCTAA	AATGCAGGCT	GCCAAAGACC	1860
TACACCTGCC	CTGGCTCTAC	AGCCACTTAC	CTGGTTTCTG	GACTGTCAAC	CTCCAGCTGC	1920
ACCTGCCCGT	AGCCAGGAA	TGAGGACCTA	ACTGAGTTTG	GCCCCAAGTC	TGACCTGGCT	1980
GTATGTCCTT	GTGGCCCAAC	CCAGCCCTGT	CTTGCTCAAT	CATGCAGCCT	CAACACTGGC	2040
CTCCAAAGTT	CCCTTAACAC	TTGCAAGATC	CTTTTACCT	GTGCATTGAG	ACTTGAGGAC	2100
ACTGTGTTCT	ATCAGAGTGG	AGAGCCATGT	TCAATACCTC	CAGCAAGCTC	TCCTGGCTCC	2160
CTGCACTGTG	CAGCTCTCTC	TTCCCAAGGT	CCCAATACCA	GCACCTCTAG	TTAGAGTTAG	2220
GGTCAGGGTC	AGGCGCTGCC	CAACATCCCA	GTAGTTTCTC	CTCTGAGACA	CATGGGCAAG	2280
AGACAATTTC	GAGTCAAGAT	TTTCCATTTC	GATCTATTTT	AAATCTTTTA	GAAATGCATT	2340
TGAAACAGTG	TGTTTGTGTT	TTCCCTTCTA	GTTAAGGGAC	TATTTATATG	TGTATAGGAA	2400
AGCTGTCTCT	TTTTTGTGTT	TTCCCTTAAAC	AAGGTCCAAA	GAAAGATGCA	AAAGGAGATC	2460
ACACCCCTGC	CCGCTGAGC	CCCGTGATAA	CAAGTCACTC	CAGACTAACC	TGTGTGCCAG	2520
ACATTGTGTC	ATTGTTGCAC	TTTGAGGTTA	TTATTATATCA	AGTTCTTGAA	GGAAGCAGAA	2580
AGAGGGAGTC	CTCTCTCCCT	CCGTGTATAG	TCTCTATGTT	TGTGCTAGTT	TTTCTTTTTT	2640
TTCTCTGTGT	CCAGTCAGCC	ACAGGGCCCG	CCTCCCTGCA	GGAATAAGGG	GTAACCACTT	2700
AGGTGTTGTT	TGGCAAGAAA	CCACACTGAC	TGATGAGGGG	TAAAAAGGAA	CCAGGTAGAG	2760
CCACTCCGGG	CAGCTGTAC	CCATTTCAGAA	CTTCTTTCCG	CAGCTGAAGA	AATGTTACAT	2820

AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAAG TGGCATTACG 2880
 TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTACAGAA 2940
 AAGCTAGCCA CTGGTATTTT GTTTTGTTTA AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA 3000
 AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAAGAA CTTTTGATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120
 CATTTCACTC CCTGTAGTC AGAAGGGCTT TATTTCTCCC TTTGATGGGG CCCCTTCTTC 3180
 TTCTCGTGTC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCACTCTAG GAAAAACAAA TGGTTTATGT 3300
 AGATAAGGGA TGCCTACTAA TGCTTTTAA AAACAAACAG GGACATTTTT ATTATAGATT 3360
 TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGGC GGCAGGGTTT 3420
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC ATTCACCAACA GGAAGCTTTT TTATACATTG CCTAAATCTA GGCCAACCA 3540
 AAAATAGTCT CATCTCTTTT TTCTCAAAAT GAGATCCGTG TTTTATTTTA GCATTAAAT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGAGC CTCAAAGTTA ATGTAAGCTG 3720
 GAAAGGTGT GTGTGTTGTC TTTTGTGTTT TGGTTAGGC TTGGTTTGT TTTTAAATTT 3780
 TTATACCTTC TAATAAATTT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG GWMCTAMARM 3840
 AAMMAAAAC AMYWTGGGG GGGCTTGGGC CTCGGAAGAA GTTTTAAACA CCACTTCGGG 3900
 TGGGGCGGCG GGGCCCAOCT AGGTACGGCG ACCACCGCGG CCCAACCGGG ACCCCAGAG 3960
 GAAACCTCG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGCGCGGG 4020
 GGAAACCGCA GAGTGTTCG TAAACACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

A151 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MWLLGPLCLL LSSAAESQLL PGNFTNECN IPGNFMCNSG RCIPGAWQCD GLPDCFPKSD 60
 EKECPKAKSK CGPTFPFCAS GIHCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
 KNGLCIDKSF ICDGQNNQD NSDEBSCSS QEPGSGQVFP TSENQLVYYP SITYAIIGSS 180
 VIFVLVALL ALVLHHRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNNVNGIQ 240
 YVASQAQNA SEVGSPPSYR BALDQRPAW YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT ABPRDSEPSQ GTEEV

A152 DNA SEQUENCE

Gene name: Transmembrane protease, serine 2 (TMPRSS2)
 Unigene number: Hs.105807
 Probeset Accession #: T48536
 Nucleic Acid Accession #: NM_005656.1
 Coding sequence: 57-1535 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTGATAAC AGCAAGATGG 60
 CTTTGAATC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAGAACAT GGATACCAAC 120
 CGGAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCGG 180
 CTCAGTACTA CCGTCCCCC GTGCCCACTG ACGCCCGGAG GGTCTGACG CAGGCTTCCA 240
 ACCCGTCAAT CTGCAAGCAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAGACTA 300
 AGAAAGCACT GTGCATCAC TTGACCTCGG GGCCTTCCCT CGTGGGAGCT GCGCTGGCG 360
 CTGGCTACT CTGGAAGTTC ATGGGCAGCA AGTGTCTCAA CTCTGGGATA GAGTGGGACT 420
 CCTCAGGTAC CTGCATCAAC CCTCTAACT GGTGTGATGG CGTGTACAC TGCCCGCGG 480
 GGGAGGACGA GAATCGGTGT GTTGCCTCT ACGGACCAAA CTTCATCCTT CAGATGTACT 540
 CATCTCAGAG GAATCTCTGG CACCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC 600
 GGGGGCCTG CAGGACATG GGCTATAAGA ATAAATTTTA CTCTAGCCAA GGAATAGTGG 660
 ATGACAGCGG ATCCACCAGT TTTATGAAAC TGAACACAAG TGCCGGCAAT GTCGATATCT 720
 ATAAAAAAT GTACCACAGT GATGCTGTCT CTTCAAAAGC AGTGGTTTCT TTACGCTGTT 780
 TAGCCTGCGG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGGC GGTGAGAGCG 840
 CGCTCCCGGG GGCTTGGCCC TGGCAGGTCA GCCTGCACGT CCAAGACGTC CACGTGTGCG 900
 GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCGCG CCAGTGGGTG GAAAGACCTC 960
 TTAACAATCC ATGGCATTGG ACGGCATTTG CCGGGATTTT GAGACAATCT TTCAATGTCT 1020
 ATGGAGCCGG ATACCAAGTA CAAAAAGTGA TTTCTCATCC AAATTATGAC TCCAAGACCA 1080
 AGAACATGA CATTGGCTG ATGAAGCTGC AGAAGCCTCT GACTTCAAC GACCTAGTGA 1140
 AACCACTGTG TCTGCCCAAC CCAAGCATGA TGCTGCAGCC AGAACAGCTC TGCTGGATTT 1200
 CCGGGTGGGG GGCAACCGAG AGACCTCAGA AGTGTGAAC GCTGCCAAGG 1260
 TGCTTCTCAT TGAGACACAG AGATGCAACA CGAGATATGT CTATGACAAC CTGATCACAC 1320
 CAGCCATGAT CTGTGCGGC TTCTGTCAGG GGAACGTGCA TTCTTGCCAG GGTGACAGTG 1380
 GAGGGCTCTT GGTCACTTCC AACACAATA TCTGTTGGCT GATAGGGGAT ACAAGCTGGG 1440
 GTTCTGGCTG TGCCAAAGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTCAAGG 1500
 ACTGGATTTA TCGACAATAG AAGGCAACCG GCTAATCCAC ATGGTCTTCG TCCTTGAAGT 1560
 CGTTTACAAA GAAACAATG GGGCTGTTTT TGCTTCCCGG TGCAATGATT ACTCTAGAG 1620
 ATGATTCAGA GGTCACTTCA TTTTATTAA ACAGTGAAC TGCTGGCTT TGGCACTCTC 1680
 TGCCACTAGT TGCAGGCTGC AGTGGCTCCC CTGCCAGCC TGCTCTCCCT AACCCCTTGT 1740

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COGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGGGG TCAATTGTGG AAGGAAGAGG 1800
GTTGGAGGCT GCCCCATTG AGATCTTCCT GCTGAGTCCT TTCCAGGGGC CAATTTTGGA 1860
TGAGCATGGA GCTGTCACTT CTCAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT 1920
GGAAAGGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTGGTAGTG 1980
TCCCCAGCCT ACTTCACAAG GGGATTITGC TGATGGGTTT TTAGAGCCTT AGCAGCCCTG 2040
GATGGTGGCC AGAATAAAAG GGACAGCCCT TTCATGGGTG GTGACGTGGT AGTCACCTGT 2100
AAGGGGAACA GAAACATTTT TGTTCCTATG GGTGAGAAAT ATAGACAGTG CCCTTGGTGC 2160
GAGGGGAACA ATTGAAAGG AACTTGCCCT GAGCACTCCT GGTGCAGGTC TCCACCTGCA 2220
CAITGGGTGG GGCTCCTGGG AGGGAGACTC AGCCTTCCTC CTCATCCTCC CTGACCTGTC 2280
TCCTAGCACC CTGGAGAGTG AATGCCTCTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340
ATGTCCGCCT CTTAGGCCTT GATAGTCATT GGAAATTGAG GTCCATGGGG GAAATCAAGG 2400
ATGCTCAGTT TAAAGTACAC TGTTTCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460
CTGAGTTCAA AGCCATCTT

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A153 Protein sequence:

Gene name: Transmembrane protease, serine 2 (TMPRSS2)
 Unigene number: Hs.105807
 Probeset Accession #: T48536
 Protein Accession #: NP_005647.1
 Signal sequence: none found
 Transmembrane domains: 85-107
 Cellular Localization: plasma membrane

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1 11 21 31 41 51
| | | | |
MALNSGSPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTQA 60
SNPVVCTQPK SPSGTVCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFPMG SKCSNSGIEC 120
DSSGTCINPS NWCDGVSHCP GGEDENRCVR LYGNPFILQM YSSQRKSWHP VCQDDWNNY 180
GRAACRDMGY KKNFYSSQGI VDDSGSTFSM KLNTSAGNVD IYKLYHSDA CSSKAVVSLR 240
CLACGVNLNS SRQSRIVGGE SALPGAWPQV VSLHVQNVHV CGGSIITPEW IVTAHCVEK 300
PLNNPWHWTA FGAILRQSPM FYGAGYQVQK VISHPNYDSK TKNDIALMK LQKPLTFNDL 360
VKPVCLPNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLIETQRC NSRYVYDNL 420
TPAMICAGFL QGNVDSQGD SGGPLVTSNN NIHWLIGDTS WSGGCAKAYR PGVYGNVMVF 480
TDWIIRQMK NG

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A154 DNA SEQUENCE

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039
 Unigene number: Hs.129179
 Probeset Accession #: AI694767
 Nucleic Acid Accession #: AI694767
 Coding sequence: 130-1086 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
CAGAGAGGCT GTATTTTCAGT GCAGCCTGCC AGACCTCTTC TGGAGGAAGA CTGGACAAAG 60
GGGGTCACAC ATTCCCTTCCA TACGGTTGAG CCTCTACCTG CCTGGTGGTG GTCCACAGTTC 120
AGCTTCTTCA TGATGGTGGG TCCCAATGGC AATGAATCCA GTGCTACATA CTTTCATCTA 180
ATAGGCCTCC CTGGTTTAGA AGAGGCTCAG TTCTGGTTGG CCTTCOCATT GTGCTCCCTC 240
TACCTTATTG CTGTGCTAGG TAACCTGACA ATCATCTACA TTGTGCGGAC TGAGCACAGC 300
CTGCTAGAGC CCATGTATAT ATTTCTTTGC ATGCTTTTCA GCATTGACAT CCTCATCTCC 360
ACCTCATCCA TGCCCAAAAT GCTGGGCATC TTCTGGTTCA ATTCCACTAC CATCCAGTTT 420
GATGCTGTGC TGCTACAGAT GTTTGCCATC CACTCCTTAT CTGGCATGGA ATCCACAGTG 480
CTGCTGGGCA TGCCCTTTGA CCGCTATGTG GCCATCTGTC ACCCACTGGC CCATGCCACA 540
GTACTATAGT TGCTCTGTGT CACCAAAATT GGTGTGGCTG CTGTGGTGGG GGGGGCTGCA 600
CTGATGGGAC CCCTTCTGTG CTTCATCAAG CAGCTGCOCT TCTGCGCTC CAATATCCTT 660
TCCCATCTCT ACTGCTTACA CCAAGATGTC ATGAAGCTGG CCTGTATGTA TATCOGGGTC 720
AATGTCGTCT ATGGCCTTAT GGTCTATCAT TCCGCCATTG GCTTGGACTC ACTTCTCATC 780
TCCTTCTCAT ATCTGCTTAT TCTTAAGACT GTGTTGGGCT TGACACGTGA AGCCCAGGCC 840
AAGGCATTGG GCATCTGCGT CTCTCATGTG TGTGCTGTGT TCATATTCTA TGTACCTTTC 900
ATTGGATTGT CCATGGTGCA TCGCTTTAGC AAGGCGGGTG ACTCTCCACT GCCCGTCATC 960
TTGGCCATA TCTATCTGCT GGTTCCTCCT GTGCTCAACC CAATTGTCTA TGGAGTGAAG 1020
ACAAAGGAGA TTGACAGCG CATCCTTCGA CTTTTCATG TGGCCACACA CGCTTCAGAG 1080
CCCTAGGTGT CAGTGATCAA ACTTCTTTTC CATTCAGAGT CCTCTGATTC AGATTTTAAT 1140
GTTAATCATTT TGGAAAGACG TATTGAGAAA AAAAATTTC TTAATAAAAA TACAACTCAG 1200
ATCCTTCAAA TATGAAACGT GTTGGGGAAT CTCCATTTT TCAATATTAT TTTCTTCTTT 1260
GTTTTCTTGC TACATATAAT TATTAAATACC CTGACTAGGT TGTGGTTGGA GGGTTATTAC 1320
TTTTCAITTT ACCATGCAAT CCAATCTAA ACTGCTTCTA CTGATGGTTT ACAGCATTCT 1380
GAGATAAGAA TGGTACATCT AGAGAACATT TGCCAAAGGC CTAAGCACAG CAAAGGAAAA 1440
TAAACACAGA ATATATAATA ATGAGATAAT CTAGCTTAAA ACTATAACTT CCTCTTCAGA 1500
ACTCCCAACC ACATGGATC TCAGAAAAAT ACTGCTTCA AAATGACTTC TACAGAGAAG 1560
AATAATTTT TCCTCTGGAC ACTAGCACTT AAGGGGAAGA TTGGAAGTAA AGCCTTGAAA 1620
AGAGTACATT TACCTACGTT AATGAAAGTT GACACACTGT TCTGAGAGTT TTCACAGCAT 1680
ATGGACCCCTG TTTTCTCTAT TTAATTTTCT TATCAACCOCT TTAATTAGGC AAAGATATTA 1740
TTAGTACCOCT CATGTAGCC ATGGGAAAAAT TGAATGTCAG TGGGGATCAG TGAATTAAT 1800
GGGGTCATAC AAGTATAAAA ATTAATAAAA AAAGACTTCA TGCCCAATCT CATATGATGT 1860
GGAAGAACTG TTAAGAGAC CAACAGGGTA GTGGGTTAGA GATTTCCAGA GTCTTACATT 1920
TTCTARAGGA GGTATTAAAT TTTCTTCTAC TCATCCAGTG TTGATTATG GAAATTCCTG 1980
GCAACAGAAC TCATGGCTTT AATCCCACTA GCTATTGCTT ATTGTCTGG TCCAATTGCC 2040
AATTACCTGT GTCTTGAAG AAGTGATTTC TAGGTTCACC ATTATGGAAG ATTCTTATTC 2100
AGAAAGCTCG CATAGGGCTT ATAGCAAGTT ATTTATTTTT AAAAGTTCCA TAGGTGTTTC 2160
TGATAGGCAG TGAGGTTAGG GAGCCACCAG TTATGATGGG AAGTATGGAA TGGCAGGTGT 2220
TGAAGATAAC ATTGGCCTTT TGAGTGTGAC TCGTAGCTGG AAAGTGAGGG AATCTTCAGG 2280

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5 ACCATGCTTT ATTGGGGCT TTGTGCAGTA TGGAAACAGG ACTTTGAGAC CGGGAAGCA 2340
 ATCTGACTTA GGCATGGGAA TCAGGCATTT TTGCTTCTGA GGGGCTATTA CCAAGGGTTA 2400
 ATAGGTTTCA TCTTCAACAG GATATGACAA CAGTCTTAAC CAAGAAACTC AAATTACATA 2460
 TACTAAAACA TGTGATCATA TATGTGGTAA GTTCAITTTT CTTTTTCAAT CCTCAGGTTT 2520
 CCTGATATGG ATTCTATNA CATGCTTTCA TCCCTTTTG TAATGGATAT CATATTGGGA 2580
 AATGCCTATT TAATACTTGT ATTTGCTGCT GGACTGTAAG CCCATGAGGG CACTGTTTAT 2640
 TATTGAATGT CATCTCTGTT CATCATTGAC TGCTCTTTGC TCATCATTTGA ATCCCCCAGC 2700
 AAAGTGCCTA GAACATAATA GTGCTTATGC TTGACACCGG TTATTTTCA TCAAACTGTA 2760
 10 TTCCTTCTGT GCTGAACACA TAGCCAGGCA ATTTTCCAGC CTTCCTTGAG TTGGGTATTA 2820
 TTAAATTTTA GCCATTACTT CCAATGTGAG TGGAAAGTGC ATGTGCAATT TTTATACCTG 2880
 GCTCATAAAA CCTCCCATG TGCAGCCTTT CATGTTGACA TTAATGTGA CTGGGGAAGC 2940
 TATGTGTTAC ACAGAGTTAA TTAACNGAA AGGCCTGGNA ATTTTTGNN AANNAAACTG 3000
 TGGCCNAGG GCCCNCAACC CTTTTNNNA ATTTGGCAAN NTCCCATTT GTANTTTGGT 3060
 15 AAGGAGGCCA GTTGGATAAG TGAAAAATA AGTACTATTG TGTC

A155 PROTEIN SEQUENCE

20 Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039
 Unigene number: Hs.129179
 Protein Accession #: not available
 Signal sequence: none found
 Pfam domain: 7tm_1 [43-293]
 Transmembrane domains: 29-51, 57-79, 82-104, 203-225, 239-261, 273-295
 25 Cellular Localization: not determined

30 1 11 21 31 41 51
 | | | | |
 MVDPNNGNESS ATYFILIGLP GLEBAQFWLA FPLCSLYLIA VIGNLTIIYI VRTEHSLHEP 60
 MYIFLOMLSG IDILISTSSM PKMLAIPWPN STTIQFDACL LQMPAIHSLS GMESTVLLAM 120
 AFDRYVAICH PLRHATVLT PRVTKIGVAA VVRGAALMAP LEVFIKQLPF CRSNILSHSY 180
 CLHQDVVKLA CDDIRVNVVY GLIIVISAIG LDSLLISFSY LLILKTVLGL TREAQAKAFG 240
 TCVSHVCAVF IPYVPPFGLS MVRFRSKRRD SPLPVILANI YLLVPPVLPN IVYGVKTKEI 300
 35 RQRILRLFHV ATHASEP

A156 DNA SEQUENCE

40 Gene name: vasoactive intestinal peptide receptor 1
 Unigene number: Hs.198726
 Probeset Accession #: X77777
 Nucleic Acid Accession #: NM_004624.1
 Coding sequence: 57-1544 (underlined sequences correspond to start and stop codons)

45 TCGGAGCCTG CGGAGGGTGG TGGTGGTGGT GGTGGTGGCC CTGCCCCGCC TCACTCATGC 60
 CTCCTCTCTC TCTGCTCTCG CTCAGGCGCC TCGGTGGCGG TTGGTGGCGG GTTAAGCGGC 120
 TGGTGGTTCG GCGCGCGCGG GCTCGCTCTC GGGGAGGCGG GGGCGGATCT CGCGCGCGCAG 180
 GCGGCGCGCG CGGAGGTGGG GTGCGCGCGG GAGGCGGCT CGAGCTTCGT GCTGCGCGCT 240
 CGCTCTTGGG CTCTCGCTG CAGGAGGAGT GTGACTATGT GCAGATGATC GAGGTGCAGC 300
 ACAAGCAGTG CTGAGGAGG GCGCAGCTGG AGAATGAGAC AATAGGCTGC AGCAAGATGT 360
 50 GGGACAACCT CACCTGCTGG CAGCCACCC CTGGGGGCCA GGTAGTTGTC TTGGCCTGTC 420
 CCCTCATCTT CRAAGCTCTT TCCTCCATTC AAGGCGCGCA TGTAAGCCGC AGCTGCACCG 480
 ACGAAGGCTG GACGCACCTG GAGCCTGGCC CGTACCCCAT TGCTGTGGT TTGGATGACA 540
 AGGCAGCGAG TTGAGATGAG CAGCAGACCA TGTCTACGG TTCTGTGAAG ACGCGCTACA 600
 CCATTGGCTA CGGCTGTCTC CTGCGCACCC TTCTGGTGGC CACAGCTATC CTGAGCCTGT 660
 55 TCAGGAAGCT CCACCTGACG CGGAATACA TCCACATGCA CCTCTTCAZA TCCTTCATCC 720
 TGAGGGCTGC CGCTGTCTTC ATCAAGACT TGGCCCTCTT CGACAGCGGG GAGTCGGACC 780
 AGTGCTCCGA GGGCTGGTGG GGTGTGAAG CAGCCATGGT CTTTTCCTCA TATTGTGTCA 840
 TGGCTAACTT CTCTGGCTG CTGGTGGAGG GCCTCTACCT GTACACCTGC CTTGCGGTCT 900
 60 CCTTCTCTCT TGAGCGGAAG TACTTCTGGG GGTACATCT CATCGGCTGG GGGTACCCA 960
 GCACATTAC CATGCTGGG ACCATCGCCA GGATCCATTT TGAGGATTAT GGTCTGCTCA 1020
 GGTGCTGGGA CACCATCAAC TCCTCACTGT GGTGATCAT AAGGGGCCCC ATCCTCACCT 1080
 CCATCTTGGT AAACCTTCAT CTGTTTATTT GCATCATCG AATCCTGCTT CAGAACTGC 1140
 GGCCCCCAGA TATCAGGAAG AGTGACAGCA GTCCATACT AAGGCTAGCC AGGTCCACAC 1200
 65 TCCTGCTGAT CCCCTGTGTT GGAGTACACT ACATCATGTT CGCCTTCTTT CGGACAATT 1260
 TTAAGCCTGA AGTGAAGATG GTCTTTGAGC TCGTGTGGG GTCTTCCAG GGTTTTGTGG 1320
 TGGCTATCCT CTACTGCTTC CTCAATGGTG AGGTGCAGGC GGAGCTGAGG CGGAAGTGGC 1380
 GGCGCTGGCA CTGACAGGTC GTCTGGGCT GGAACCCCAA ATACCGGCAC CGTGGGAG 1440
 GCAGCAACGG CGCCAGTGC AGCAAGCAGG TTTCCATGCT GACCGCGTC AGCCAGGTG 1500
 70 CCGCGCGCTC CTCCAGCTTC CAAGCGAAG TCTCCCTGGT CTGACCAACA GATCCACAGC 1560
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 GGGCGCGCCA GCGCGGCCCT TGGGCTGGGA GGCTGCCGCC GCGCCCTGG TCTGTGTTC 1680
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 75 AGGCCCCCTA CGCCAAATCAA GGGCAAAAAG TCTACATACT TTACCTCTGA CTCTGCCCCC 1860
 TGCTGGCTCT TCTGCCCAAT TGGAGGAAAG CAACCGGTGG ATCTCTCAAC AACACTGGTG 1920
 TGACCTGAGG GCAGAAAGGT TCTGCCCGG AAGGTCAACA GCACCAACAC CACGATAGTG 1980
 CTGAAATTT CACCATTGCT GTCAAGTTC TTTGGGTAA GCATTACCAC TCAGGCATT 2040
 80 GACTGAAGAT GCAGCTCACT ACCCTATTCT CTCTTACGC TTAGTTATCA GCTTTTAAA 2100
 GTGGGTATT CTGGAGTTT TGTGTGAGA GCACACCTAT CTAGTGGTT CCCCACGGA 2160
 GTGGAAGTGC CCTTGGGTCA GTCTGGTGG AGGACGGTGC AACCCAGGA CTGAGGAGT 2220
 CTGAAGCTC TGGGAAATGA GAAGGCAGCC ACCAGGAAT GCTAGGCTC GGACTAAGCC 2280
 TACCTGCTCT CCAAGTCTCA GTGGCTTCAT CTGTCAAGTG GGACTCTGTC ACACAGCCA 2340
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5 AAGCAGATCC TCACCTCTGCT ACACATACAG GATTTGAAGT CAGATCTGTC TGATAGGAAT 2520
 GTGAAAGCAC GGAATCTTAC TGCTAACTTT TGTGTATCGT AACCAGCCAG ATCCTCTTGG 2580
 TTATTTGTTT ACCACTTGTA TTATTAATGC CATTATCCCT GAATTCCTCT TGCCACCCCA 2640
 CCTCCCTGG AGTGTGGCTC AGGAGGCTC CATCTCATGT ATCATCTGGA TAGGAGCTGG 2700
 CTGGTCAACAG CCTCTCTGCT CTGCCCTTCA CCCCAGTGGC CACTCAGCTT CCTACCCACA 2760
 CCTCTGCCAG AAGATCCCTT CAGGACTGCA ACAGGCTTGT GCAACAATAA ATGTTGGCTT 2820
 GGAAGAAAAA AAAA

10 A157 Protein sequence:
 Gene name: vasoactive intestinal peptide receptor 1
 Unigene number: Hs.198726
 Probeset Accession #: X77777
 Protein Accession #: JC2195
 Signal sequence: none found
 15 Transmembrane domains: 181-202, 214-236, 255-277, 290-311, 332-354, 377-399, 408-430
 Cellular Localization: plasma membrane

20 1 11 21 31 41 51
 | | | | |
 MPPPLLRLR RLGGWSAVT RLVVAAAGAR SRGGRGSRG AGGGGRGVA RRRRLRLRAA 60
 RSLGSLQ ECDYQMI EV QHKQCLEEAQ LENETIGCSK MWDNLTCWPA TPRGQVVLA 120
 CPLIFKLFSS IQGRNVRSC TDEGWHLEP GPYPIACGLD DKAASLDLQ TMYGVSVKTG 180
 25 YTIGYGLSLA TLLVATAILS LFRKLHCTRN YIHMHLFISF ILRAAAVPIK DLALFDSGES 240
 DQCEGSGVGC KAAMVFPQYC VMANFFWLLV EGLYLYTLA VSPFSEKRYF WGYILIGWGV 300
 PSTFTMWVIT ARIHFEDYGL LRCWDITNSS LWIILKGPIL TSILVNFIPL ICIIIRILLQK 360
 LRPPDIRKSD SSPYRLARS TLLLIPLFGV HYIMFAPFPD NFKPEVMKVF ELVVGSEFQGF 420
 VVAILYCPFN GEVQAELEPR WRRWHLQGV L GWNPKYRHPG GSGNGATCST QVSMLTRVSP 480
 30 GARRSSSFQA EVSLV

A158 DNA SEQUENCE
 Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 35 Nucleic Acid Accession #: AL133619
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
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 ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCGCCCA GCTGCGCGAC CCCGGGCTCT 60
 OGGCGCGGCG GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCGCGA GAGCCCGCAG 120
 CTCAGGCAGA GCGACCCGCA GAAACGGAAC CTGGACCTGG AGAAAGCCT GCAGTTCCTG 180
 CAGCAGCAGC ACTCGAGATG GCTGGCCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240
 45 GAAACCAAGG GTAGGCGGGC GCGGGGCGCT AGGCGCGGCC TGCCCTCCCA GGCACACTCA 300
 ACACTGCGCG TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CCTGGGCTCA 360
 GGGGGAACAC AGGACGGGGA GCCCCTCCAG ACTGTCTTGG CCCACCTGGC TGCACTGGCC 420
 CCTGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGTACCTCT 480
 AGCCGTGGCT GGAAGATGTT ATGCAGCCAA GCACAGCAGC TGCTGCTCTC GGGAAAGCCC 540
 50 GGGCCTGAGG TCATTGCAAG GCGGCAAGGT GCCACAGGCT GCTCCCGAGA CCTCCCTCT 600
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 CCTCAGATTG CTGCTGTGGC CAGGCCCAAG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720
 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780
 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCTCTG TTCTTGCCA CTTGTCCAAG 840
 55 GCATTTCCCC ATCTTGACAG CGGCCCCAC CAGGCCAGG ATCCTGGGCT GTGGTCTCAA 900
 GCTCACTTCC CATTAATCTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGA 960
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 GACATGAGAG AGGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG 1080
 CTGTTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CCGTCACTGC TGGGGAAGCT 1140
 60 GACAGGACAC GGAAGAGGCG CATGCTTCTC CTGGGACCT GCTGTTCAT GTGTCCCAAG 1200
 CCTCTCTGCT TTCCAGATGG CCCCTCAGGA AACCACCTTT CCAGGGCTTC TGCTCCCTTG 1260
 GGGCTCTGCT GGGTCTGCAT CAACGAGTGG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC 1320
 AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGG 1380
 GGGGTAGAGC CCGCACTGT GCGCTCTCTC GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440
 65 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500
 TCCTTCAACA AGCAAGATTC AAAAGCTGAC GTCTCCAGA AGGCGGACCT GGAAGAGGAG 1560
 CCCTACTTTC ACAACAGCAA GCTGGACAAA GTTCTTGGGG TACAAGGSCA GGCCAGAAAG 1620
 GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACAGGGC 1680
 AGGCAGATGG GGGCGGGGGC ACACCCCOCA ATGATCTTGC CCTTCCCTCT GCGAAAGCCC 1740
 70 ACCACACTTA GGCAGTGGGA AGTGTCTATC CCGAGCTGTG GGAATACCAA CCTCTGCGAG 1800
 ACCGAGAGC TGGCGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860
 CCGAGGAGAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCAA GGTCTCCACC 1920
 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCGTGGGCGG AGCGTGCCAT CCGTCCCGCA 1980
 CTGAAGCAGA CCGCAAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GCAATGCGAG 2040
 75 AAAAGGCGCC TGCATGCTC AGTGCTTTGA

A159 Protein sequence:
 Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 80 Protein Accession #: T43457
 Signal sequence: none found
 Transmembrane domains: 303-322
 Cellular Localization: not determined

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1      11      21      31      41      51
5      |      |      |      |      |
MSGAGVAA GT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
QQQHSEMLAK LHEEIEHLKR ENKGEFARGP RPALPPQAH S TLPLPQHRNT AINSSTRLGS 120
GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAA TS SRGWTMLCSQ AQHVLLSGSP 180
GPEVIAGRQV ATGCSPLDLP PSRAEMGRNP WDSPPCAPSL PQIAAVARPR ISSPMALSPH 240
MLGAQGIWTH SIQGSPLAIW AATMGTKGGS RVLFPCHLSK ALPHPDSPGH PAQDPGLWSQ 300
10     AHFPLSLGLG L TSGGHLTG WSQPGNIAAG AVPRALPSQG DMEKGVGGP FPSRCGNSSE 360
LFWAKGSPSR QPQPCBAGDA DRTREEMLS LGTCCSMPCK PSCFPDGP SG NHLSTRASAPL 420
GARWVCINGV WVEPPGSPSA RLKEGSSRTH RFGGKRGRLA GGSADTVRSP ADSLSMSSFP 480
SVKSISNSAN SQGKARPPQ SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQGOARK 540
EKAESNAGA ACMGNSQHQG RQMGAGAHPP MILPLPLRKP TTLRQCSEVLI RELWNTNLLQ 600
15     TQELRHLKSL LEGSQRPQAA PEEASPPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA 660
LKQTPKNFA ERQKRLQAMQ KRRLHRSVL

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A160 DNA SEQUENCE

Gene name: LIV-1 protein, estrogen regulated

Unigene number: Hs.79136

Probeset Accession #: U41060

Nucleic Acid Accession #: NM_012319.2

Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

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CTGTGCGCGA ATTGCGCAGC AGACCGCGTG TCGGCGCCTG GTAGAGATTT CTGAAGACA 60
CCAGTGGGCC CGTGTGGAAC CAAACCTGCG CGCGTGGCGG GGCCGTGGGA CAACGAGGCC 120
GCGGAGACGA AGGCGCAATG GCGAGGAAGT TATCTGTAAT CTGTATCCTG ACCTTTGCCC 180
TCTCTGTAC AAATCCCTCT CATGAACATA AAGCAGCTGC TTCCCCAG ACCACTGAGA 240
AAATTAGTCC GAATTGGGAA TCTGGCATT AATGTGACTT GGCATTTTCC ACACGGCAAT 300
ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAAATA TTCTTTGTCA GTTGAAGGGT 360
35     TCAGAAAAAT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420
ACCAACGACA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480
AGCATCACTC AGACCAAGAG CATCACTCTG ACCATGATCA TCACTCTCAC CATATCATG 540
CTGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCAGCA CCATGACTCA GATAGTTTCA 600
GTAAAGATCC TAGAAACAGC CAGGGGAAGG GAGCTCACCG ACCAGAATAT GCCAGTGGTA 660
40     GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG 720
TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTTCTC 780
CCAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCAATC AAAGAGCCGG GTGAGCCGGC 840
TGGCTGGTAG GAAAAACAAAT GAATCTGTGA GTGAGCCCGG AAAAGGCTTT ATGTATTCCA 900
45     GAAACACAAA TGAAAATCTCT CAGGAGTGT TCAATGCATC AAAGCTACTG ACATCTCATG 960
GCATGGGCTA CCAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA 1020
TCAACCAAT TGATGCTAGA TCTGTCTGA TTCAACAAG TGAAAAGAGG GCTGAAATCC 1080
CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTGGTGG TTTTATAGCC ATTTCCATCA 1140
TCAGTTTCTC GTCTCTGCTG GGGGTATCT TAGTGCTCT CATGAATCGG GTGTTTTC 1200
50     AATTTCTCCT GAGTTTCTCT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTT 1260
TACACCTTCT CACCACTTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG 1320
CAATGGAAAT GAAAAGAGGA CCACCTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA 1380
GTGCTTATTT TGATTCCAGG TGAAGGGTTC TAACAGCTCT AGGAGGCTGT TATTTTCATG 1440
55     TTCTTGTGTA ACATGTCTTC AACAATTTAA AGATAAGAAG AAAAAGAAAT 1500
AGAAGAAACC TGAAAATGAT GATGATGTGG AGATTAAAG GCAATGTGTC AAGTATGAAT 1560
CTCAACTTTC AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCTATTTAC 1620
GAGCAGACTC ACAAGAGCCC TCCCCTTTG ATTCTCAGCA GCCTGCAGTC TTGGAAGAAG 1680
AAGAGGTGAT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740
60     GGTGCAAGAA TAAATGCCAT TCACATTTCC ACGATACACT OGGCCAGTCA GACGATCTCA 1800
TTCACACCA TCATGACTAC CATCATATTC TCCATCATCA CCACACCAA AACCACCATC 1860
CTCAGCTCA CAGCCAGGCG TACTCTGGG AGGAGCTGAA AGATGCGGCG GTGCCACTT 1920
TGGCCTGGAT GGTGATAATG GGTGATGGCC TGCACATTT CAGCGATGGC CTAGCAATTG 1980
75     GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTGTCT GTGTTCTGTC 2040
ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA 2100
AGCAGGCTGT CCTTTATAAT GCATTGTGAG CCAATGCTGGC GTATCTTGGG ATGGCAACAG 2160
65     GAATTTTCAT TGGTCATTAT GCTGAAAATG TTTCTATGTG GATATTGCA CTTACTGCTG 2220
GCTTATTCAT TGGTTTGTCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA 2280
GTGACCATGG ATGTAGCGCG TGGGGGTATT TCTTTTACA GAATGCTGGG ATGCTTTTGG 2340
70     GTTTTGGAA TATGTTACTT ATTTCCATAT TTGAACATAA AATCGTGTTC CGTATAAAT 2400
TCTAGTTAAG GTTTAAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGGTCAT 2460
AGGGAGATGA GTTTGTATGC TGTACTATGC AGOGTTTAAA GTTAGTGGGT TTTGTGATTT 2520
TTGTATTGAA TATTGCTGTC TGTACAAAG TCAGTTAAAG GTACGTTTAA ATATTTAAGT 2580
TATTCTATCT TGGAGATAAA ATCTGTATGT GCAATTCACC GGTATTACCA GTTTATTATG 2640
80     TAAACAAGAG ATTTGGCATG ACATGTTCTG TATGTTTCAG GGAATAATGT CTTTAATGCT 2700
TTTTCAAGAA CTAACACAGT TATTCCTATA CTGGAATTTA GGTCTCTGAA GAACTGCTGG 2760
TGTTTAGGAA TAAGAAATGT CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA 2820
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AAAAATCACA AAATTTGTGT TAAATTAGAG GGGAGAAAT TAGAATTAAG TATAAAAAGG 2940
CAGAATTAGT ATAGATACA TTCAATTAAC ATTTTGTGCA GGATTATTTC CCGTAAAAAC 3000
GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT 3060
AAATATATTT AATGAATTCA AGCAATATAC ACTTGACCAA GAAATTTGAA TTTCAAAATG 3120
75     TTTGTCGGGG TTATATACCA GATGAGTACA GTGAGTAGTT TATGTATCAC CAGACTGGGT 3180
TATTGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTCTGTGTT ACCTGGTTTA 3240
CAAAATTATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAAACT ACCTAAGTA 3300
80     CATTTTGATT OGATTACAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCATTGT 3360

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GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGCTCTGTG GCATTCTCTA 3420
GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

5

A161 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
Unigene number: Hs.79136
Protein Accession #: NP_036451
Signal sequence: 1-21
Pfam domain: Zip[591-743]
Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745
Cellular Localization: plasma membrane

10

15

1	11	21	31	41	51	
MARKLSVILI	LTFALSVTNP	LHELKAAAF	QTTEKISFNW	ESGINVDLAI	STRQYHLQOL	60
FYRYGENNSL	SVGEFRKLLQ	NIGIDKIKRI	HIHHDHDS	DHEHSDHER	HSDHEHSDH	120
EHHSDEHDS	HMNHAASGKN	KRKALCPDHD	SDSSGKDPNR	SQKGAHRPE	HASGRNRVKD	180
SVSASEVTST	VYNTVSEGT	PLETIETPRP	GKLFPKDVSS	STPPSVTSKS	RVSRLAGRKT	240
NESVSEPRKG	FMYSRMTNEN	PQECFNASKL	LTSHGMGIQV	PLNATEFNYL	CPAIIINQIDA	300
RSCLIHTEK	KAEIPPKTYS	LQIAWVGFI	AISIISPLSL	LGVLVPLMN	RVFFKPLLSF	360
LVALAVGTL	GDAPLHLLPH	SHASHHSHS	HEEPAMEMKR	GPLFSLSSQ	NIEESAYFDS	420
TRKGLTALG	LYPMFLVEHV	LTLIKQFKDK	KKRNQKPKEN	DDDVEIKKQL	SKYESQLSTN	480
EKVVDTRDT	EGVLRADSQ	PSHFDSSQPA	VLEEEVEMIA	HAHPQEVYNE	VVPRGCKNKC	540
HSHPHDTLQ	SDDLIHSHH	YHILHHHHH	QNHHPHSHSQ	RYSREELKDA	GVATLAWMVI	600
MDGLHNFSD	GLAIGAAFT	GLSSGLSTV	AVFCHPELPE	LGDFAVLLKA	GMTVQKAVLY	660
NALSAMLAYL	GMATGIFIGH	YAENVSMWIP	ALTAGLFMYV	ALVDMVPEML	HNDASDHGCS	720
RMGYFFLQNA	GMLLPGFIML	LISIFEHKIV	PRINF			

30

A162 DNA sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.87223
Probeset Accession #: AA250737
Nucleic Acid Accession #: NM_001203
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

35

40

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CGCGGGGCGC	GGAGTCGGCG	GGGCCTCGCG	GGACGCGGGC	AGTGCAGAGA	CGCGGGCGCT	60
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GTGAAGAGAA	AGGAAGATCA	TTTCATGCCT	TGTTGATAAA	GGTTCAGACT	TCTGCTGATT	180
CATAACCAT	TGGCTCTGAG	CTATGACAAG	AGAGGAAACA	AAAAGTTAAA	CTTACAAGCC	240
TGCCATAAGT	GAGAAGCAAA	CTTCCTTGAT	AACATGCTTT	TGCCAAGTGC	AGGAAAATTA	300
AATGTGGGCA	CCAAGAAAGA	GGATGGTGAG	AGTACAGCCC	CCACCCCGCG	TCCAAAGGTC	360
TTGCGTGTGA	AATGCCACCA	CCATTGTCCA	GAAGACTCAG	TCAACAATAT	TTGCAGCACA	420
GACGGATATT	GTTCACGAT	GATAGAAGAG	GATGACTCTG	GGTTGCCTGT	GGTCACTTCT	480
GGTTGCCTAG	GACTAGAAGG	CTCAGATTTT	CAGTGTGCGG	ACACTCCCAT	TCCTCATCAA	540
AGAAGATCAA	TTGAATGCTG	CACAGAAAGG	AACGAATGTA	ATAAAGACCT	ACACCCCTACA	600
CTGCCTCCAT	TGAAAAACAG	AGATTTTGT	GATGGACCTA	TACACCACAG	GGCTTTACTT	660
ATATCTGTGA	CTGTCTGTAG	TTTGCTCTTG	GTCTTATCA	TATTATTTTG	TTACTTCCGG	720
TATAAAAGAC	AAGAAACAG	ACCTCGATAC	AGCATTGGGT	TAGAACAGGA	TGAAACTTAC	780
ATTCTCTCTG	GAGAAATCCCT	GAGAGACTTA	ATTGAGCAGT	CTCAGAGCTC	AGGAAGTGGA	840
TCAGGCTCC	CTCTGCTGGT	CCAAGGACT	ATAGCTAAGC	AGATTGAGAT	GGTGAACAG	900
ATTGGAAGAG	GTGCTATGG	GGAAGTTGG	ATGGGAAAGT	GGCGTGGCGA	AAAGGTAGCT	960
GTGAAGTGT	TCTTCACAC	AGAGGAAGCC	AGCTGGTTCA	GAGAGACAGA	AATATATCAG	1020
ACAGTGTGTA	TGAGGCATGA	AAACATTG	GGTTTCATTG	CTGCAGATAT	CAAAGGGACA	1080
GGGTCTCTGA	CCAGTTGTA	CCTAATCACA	GACTATCATG	AAAATGGTTC	CCTTTATGAT	1140
TATCTGAAGT	CCACCAACCCT	AGACGCTAAA	TCAATGCTGA	AGTTAGCCTA	CTCTTCTGTC	1200
AGTGGCTTAT	GTCATTACA	CACAGAAATC	TTTAGTACTC	AAGSCAAACC	AGCAATTGCC	1260
CATCGAGATC	TGAAAGTAA	AAACATTCTG	GTGAAGAAAA	ATGGAACCTG	CTGTATTGCT	1320
GACCTGGGCC	TGGCTGTATA	ATTTATTAGT	GATACAAATG	AAGTTGACAT	ACCACCTAAC	1380
ACTCGAGTTG	GCACCAAAAG	CTATATGCCT	CCAGAAAGTGT	TGGACGAGAG	CTTGAACAGA	1440
AATCACTTCC	AGTCTTACAT	CATGGCTGAC	ATGTATAGTT	TTGGCCTCAT	CCTTTGGGAG	1500
GTGCTAGGA	GATGTGTATC	AGGAGGTATA	GTGGAAGAA	ACCAGCTTCC	TTATCATGAC	1560
CTAGTGCCCA	TTATGAGGAC	ATGAGGGAGA	TTGTGTGCAT	CAAGAAGTTA		1620
CGCCCTCAT	TCCCAAAACG	GTGGAGCAGT	GATGAGTGTC	TAAGGCAGAT	GGGAAAATC	1680
ATGACAGAA	GCTGGGCTCA	CAATCCTGCA	TCAAGGCTGA	CAGCCCTGCG	GGTTAAGAAA	1740
ACACTTGCCA	AAATGTCAGA	GTCCAGGAC	ATTAAACTCT	GATAGGAGAG	GAAAAGTAAG	1800
CATCTCTGCA	GAAAGCCAAC	AGGTACTCTT	CTGTTTGTGG	GCAGAGCAAA	AGACATCAAA	1860
TAAGCATCCA	CAGTACAAAG	CTTGAACATC	GTCTGCTTTC	CCAGTGGGTT	CAGACCTCAC	1920
CTTTCAGGGA	GCGACCTGGG	CAAGACAGAG	GAAGCTCCCA	GAAGGAGAGA	TTGATCCGTG	1980
TCTGTTGTA	GGCGAGAGAA	CGTGGGTA	ACTTGTTCAA	GATATGATGC	AT	

75

A163 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.72472 / Hs.87223
Probeset Accession #: AA250737 / U89326
Protein Accession #: NP_001194
Signal sequence: 1-13
Transmembrane domains: 128-144
PFAM domains: activin_receptor [30-111], protein kinase [204-491]
Cellular Localization: plasma membrane

80

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1      11      21      31      41      51
|      |      |      |      |      |
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   DSGLPVVTSG CIGLEGSDFQ CRDTPIPHQR RSEECCTERN ECKNDLHPTL PPLKNRDFVD 120
   GPIHRRALLI SVTVCSLLLV LIILFCYFRY KRQSTRPRYS IGLEQDETYI PPGESLRDLI 180
   EQSQSSSGSGS GLPLLVRQTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTTEAS 240
   WFRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
10  MLKLAYSSVS GLCHLHTEIF STQKPAIAH RDLKSKNIV KNGTCCCIAD LGLAVKFISD 360
   TNEVDIPNPT RVGTIKRYMPP EVLDESLNRN HFQSYIMADM YSFLILWEV ARRCVSGGIV 420
   EBYQLPYNHL VPSDPSYEDM REIVCIKCLR PSFPNRNSSD ECLRQMGKLM TECWAHNPAS 480
   RLTAALRVKKT LAKMSESQDI KL

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A164 DNA sequence

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15  Gene name: ESTs
   Unigene number: Hs.157601
   Probeset Accession #: W07459
   Nucleic Acid Accession #: AC005383
20  Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
25  GACAGTGTTC GCGGCTGCAC GCTCGGAGS CTGGGTGACC GCGGTAGAAG TGAAGTACTT 60
   TTTTATTGCG AGACCTGGGC OGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACCTC 120
   CCTGGCGGTA GTTCTCCGGA CCTCAGCCGG GTCCGGTCTG GCCGCCCTCT CCCAGGAGAG 180
   ACAAACAGGT GTCCACGTG GCAGCCGCGC CCCGGGCGCG CCTCCTGTGA TCCCGTAGCG 240
   CCCCTGTGCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCCCGGGCAC CGAGCGCTGG 300
   TGCGCGCTCT CCTTCGGTTA TATCAACATG CCCCTTTTCC TGTGTCTGGA GGCCGTCTGT 360
30  GTTTTCCTGT TTTCCAGAGT GCCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAACAAA 420
   GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480
   ATCATGTTTC TGTAGATGG GTCTAACAGC GTCCGGAAAG GGAGCTTTGA AAGGTCCAG 540
   CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CGAGAGAGGT CAGAGTGGGA 600
   GCATTCCAGT TCAGTTCCAC TCCTCATCTG GAATTCCTCT TGAATTCATT TTCAACCCAA 660
35  CAGGAAGTGA AGGCAAGAAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720
   CTGTCTCTGA AATACCTTCT GCACAGAGGG TTGCCTGGAG GCAGAAATGC TTCTGTGCCC 780
   CAGATCCTCA TCATCGTCAC TGATGGGAAG TCCCAAGGGG ATGTGGCACT GCCATCCAG 840
   CAGCTGAAGG AAGGGGTGTG CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG 900
   GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCAGC TGCTGTGGGC TGAGCAGGTG 960
40  GAGGATGCCA CCAACGGCCT CTTCAGCACC CTCAGCAGCT CGGCATCTG CTCCAGCGCC 1020
   ACGCCAGACT GCAGGGTCGA GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGCTCCGG 1080
   GAGTTGCTCG GCAATGCCCC ATGCTGGAGA GGATGCGGCG GGACCTTTCG GGTGTCTGGT 1140
   GCACACTGTG CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTGTC CACCTGCTAC 1200
   AGGACCACTT GCCCAGGCCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260
45  CCAGAAGGAC TGGACGGCTA CCAAGTGCCT TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC 1320
   TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCCGACTCC TCTTCTGCTT GGACAGCTCT 1380
   GCGGGCACC A CTCTGGACGG CTTCCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG 1440
   GCGTACTGCA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500
   CTGGTGGCGG TGCTGTGGGG GGAGTACCAG GATGTGCTCG ACCTGGTCTG GAGCCTCGAT 1560
50  GGCAATCCCT TCCGTGGTGG CCCACCTCTG ACGGCGAGTG CCTTGCAGCA GCGGCGAGAG 1620
   CGTGGCTTGG GAGAGGCCAC CAGGACCGGC CAGGTAGAGT GGTGGTTTGG 1680
   CTCATCTGAT CACTCTCCGA GGATGAGGTT GCGGGCCGAG CGGCTCAGCG AAGGGCGCGA 1740
   GAGCTGCTCC TCTCTGGTGT AGGCAGTGAG GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800
   GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCNA CCAATTCCT 1860
55  GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG CGGCCAGGTT GCGGACACA AGCCCTGGAC 1920
   CTGCTCTTCA TGTGGACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980
   AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCCGC 2040
   CTGGTGGTGT ATGGCAGCCA GGTGCAGACT GCCTTCGGGC TGGACACCAA ACCACCCCG 2100
60  GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCTACCTAG GTGGGTGGG CTGAGCCGGC 2160
   ACCGCCCTGC TGCACATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTGGT 2220
   GTCCCCAAAG CTGTGGTGGT GCTCAGAGGC GGGAGAGGCG CAGAGGATGC AGCCGTCTCT 2280
   GCCCAGAAAG TGAGGAACAA TGGCATCTCT GTCTTGGTGG TGGGCGTGGG GCCTGTCTTA 2340
   AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC CGGATTCCC TGATCCAGST GGCAGCTTAC 2400
65  GCCGACCTGC GGTACCAACA GGACGTGCTC ATTGATGGC TGTGTGAGGA AGCCAAGCAG 2460
   CCACTCAACC TCTGCRAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CTGACAGAAT 2520
   GGGAGCTATC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC OCCACTGCGA GAACCGTGAG 2580
   TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GATGGATTTC TTAGAGCGCC CTGAGGCAC 2640
   ATGGCTCCCG TGCAGGAGGG CAGCAGCGGT ACCCTCCCA GCACTACAG AGAAGGCCCTG 2700
70  GGCAGTAAA TGGTGCCTAC CTCTGGAAT GTCTGTGCC CAGGTCCTTA GAATGTCTGC 2760
   TTCCCGCGGT GGCAGGAGCC ACTATTCTCA CTGAGGAGG AGGATGTCCC AACTGCAGCC 2820
   ATGCTGCTTA AGCAAGAA AGCAGCTGAT GTCACCACA AACGATGTTT TTGAAAAGTT 2880
   TTGATGTGTA AGTAATAACC CACTTCTGTG ACCTGCTGTG CCTTGTGAG GCTATGTCAT 2940
   CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCTGGAAG ACTTAAATTT AGCGGCTGGA 3000
75  CGTTCCTTTG CACACAATCA ATGCTGCGCA GAATGTTGTT GACACAGTAA TGCCGAGCAG 3060
   AGGCTTTTAC TAGAGCATCC TTTGAGCGGC GAAGGCCAAG GCCTTTCAAG ATGGAAGACA 3120
   GCAGCTTTTC CACTTCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAGGGGG 3180
   CTGAGGGGAC GTTTGTGACT TCTTGGCGAC TGCTTTTGT GTGTGGAAGA GACTTGGAAA 3240
   GGTCTCAGAG TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GGGCTGAGT 3300
80  TGTGCATGGG CCCAGGCTCG GAGGGCCAGG TAAATTCGTT CTGAGTCGTG AGCAGTGTC 3360
   ACCTTGAAGG TCTTC

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A165 Protein sequence

Gene name: ESTs
 Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGM domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
MPPFLLEAV CVPLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMPLLDGSN 60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILLIIVTDG KSQGDVALPS KQLKERGVTV 180
FAVGVRPFRW EELHALASEP RGQHVLLEAQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLMEV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVPLTHPATC YRTTCPGPCD 300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLVLLDS SAGTTLDGFL 360
RAKVVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVNSL DGIPFRGGPT 420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVS 480
EAVRAELSEI TGSPKHVMVY SDPQDLFNQI PELQGLCSR QRPGRTOAL DLVFMLD TSA 540
SVGPENFAQM QSFVRSCALQ FEVNPDVTVV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
APYLVGGVSA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLRRNGI 660
SVLVVGVGPV LSEGLRLLAG PRDSLHVAA YADLRYHQDV LIENLQGEAK QPVNLCKPSP 720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
RTFPPSNYREG LGTEMVPTFW NVCAPGP

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A166 DNA sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR
 Unigene number: Hs.37744
 Probeset Accession #: AA011176
 Nucleic Acid Accession #: AF272890
 Coding Sequence: 87-1520 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
TGCTACCCCG GCCCGGGCTT CTGGGGTGTG CCCCACACAC GGCACAGCCC TGCCACACCC 60
CCCGCCCGCG GCCTCCGCGAG CTGCGCATGG GCGCGGGGGT GCTGCTCTCG GCGCGCTCGG 120
AGCCCGGTAA CCTGTGCTCG GCGCGACCGC TCCCAGACGG CGCGGCCACC GCGCGCGCGC 180
TGCTGTGTGC CCGGTGCGCG CCGGCTCGT TGCTGCTTCC CGCCAGCGAA AGCCCGGAGC 240
CGCTGTCTCA GCACTGGACA GCGGGCATGG GTCTGCTGAT GCGGCTCATC GTGCTGCTCA 300
TCGTGGCGGG CAATGTGCTG GTGATGCTGG CCATCGCCAA GACGCGCGGG CTGCAGACGC 360
TCACCAACCT CTTCATCATG TCCCTGGCCA GCGCGGACCT GGTATGCGGG CTGCTGGTGG 420
TGCCGTTTCGG GGCACCATC GTGGTGTGGG GCGGCTGGGA GTACGGCTCC TTCTTCTGCG 480
AGCTGTGGAC CTCACTGGAC GTGCTGTGCG TGAAGGCCAG CATCGAGACC CTGTGTGTCA 540
TTGCCCTGGA CCGCTACCTC GCCATCACCT CGCCCTTCCG CTACCAAGAG CTGCTGACGC 600
GCGCGCGGGC GCGGGGCTCT GTGTGCAAGG TGTGGGCCAT CTGCGGCTCG GTGTCTTCC 660
TGCCCATCCT CATGCACTGG TGGCGGGCGG AGAGCGAAGA GCGCGCGCGC TGCTACAACG 720
ACCCCAAGTG CTGCGACTTC GTACCAACCC GGGCCTACGC CATCGGCTCG TCCGTAGTCT 780
CCTTCTAAGT GCCCCTGTGC ATCATGGCCT TCGTGTACCT GCGGGTGTTC CGCGAGGCC 840
AGAAGCAGGT GAAGAAGATC GACAGCTGCG AGCGCGGTTT CCTCGGCGGC CCAGCGCGGC 900
CGCCCTCGCC CTGCGCTCGC CCGCTCCCGC GCGCGCGGCC CCGCGCGGCC 960
CGCGCGCGGC CGCGCGCAC GCGCGGCTGG CCAACGGGGG TGCGGGTAAG CGGCGGCGCT 1020
CGCGGCTCGT GGCCTTACGC GAGCAGAAGG CGCTCAAGAC GCTGGGCATC ATCATGGGGG 1080
TCTTCAAGCT CTGCTGGCTG CCTTCTTCTT TGCGCAACGT GGTGAAGGCG TTCCACCGCG 1140
AGCTGGTGCC CGACCGGCTC TTGCTCTTCT TCAACTGGCT GGGCTAAGCC AACTCGGCTC 1200
TCAACCCATC CATCTACTGC CGCAGCCCGC ACTTCGCAA GGCCTTCCAG GACTGCTCT 1260
GCTGCGCGCG CAGGCTGCCC GCGCGGCGCC ACGCGACCCA CGGAGACCGG CGCGCGGCTC 1320
CGGCTGTCTT GCGCGGCGCC GACCCCGCGC CATCGCGCGG GCGCGGCTCG GACGACGACG 1380
ACGACGATGT CGTCGGGGCC ACGCGCGCGC CGCGGCTGCT GGAGCCCTGG GCGGCTGCA 1440
ACGCGGGGCG GCGGGCGGAC AGCGACTCGA GCCTGGACGA GCGGTGCGCG CCGGCTTTCG 1500
CCTCGGAATC CAAGGTGTAG GCGCGGCGCG GCGGCGCGGA CTCCGGGCAC GCTTCCAG 1560
GGGAACGAGG AGATCTGTGT TTACTTAAGA CGATAGCAG GTGAACCGA AGCCACRAT 1620
CCTGCTCTGA ATCATCCGAG GCAAGAGAA AAGCCACGGA CCGTTGCACA AAAAGGAAAG 1680
TTTGGGAAGG GATGGAGAG TGGCTTGTG ATGTTCTTGT TTG

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A167 Protein sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR
 Unigene number: Hs.37744
 Protein Accession #: AA011176
 Signal sequence: none found
 Transmembrane domains: 62-84, 95-117, 135-157, 177-198, 226-248
 Pfam domain: 7tm_1 [75-377]
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MGAGVLVLGA SEPNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQQWTAG 60
MGLLMALIVL LTVAGNVLVI VAIKTPRLQ TLTNLFIMSL ASADLVMGLL VVPFGATIVV 120

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WGRWEYGSFF CELWTSVDVL CVTASIELTC VIALDRYLAI TSPFRYQSLL TRARARGLVC 180
 TWVAISALVS[~] FLPIIMHWMR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSPYVPLCIM 240
 AFVYLRFVRE AQKQVKKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPP RPAAAAAATAP 300
 LANGRAGRKR PSRLVALREQ KALKTLGIIM GVFTLCNLPF FLANVVKAFH RELVPDRLFV 360
 PFNWLGYANS APNPIIYCRS PDKRAFOQL LCCARRAARR RHATHGDRFR ASGCLARPGP 420
 PPSPGAASDD DDDDVVGATP PARLLEPWAG CNGGAAADSD SSLDEPCRPG FASESKV

A168 DNA sequence

Gene name: CEGP1
 Unigene number: Hs.222399
 Probeset Accession #: AA256485
 Nucleic Acid Accession #: AJ400877
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GGGCTCCGCG CACACCTCCC CGGCGCGCGG CCGCCACCGC CCGCACTCCG CCGCCTCTGC 60
 CGCAACCGCG TGAGCCATCC ATGGGGGTGG CGGCGCGCAA CCGTCCCGGG GCGGCCTGGG 120
 CGGTGCTGCT GCTGCTGCTG CTGCTGCCGC CACTGCTGCT GCTGGCGGGG GCCCTCCCGC 180
 CGGTCGCGGG CCGTCCCGCG GGGCGCGCAG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240
 ATGACTGCCA TGCCGACGCC CTGTGTGAGA ACACACCCAC CTCCTACAAG TGCTCCTGCA 300
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAAATGAGC 360
 TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACCTGTT 420
 TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG 480
 AGAACAAATG CCGCTGCCAG CATACCTGTG TCAAGTTCAT GGGGAGCTAT GAGTGTCTGT 540
 GCAAGGAGGG GTTTTTCCTG AGTGACAATC AGCACACCTG CATTCACCGC TCGGAAGAGG 600
 GCCTGAGCTG CATGAATAAG GATCAGCGCT GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660
 GCAGCGTCGC CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720
 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780
 GCGGAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840
 AGCGAGAGGA CACTGTCTCG GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900
 ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAT GGAGGCTGTG 960
 ACGCACCTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGCTCTGTT GGATTCACTC 1020
 TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT 1080
 GTGATCATTT TGCAAAAAC ATCGTGGGCA GTTTTGACTG CGGCTGCAAG AAAGATTATA 1140
 AATTATTAAAC AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT 1200
 GTGACCAACG CTGCATCAAC CACCCTGGCA CATTTGCTTG TGCTTGCAAC CGAGGCTACA 1260
 CCTGTATGG CTTCACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320
 GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAGTGCCAC CTGGGTGACA 1380
 AGCTCCACTG GAATAAAAAA GACTGTGTGG AAGTGAAGGG GCTCCTGCCC ACAAGTGTGT 1440
 CACCCCGTGT GTCCCTGCAC TGGGTGAAGA GTGGTGGAGG AGACGGGTGC TTCTCAGAT 1500
 GTCACTCTGG CATTCACCTC TCTTCAGATG TCACCACCAT CAGGACAAGT GTAACCTTTA 1560
 AGCTAAATGA AGGCAAGTGT AGTTTGAAAA ATGCTGAGCT GTTTCCCGAG GGTCTGCGAC 1620
 CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTAAGTA AACCTTACAT 1680
 GCAGCTCTGG CAAGCAAGTC CCAGGAGCCC CTGGCCGACC AAGCACCCCT AAGGAAATGT 1740
 TTATCACTGT TGAGTTTGA CTTGAAACTA ACCAAAAGGA GGTGACAGCT TCTTGTGACC 1800
 TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACGCTCAGAA 1860
 AGGCGGTCCA CAGGGAGCAG TTTCACTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA 1920
 AAAAGCCTCC TAGAACATCT GAACGCCAGG CAGAGTCCGT TGGAGTGGGG CAGGCTCATG 1980
 CAGAAAAACA ATGTGTGAGT TGCAGGCTG GGACCTATTA TGATGGAGCA CGAGAACGCT 2040
 GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAAATGACT TGTGAACCAT 2100
 GCCCAAGACC AGGAAATTTCT GGGGCCCTGA AGACCCGAGA AGCTTGGAAAT ATGCTGGAAT 2160
 GTGGAGGTCT GTGTCAACCT GGTGAATATT CTGCAGATGG CTTTGACCTT TGCCAGCTCT 2220
 GTGCCCTGGG CACGTTCCAG CCGTGAAGCTG GTCGAACTTC CTGCTTCCCT TGTGGAGGAG 2280
 GCCTTGCCAC CAACATCTAG GGAGCTACTT CCTTTCAGGA CTGTGAAACC AGAGTTCAAT 2340
 GTTCACCTGG ACATTCTAC AACACCAACA CTCACCGATG TATTCGTTGC CCAGTGGGAA 2400
 CATACCAGCC TGAATTGGA AAAAATAATT GTGTTTCTTG CCCAGGAAAT ACTAOGACTG 2460
 ACTTTGATGG CTCCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520
 GAGATTTCAC TGGGTACATT GAATCCCCAA ACTACCCAGG CAATTACCCA GCCAACACCG 2580
 AGTGTAACTG GACCATCAAC CCACCCCCCA AGGCGCGCAT CCTGATCGTG GTCCCTGAGA 2640
 TCTTCTGCCC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGGGAGAA ACCTCTTCAT 2700
 CCAATTCTGT GACAACATAT GAAACCTGCC AGACCTACGA ACGCCCCATC GCCTTCACCT 2760
 CCAGGTCAA GAAGCTGTGG ATTCAATTCA AGTCCAATGA AGGGAACAGC GCTAGAGGGT 2820
 TCCAGTCCCC ATACGTGACA TATGATGAGG ACTACCGAGA ACTCATTGAA GACATAGTTC 2880
 GAGATGGCAG GCTCTATGCA TCTGAGAAC ATCAGGAAAT ACTTAAGGAT AAGAACTTTA 2940
 TCAAGGCTCT GTTTGATGTC CTGGCCCATC CCCAGAACTA TTTCAAGTAC ACAGCCAGG 3000
 AGTCCCGAGA GATCGTTTCA AGATCGTTCA TCOGATTGCT ACGTTCCAAA TGTGTCAGGT 3060
 TTTTGAGACC TTACAAATGA CTCAGCCAC GTGCCACTCA ATACAAATGT TCTGCTATAG 3120
 GGTGGTGGG ACAGAGCTGT CTTCTCTCTG CATGTCAGCA CAGTGGGTA TTGCTGCTAG 3180
 CGGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATAAT TTGGTAAAT 3240
 GAATCTGGTT TTCTTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300
 GACTCTTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CGGCTGGCTG GAGCTGGACT 3360
 TTGGTCAGCC TAGGTGAGAC TCACTGTGCC TTCTGGGGTC TTAATCTTCC TCAAGGAGTC 3420
 TGTATGGGAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACCTTCAG TTCTCTAGC 3480
 CCGGCCCTCT CTAAGGGAGC CCTCTGCACT CGTGTGACGG CTCTGACCAG GCAGAACAGG 3540
 CAAGAGGGGA GGAAGAGAGA CCCCTGCAGG CTCCCTCCAC CCACCTTGAG ACCTGGGAGG 3600
 ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACCTG 3660
 AGTTCTAAGC AGTGTCTGTG AAAAAAATAA TTAGAAATAA ATAAAACTA 3720
 AGCACTTCTG GAGACAT

A169 Protein sequence

Gene name: CEGP1
 Unigene number: Hs.222399

Probeset Accession #: AA256485
 Protein Accession #: CAB92285
 Signal sequence: 1-31
 Transmembrane domains: none
 PFAM domains: EGF-like_domains [49-84,132-167,177-213,286-321,407-442] CUB_domain [809-918]
 Cellular Localization: may be secreted

10 1 11 21 31 41 51
 MGVAGNRNRP AANAVLLLLL LPPPLLLLAG AVPPGRGAA GPQEDVDECA QGLDDCHADA 60
 LCQNTPTSYK CSCRPYQGE GRQCEDIDEC GNEINGGCVH DCLNIPGNVYR CTCFDGFMLA 120
 HDGHNCLDVD ECLENNNGCQ HTCVNVMSY ECCCCKEGFPL SDNQHTCIHR SEEGLSCHMK 180
 15 DHGCSHICKE APRGSVACB RPFGLAKNQ RDCILTCNHG NGGQCHSCDD TADGPECSCH 240
 PQYKMTDGR SCLEREDTVL SVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCRTCKDT 300
 STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFLLLTDEK 360
 SQQDVDECSL DRPCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGQQVCVN 420
 TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480
 20 SSDVTIRTIS VTFKLNEGKC SLKNAELFPE GLRPALEKH SSVKESFRYV NLTCSSGQV 540
 PGAPGRPSTP KEMFITVSEF LETNQKEVTA SCOLSCIVKR TEKRLRKAIR TLRKAVHREQ 600
 FHLQLSGMML DVAKKPPRPS ERQAESCQVG QGHAEQCQVS CRAGTYVDGA RERCILCPNG 660
 TTFNEGGQMT CEPKPRPGNS GALKTPRAWN MSECGLCQP GEYSADGFAP CQLCALGTFO 720
 PEAGRTSCFP CGGLGATKHQ GATSFQDCET RVQCSPGHFI NTTTHRCIRC FVGTYQPEFG 780
 25 KNNCVSCPGN TTTFDQSTN ITQCKNRCG GELGDTGYI ESPNYPGNYP ANTECTWTIN 840
 PPPKRRILIV VPEIFLPIED DGDYLVMRK TSSNSVTYI ETCQTYERPI AFTSRSKKLW 900
 IQFKSNEGNS ARGFQVFPYT YDEYQELIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960
 LAHPQNYFIY TAQESREMPF RSFIRLLRSK VSRFLRPYK

30 A170 DNA sequence
 Gene name: DEME-6 protein (KIAA0452)
 Unigene number: Hs.125783
 Probeset Accession #: AL039402
 Nucleic Acid Accession #: AF007170
 Coding sequence: 1-1725 (underlined sequences correspond to stop codon)

35 1 11 21 31 41 51
 AAGGAGGCGG CCTCCGGGAA AAGCGACCGC AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60
 CTGGACCACT GCATGACCGC CTGGACCTC TTCTCTACCA ACCAGTCTCT AGAAGCACTC 120
 40 AGCTACTCTA AGCCCAAGAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180
 CTGGAGATGC AGGCCATGAT GACCTTTGAC CCTCAGGACA TCCTGCTTGC CGGCAACATG 240
 ATGAAGGAGG CACAGATGCT GTGTCAAGG CACCGAGGA AGTCTTCTGT AACAGATTCC 300
 TTCAGCAGCG TGGTGAACCG CCCACGCTG GGCCAATTCA CTGAAGAAGA AATCCACGCT 360
 GAGGTCTGCT ATGCAGAGTG CCTGCTGCAG CGAGCAGCCC TGACCTTCTT GCAGGACGAG 420
 45 AACATATGCA GCTTCATCAA AGGCGGCATC AAAGTTOGAA ACAGCTACCA GACCTACAAG 480
 GAGCTGGACA GCCTTGTTCA GTCTCACA TACTGCAAG GTGAGAACCA CCGCACTTTT 540
 GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCTACT 600
 AGGATCCTGA GGCCTGTGGA GTTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660
 CAGCTGGAGG AGGGAGCGTG AGGGCAGAGC TTCCGCTCTG TGCTCTGTGT CATGCTCTCTG 720
 50 CTGTGCTACC ACCTTCTCT CACCTTCTGT CTGGTACTG GGAAGCTCAA CATCGAGGAG 780
 GCGAGAGAGC TCTTGAAGCC CTACCTGAAC CGGTACCTTA AGGTGCCAT CTCTCTGTTC 840
 TTTGCAAGGA GGAATTGAAG CATTAAAGGC AACATTGATG CAGCCATCG GCGTTTCGAG 900
 GAGTGTCTGT AGGCCAGCA GCACTGAAG CAGTTTCAAC ACATGTGCTA CTGGGAGCTG 960
 55 ATGTGTGTCT TCACCTACAA GGGCCAGTGG AAGATGTCTT ACTTCTACGC CGACCTGTCT 1020
 AGCAAGGAGA CTGCTGTGTC CAAGGCCACC TACATTAC TGAAGGCCG CTACCTCAGC 1080
 ATGTTTGGGA AGGAGGACCA CAAGCCGTTT GGGGACGAG AAGTGAANTT ATTTGAGCT 1140
 GTGCCAGGCC TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTGCCATC 1200
 CGGAAGTCCC GGCCTACTT CTCTCTCAAC CCTATCTGCG TGCCAGTGCC TGCTCTGGAA 1260
 60 ATGATGTACA TCTGGAACGG CTACGCGGTG ATTGGGAAGC AGCGAAACT CACGGATGGG 1320
 ATACTTGAGA TTATCACTAA GGCTGAAGAG ATGCTGAGA AAGGCCAGA GAACGAGTAC 1380
 TCAGTGGATG ACGAGTGCTT GGTGAAATTG TTGAAAGGCC TGTGTCTGAA ATACCTGGGC 1440
 CGTGTCCAGG AGGCCAGGA GAATTTTAGG AGCATCTCTG CCAATGAAA GAAATTTAAA 1500
 65 TATGACCACT ACTTGATCCC AAACGCCCTG CTGGAGCTGG CCCTGCTGCT TATGGAGCAA 1560
 GACAGAAAGC AAGAGGCCAT CAACTTTTG GAATCTGCCA AGCAAACTA CAAGAATTAC 1620
 TCCATGGAGT CAAGGACACA CTTTGAATC CAGGCAGCCA CACTCCAAGC CAAGCTTCC 1680
 CTAGAGAACA GCAGCAGATC CATGGTCTCA TCAGTGTCTT TGTAGCTTTG TGCAGCAGTT 1740
 CGGGCTGGA AGACAGAGAG AGCTGGACAG AGCTCCTGAA AACATTTCAA AATACCCCT 1800
 70 CCCCTGCCCT TGCCCTGCTT TTGGGGTCCA CGGCACTCC AGTTGGATGG CACAACATAG 1860
 TGTATCCGTG CAGAAGCGA GCTGGCATT TCAACAGTGT AGCCAAGGGC CTTTGCCAAG 1920
 GGCAGAGCAG GTGGAGCCCT CTGCCCTGCC TATCACACAT ACGGGTACTT GCTTTTCACT 1980
 GTGATGTTTA AGAAGATGTA TGAACAGTTT ACATTTTCTT TAGAATAACA TTGATGGGAT 2040
 CACAGTTGGC TTTAAAAACC AACAACAATC AACCACCTGT AAGTCTTTGT CTTCACCTAT 2100
 75 TATCATCTGG AGGTAAATCT CTTTATATGA TGATGCCAAA GGGCAAAATG CTTTTCAAAT 2160
 TCAGCAAGTT CTCAGCTTGT GTGAOAGGAG GTCTTTCAGA GGACCTGAGG AATGCCTGGG 2220
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 80 AGTAGAAAT AGCAGGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCAGG 2460
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 CTGAAACCACT TGGGAATAAT TTATGAAACA TAAAAATCTT CTGTACTTCA CTCAAAGGTA 2580
 CATTGTCTTA CTGACAGCAT TTTTGTAAAA ACTGTTATTC TTGAAAAAAA AAAAAAATAA 2640
 AA

A171 Protein sequence

Gene name: DEME-6 protein (KIAA0452)
 Unigene number: Hs.125783
 Probeset Accession #: AL039402
 Protein Accession #: AAC39582
 Signal sequence: none
 Transmembrane domains: 210-226
 Cellular Localization: plasma membrane

10 1 11 21 31 41 51
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 MTALDLFLTN QFSEALSYLK PRTKESMYHS LTYATILEMQ AMMTFDPQDI LLAGNMKKA 60
 QMLCQRHRRK SSVTDSFSSL VNRPTLGQFT EEBIHAEVCY AECLLQRAAL TFLQDENMVS 120
 FIRGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHPEGGV KLGVGAFNLT LSMPLPTRILR 180
 15 LLEFVFGSGN KDYGLQLLEE GASGHSFRSV LCVMLLLCYH TFLTFLVLTG NVNIEEAERL 240
 LKPYLNRYPK GAIFLFFAGR IEVIKGNIDA AIRRFEECC E AQHWKQFHH MCYWELMWCF 300
 TYKGQWMSY FYADLLSKEN CWSKATYIYM KAAYLMSFGK EDHKPFQDDE VELFRAVPGI 360
 KLKIAGKSLP TEKPAIRKSR RYFSSNPISL PVPALMMYI WNGYAVIGKQ PKLTDGILEI 420
 20 ITKAEEMLEK GPENEYSVDD ECLVKLLKGL CLKYLGRVQE AEENFRSISA NEKKIKYDHY 480
 LIPNALLELA LLLMEQDRNE EAIKLLESAK QNYKYNYSMB RTHFRIQAAT LQAKSSLENS 540
 SRSMVSSVSL

25 A172 DNA sequence
 Gene name: EST
 Unigene number: Hs.200102
 Probeset Accession #: AL117406
 Nucleic Acid Accession #: none found
 Coding sequence: 1-4044 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
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 35 GGCCCTCGGA GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCCACCG 180
 TGGGGAGAGT ATGATGCTGC CTTGAGAAC C ATGATTCCTT TCGTCCCAA GCCGAGGTTT 240
 CCTGCCCCCC AGCCCTCGGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCATGGCTC 300
 ACCCCGCTCA TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCTCCACTG 360
 TCAGTCCATG ATGCGCTCAGA CAAAAATGTC CAAAGGCTTC ACOCCTTTG GGAAGAAGAA 420
 40 GTCTCAAGGC GAGGGATTGA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA 480
 ACAAGGTGTA TTTTCGATGC ACTTCTGGGC ATCTGCTTCT GCATGTCAG TGTACTCGGG 540
 CCAATATTGA TTATACCAA GATCCTGGAA TATTAGAAG AGCAGTGGG GAATGTTGTC 600
 CATGGAGTGG GACTCTGCTT TGCCCTTTT CTCTCOGAAT GTGTGAAGTC TCTGAGTTTC 660
 TCCTCCAGTT GGATCATCAA CCAACGACA GCCATCAGGT TCCGAGCAGC TGTTCCTCTC 720
 45 TTTGACCTTG AGAAGCTCAT CCAATTTAAG TCTGTAATAC ACATCACCTC AGGAGAGGCC 780
 ATCAGCTTCT TCACCGGTGA TGTAACTAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA 840
 GTACTGATCA CTTGCGCATC GCTGGTCATC TGCAGCATTT CTCTCTACTT CATTATTGGA 900
 TACACTGCAT TTATTGCCAT CTTATGCTAT CTCTGCTT TCCACTGGC GGTATTCTAG 960
 50 ACAAGATGAG CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGGACCA GGCATCCGT 1020
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 55 TTTGAGGAGG CCACCTTGTG ATGGCAACAG ACCGTGCTCG GATGCTCAA TGGGGCACTG 1380
 GAGCTGGAGA GGAACGGGCA TGCTTCTGAG GGGATGACCA GGCCTAGAGA TGCCCTCGGG 1440
 CCAGAGGAAG AAGGGAACAG CCTGGGCCA GAGTTGCACA AGATCAACCT GGTGTGTGCC 1500
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 60 GCCATCTGG AGGAGATGCA CTGTCTGAG GGTCTGCTGG GGTGCGAGG AAGCCTGGCC 1620
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 65 CTGCTGGAGC ACCCCTGTGC TGCTGTGGAC GCCACGTTGG GGAAGCATAT TTTGAGGAG 1920
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 GAAGCCACTT CGGACATGTT GCAGGACACA GCAAAGATAG CAGAGAAGCC AAAGGTAGAA 2160
 70 AGTCAGGCTC TGGCCACCTC CTTGGAAGAG TCTCTCAACG GAATGCTGT GCGGAGCAT 2220
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 CTTGTGACCT TGGCTGTGTC CCGTGTCTGT GCTTTTGGCA TTTCTCCAC CCCCTACTCC 3120

5	TTTAAAGTCA	TGGCTGTCAA	CATCGTGTCTG	CAGCTGGCGT	CCAGCTTCCA	GGCCACTGCC	3180
	CGGATTGGCT	TGGAGACAGA	GGCACAGTTC	ACGGCTGTAG	AGAGGATACT	GCAGTACATG	3240
	AAGATGTGTG	TCTCGGAAGC	TCCTTTACAC	ATGGAAGGCA	CAAGTTGTCC	CCAGGGGTGG	3300
	CCACAGCATG	GGGAAATCAT	ATTTCAGGAT	TATCACATGA	AATACAGAGA	CAACACACCC	3360
	ACCGTGTCTC	ACGGCATCAA	CCTGACCATC	CGCGGCCACG	AAGTGGTGGG	CATCGTGGGA	3420
10	AGGACGGGCT	CTGGGAAGTC	CTCCTTGGGC	ATGGCTCTCT	TCCGCTGGT	GGAGCCCATG	3480
	GCAGGCCGGA	TTCTCATTGA	CGGOGTGGAC	ATTTCAGCA	TCCGCTTGA	GGACTTGGCG	3540
	TCCAGCTCT	CAGTGATCCC	TCAAGATCCA	GTGCTGCTCT	CAGGAACCAT	CAGATTCAAC	3600
	CTAGATCCCT	TTGACCGTCA	CACTGACCAG	CAGATCTGGG	ATGCCTTGA	GAGGACATTC	3660
	CTGACCAAGG	CCATCTCAAA	GTTCCTCCAA	AAGCTGCATA	CAGATGTGGT	GGAAAAAGGT	3720
15	GGAAACTTCT	CTGTGGGGGA	GAGGCAGCTG	CTCTGCATTG	CCAGGGCTGT	GCTTCGCAAC	3780
	TCCAAGATCA	TCCTTATCGA	TGAAGCCACA	GCCTCCATTG	ACATGGAGAC	AGACACCTTG	3840
	ATCCAGCGCA	CAATCGGTGA	AGCCTTCCAG	GGCTGCACCG	TGCTCGTCAT	TGCCACCCGT	3900
	GTCAACCATG	TGCTGAAGTG	TGACCAATC	CTGGTTATGG	GCAATGGGAA	GGTGGTAGAA	3960
	TTTGATCGGC	CGGAGGTACT	CGGGAAGAAG	CCTGGGTCTAT	TGTTCCGACG	CCTCATGGCC	4020
20	ACAGCCACTT	CTTCACTGAG	ATAAGGAGAT	GTGGAGACTT	CATGGAGGCT	GGCAGCTGAG	4080
	CTCAGAGGTT	CACACAGGTG	CAGCTTOGAG	GCCCAAGTC	TGCGACCTTC	TTGTTTGGAG	4140
	ATGAGAACTT	CTCCTGGAAG	CAGGGGTAAA	TGTAGGGGGG	GTGGGATTG	CTGGATGGAA	4200
	ACCTTGAAT	AGGCTACTTG	ATGGCTCTCA	AGACCTTAGA	ACCCAGAAC	CATCTAAGAC	4260
	ATGGGATTCA	GTGATCATGT	GGTTCTCCTT	TTAACTTACA	TGCTGAATAA	TTTTATAATA	4320
25	AGGTAAGC	TTATAGTTT	CTGATCTGTG	TTAGAGTGY	TGCAATGCT	GTACTGACTT	4380
	TGTAAATAT	AAACTAAGG	AAAACTCAA	AAAAA	AAAAA	AAAAA	
	<u>A173 Protein sequence</u>						
	Gene name: EST						
	Unigene number: Hs.200102						
30	Probeset Accession #: AL117406						
	Protein Accession #: none found						
	Signal sequence: none found						
	Transmembrane domains: 169-185, 199-215, 275-291, 304-320, 387-403, 770-786, 829-845, 907-923, 927-943, 1018-1034						
	PFAM domains: ABC transporter [502-673], ABC_membrane_region [163-432, 771-1060]						
35	Cellular Localization: plasma membrane						
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	WGKYDAALRT	MIFPRPKPRF	PAPQPLDNAG	LFSYLTVSWL	TPLMIQSLRS	RLDENTIPPL	120
40	SVHDSQDNV	QRLHRLWEEB	VRRGIEKAS	VLLVMLRFQR	TRLIFDALIG	ICFCIASVLG	180
	PILIIPKILE	YSEBQLGNVV	HGVGLCFALF	LSECVKSLSP	SSSWINQRT	AIRFRAAVSS	240
	FAFEKLIQFK	SVIHITSGEA	ISFFTGDVNY	LFEVGYGGLP	VLITCASLVI	CSISSYFIIG	300
	YTAFIAILCY	LLVFPLAVFM	TRMAVKAQHH	TSEVSDQRIK	VTSEVLTCIK	LKMYTWEKP	360
	FAKIEGMES	LTFCSPKPGG	MAPSMLASLN	LLRLSVFFVP	IAVGLTNSK	SAVMRFKIFP	420
45	LQESPVFFVQ	TLQDPKALV	FEEATLSWQQ	TCPGIVNGAL	ELERNHASE	GMRPRDALG	480
	PEEENSLGF	ELHKNLVVS	KGMMLGVCGN	TGSGKSSLLS	AILEEMHLE	GSVGVQGSLS	540
	YVPQANIVS	GNIRENIMG	GAYDKARYLQ	VHCCSLNRD	LELLPFGDMT	EIGERGLNLS	600
	GGQKQRLSA	RAVYSRQIY	LLDDPLSAVD	AHVGHIFEE	CIKRTLGRKT	VVLVTHQLQY	660
	LEFCQIILL	ENKICENGT	HSELMQKKGK	YAQLIQKMHK	EATSDMLQDT	AKIAEKPKVE	720
50	SQALATSLBE	SLANGAVPEH	QLTQBEEMEE	GSLSWRVYHH	YIQAAGGYMV	SCIIFPFVVL	780
	IVFLTIPFSP	WLSYMLEQGS	GTNSSRESNG	TMADLGNLAD	NPQLSFYQLV	YGLNALLLIC	840
	VGVCSSGIPT	KVTRKASTAL	HNKLFNKVFR	CPMSFFDTIP	IGRLINCFAG	DLEQLDQLLP	900
	IFSEQPLVLS	LMVIAVLIV	SVLSPYILLM	GAIMVICFI	YTMFKAIG	VFKRLNYSR	960
	SPLFPHILMS	LQGLSIIHYV	GKTEDFISQF	KRLTDAQNNY	LLLFLSSTRW	MALRLIIMTN	1020
55	LVTLAVALFV	AFGISSTFYS	PKVMVNIIVL	QLASSPQATA	RIGLETBAQF	TAVERILQYM	1080
	KMCVSEAPLH	MEGTSCFPQGW	PQHGBIIPQD	YHMKYRDNTF	TVLHGINTLI	RGHVVGVIGV	1140
	RTSGSKSSLG	MALFRLVEPM	AGRILIDGVD	ICSIGLEDLR	SKLSVIPQDP	VLLSGTIRFN	1200
	LDPFDRHTDQ	QIMDALERTF	LTKAISKFPK	KLETDVVENG	GNFSVGERQL	LCIARAVLRN	1260
	SKILIDEAT	ASIDMETDTL	IQRTIREAFQ	GCTVLVIAHR	VTTVLNCDHI	LVMNGKRVVE	1320
60	FDRPEVLRKX	PGSLFAALMA	TATSSLR				
	<u>A174 DNA sequence</u>						
	Gene name: ESTs						
	Unigene number: Hs.128899						
	Probeset Accession #: AA983251						
65	Nucleic Acid Accession #: AA983251						
	Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)						
70	1	11	21	31	41	51	
	ATGCTGTCTG	GCTTCTTGAT	GAGTCCAGT	ACCCAGCACAC	GAGCACAGTA	CACTCCCGGA	60
	GGAAAGAAAC	TTCCGTGGGA	GGCTTCCATC	GGTGGGCACA	CCTCCGAGG	GGGAGGCAGC	120
	GACCGGGAGA	GGGAGAGCCG	GCCGAGGCT	GCGGGCTCC	TGTGGGACCG	CGCTGCAGCC	180
	GGGAGGCGG	AGAAGGGGAA	CGGGGCGAG	CGCGCGGCT	GGATCCGCGC	CCAGCAGCAG	240
75	CGCGGCGCG	CGCCAGCTGG	GCAGGCTCCC	GGGACTGGGG	CTGGGGGCGC	GCAAGACCTC	300
	CGCTCGCTC	CTGGACGCTC	CGGGGGGAGG	GTCCGGTTGC	CAGTGAAACC	TCCAGAGGCT	360
	TCCGAGCGAC	AGCCCGGGGG	GCTTCTGAC	TGCATCCCGA	GATTTCCATC	AGCGAGTGCA	420
	ACTCATAGG	CAGTCCCTAA	GGGACCGGG	CCACCGGCTG	AGGACGGGGA	TGGCTTAGGA	480
	GCTCCTGGAC	CTAGGGCCCG	GCGTCTGCG	CTCCTGGGCG	TGCGGCAGCA	GGGAGTGGC	540
80	CGCGCGGAA	AGCGCGCGG	GACAGTCAGT	GACGAGGCC	GGGGTTCGCG	GGGGCCACGA	600
	CTTCTCGGAG	ACCGTCTGCG	GCTCTCTGGA	GACGCGCTGT	CGCGGCCACG	GGTGGTGCCA	660
	TGTGGGCGC	TGCGCGCTCG	TCCGTCTCCT	CATCTCTGAA	CGCGGCTTGG	CTCCTGCAGC	720
	TGCTGCTGGC	TGCGCTCTGT	GCGGCGGGGG	CGAGGGCCCA	GCGGCGAGTA	CTGCCACGGC	780

5 TGGCTGGAGC CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTGACGGC 840
 GGGGACGCCA CCATCTGCTG OGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
 GGGCGCTTGG ACCAGGGGCG CTGCGACAAT GACCGCCAGC AGGCGGCTGG CGAGCCCTGGC 960
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 GGAGACGGCG AGGGTGCGCC CCCACCGGTG AGGCGCTGGC AGCGGTGCTC CCCTGAAGGC 1080
 TCCCGAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCGG TGCCAGACGC 1140
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 10 CTGGTGGCAG CCGTGTGCTG CAGATGTCTC CGGCTAAGC AGGATCCCA GCAGAGCOGA 1320
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 15 CAGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTTCATG ACGGCTGCA GCCTGGCTAC 1680
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 50 TTTTAAATA ACCAAGGCA GGGGAAATC ATTTTACTTA TTAATAATA TTTTATGATG 3660
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A175 Protein sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular Localization: not determined

1 11 21 31 41 51
 MLSGFLMSPS TQHQRAYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
 GEAKEGNRGE PPAWIRAQQQ PRPPPAGQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPPPEA 120
 65 SGRQPRGPSD CIPRFPASAS THKAVPKGTG PPAEDGDLG APGPRARRRR LLGVAEESSG 180
 PRGRRTGTVS DEARGSPGR LLDGRPALSG DALSAAPRVV CGALAARPS HPPTPLRSCS 240
 CCWLRCWRRG RGPSEYCHG WLDAGQVWRI GFQCPERFDG GDATCCGSC ALRYCCSSAE 300
 ARLDQGGCDN DRQAGGEPG RADKDGPRRL GRASCLRGTO GDGEGAPFPV RAWQRCSPFG 360
 70 SPKGRQLLRA FPGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPLIVGS VFVAFIILGS 420
 LVAACCCRL RPKQDPQQR APGGNRLMET IPWIPSASTS RGSSSRQSST AASSSSSANS 480
 GARAPPTRSQ TNCLPBGTM NNVYVNMPTN PSVLMCQAT QIVPHQGYL HPYVGYTVQ 540
 HDSVPMTAVP PFMGLQPGY RQIQSPFFHT NSEQMYPAV TV

A176 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GCCCTTGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60

5 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
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 CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCGCG CCCACTGGGG 240
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTGG GGGAGCTGCT GGCTGCAGCC 300
 TGTGCCAGCC GGGCCCTGCC CCGTCTCTCC TCCGGGCCCC CCTGCCCTGC CCTGACGTCC 360
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAATCG 480
 GCGCTCATTA AGCAGCTGTT TGAGGCCCCG GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540
 10 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCC CCAGGGCCAG CCTGGCACTC 600
 AGCCCTTCGA GGGTGGGGCG CCCATCGCAC CCACCTCTC TGGCTGGAGA CCCCGGCAG 660
 GCCCAGCCAC AGTCCCGGAG TGGGCGCCTT CCTGCCGCC TTGCCAGATG GGCTCCCCAG 720
 GCCTGCCCCC AGGTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG 780
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGAG CTACTACTGG CCGCTGTCTG 840
 15 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCGCG TTTCCAGCGG TGCGCGCCTG 900
 GGTCCTCTCT TCAGGAAAAG GCACTGCCCA CGCCAGGCTG CACTTCCAC AACGGGCAGC 960
 AGAGGGCGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGTG GGGACGGCCT 1080
 GTAAGCGGGG GGTGCTCTGC TGGCTGGGGA GCCCAGGGA TAGCGGTGG ACTTCAGGTT 1140
 CTGGCCACAG CTGAGGGACC CTGCTGCAG CGGATCGGCA CGCGGGGTG GCGAGAGCTT 1200
 20 GGCTGTGATG TGCTTCCAC AGACCTGGG GTGATGGCCT TCCCTCTCTT GCGCGGAGCG 1260
 TTGCCCCACG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCGAG AGGGCCCCCA 1320
 GACAGCTCCC AGGCACGTC TAGGCAAGC CTGTTTCCCC CGACTCAGGA TTTCGAAGGC 1380
 CTGGGGTCTT GCTCACCCCC CTTTGCTCTC ACGCCAGCC TGTCCCGAG TTTCAGCTGG 1440
 25 GAGAGGGCAG CTCCCTCAGC CAAGAAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500
 GGCAGGTCCC CTGGGTGTGC ACTCCCTCAG CCCCTGCCCA GGCCCACTCC CGCTGGTGCT 1560
 GGAGTACGCA CTGGTGGGGG GGCCCTGTCT AGCCCAACTT GGAGGGTCCC AGTGTACCA 1620
 GAACAGGGG CAGGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680
 TCAGTGTGTG TGGGGCGCAG GGCTCCGAT GCGGGGTGAG TGCGTGGGGG GCGCAGGGCC 1740
 30 CCCGATGCGG GGTCACTGCG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCATTTGGT 1800
 ACATGTCTCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCACTC 1860
 CCTTCCGAGG CCGAGCTCCA TGCTAACCTG CCCACAGCAA CCCACAGAG CCACATTTCC 1920
 TGCTGCACCT GGTCTGCAGG GGTGTCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1980
 GCCCTCCTAC CTTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAGGATG TCAGGCTTGG 2040
 35 ACCTCCTGGG CAGGAAAGGG TGCAGGTCTT GAGGGCTGTG GCCCCACAGC CCCAGCACCC 2100
 AGGTGGACTG CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAAGCC CCGTTCAGCA 2160
 GGCTGGGCTC TGCCCAACAG GGCTCCCCA CGTCTGCCCT TGAGGGTGCC TGCCATGCC 2220
 TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCG 2280
 GGTGACTTCA TCAGGAGACC GCCACATAG AGCTGGAGCC CGCAGCTGAA GCGAAATGT 2340
 40 GAGACAGGCT GGCACCTCCG GAAAACTGC CTTTCAGCCT TGGTGTCCG TGCAAGGTGA 2400
 AAAGAATAG GTCTCCCGAG TTTACAGCTT GAAATCAGGC TAGTGAGTG CCCTGGAGAC 2460
 CAGAGGGGA GAATTTAAG GCCCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520
 GCAGACCTG CCGGAGCCTT GCGCTAGGAC GCTGGGGGG TCAGTCTCCG TGCAGGATGT 2580
 GAGCAGCGTC CCGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGAGGT ACATACAGT 2640
 45 CGGTGCACAC TGTGATGACA CCGGAAAATG TCTCAGGATG TTGAAATGT TCTTTGGGG 2700
 CAGAAATGTC CCAAGTTGAG AATCTGCCCC AGAGGAACAC ACCACACCA GGCCTCAGGA 2760
 TTTGTGTGTG ATCAAGTTCC AAGGAAAAGG AACATCTCAG CCGGGCGTGG TGGTTACGC 2820
 TTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
 CCCCATCTCT ACARAAGAA AAAAAAGAGG AAAGAAAATG AGAGATCCAG GTTTAAAAAT 2940
 50 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAACAC AGATTGACTC 3000
 TAGACCCACT TACTAGAAAT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060
 AGAAATAAAA GAGATTCTG GAAACATGAA AAAAAA

A177 DNA SEQUENCE

55 Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

60 1 11 21 31 41 51
 | | | | |
 GGGAAACACC GGGCCGCGGT GCGGCGAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
 TCCCTGTGTG ACCTCTCGOG TCTCTCTCTC TTCTCCAGGT TTGCTGGCTG CAGTGGCGGG 120
 65 CCTCCGAGCC GTGCCGGGGG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCTT GGGCTGCCCT GGCAGAGACC 240
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACGTGTGG GAATGGCGAG ACAGTCCAGG 300
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCAATCCAAA CGTATCTTAC 360
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCTGAAAAT GGCAGGGGTC 420
 70 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
 ACAGCATCAC GGGCGCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540
 AGACAGGCTG GTTGTGTGTG AATAAGCCAC TGGACCAGGA GGAGATTGCC AAGTATGAGC 600
 TCTTTGGCCA CGCTGTGTCA GAGAAATGGT CTTCACTGGA GGACCCCATG AACATCTCCA 660
 TCATCGTAC CGACCAAGAT GACCAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
 75 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA 840
 AGGACCCACA CGACTCATG TTCACAATTC ACGGAGCAGC AGGCACCATC AGCGTCATCT 900
 CCAGTGGCCT GGAACGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
 TGGATGGGGA GGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCTTT GATGCCAATG 1020
 80 ACAATGCTCC CATGTTTGAC CCCAGAAAT ACAGGGCCCA TGTGCTGAG AATGCACTGG 1080
 GCCATGAGGT CCAGAGGCTG ACGGTCACTG ATCTGGAGCC CCCCAACTCA CCAGCGTGGC 1140
 GTGCCACCTA GGTATCATG GCGGGTACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
 CTGAGAGCAA CCAGGGCATC CTGACAAACA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
 AGCACCCCTT TACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAG CTCCCAACCT 1320
 CCACAGCCAC CATAGTGTGC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380

5 CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
 CTGCAGAAGA CCCTGACAAG GAGAATCAAA AGATCAGCTA COGCATCCTG AGAGACCCAG 1500
 CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTAC AGCTGTGGGC ACCCTCGACC 1560
 GTGAGGATGA GCAATTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
 ATGGAAGCCC TCCCACTACT GGCAAGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
 ACCATGGCCC AGTCCCTGAG CCCCCTCAGA TCACCATCTG CAACCAAGC CCTGTGCGCC 1740
 ACGTGTCTGA CATCAOGGAC AAGGACCTGT CTCCCCACAC CTCCCCCTTC CAGGCCCCAGC 1800
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 10 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTTT TCTCTGTCTG 1920
 ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGOGAC TGCCATGGCC 1980
 ATGTGCAAAAC CTGCCCTGGA CCGTGGAAGG GAGGTTTCAT CCTCCCTGTG CTGGGGGGCTG 2040
 TCCTGGCTCT CTGTGTTCTC CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100
 TCAAGGAGCC CCTCTACTC CCAGAAGATG ACACCGTGA CAACGTCTTC TACTATGGCG 2160
 15 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
 AGGCCAGGCC GGAGGTGGTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
 AGGCGGCTAA CACAGACCCC ACAGCCCGCC CCTACGACAC CCTCTGGTGG TCGACTATG 2400
 AGGGCAGCGG TCCGACGCC GGTCCCTGGA GCTCCCTCAC CTCTCCGCC TCGACCAAG 2460
 20 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520
 ACGTGGCGGG GGAGGAGCAG TAGGGCGCCT GCCTGCAGGG CTGGGGACCA AACGTGAGGC 2580
 CACAGAGCAT CTCGAAGGGG TCTCAGTTCC CCTCTCAGCT GAGGACTTCG GAGCTTGTCA 2640
 GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
 TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760
 25 CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2820
 TGCTCAACCC TGTGTCTGCG GCCTGGGCCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAATGGA ACCTCTCTAG GCCTCCTGGT GCAACTTAAT TTTTCTTTT AATGCTATCT 2940
 TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCGAGA GCTGCTGGGC CCACTGGCCG 3000
 TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT 3060
 30 ATACTGAGTG TGCTTAGGTT GCOCCTTATT TTTTATTTTC CCTGTGCGT TGCTATAGAT 3120
 GAAGGGTGAG GACAATCTGT TATATGTACT AGAAGCTTTT TATTAAGAA A

A178 Protein sequence:

35 Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675
 40 Cellular localization: plasma membrane

45 1 11 21 31 41 51
 MGLPRGPLAS LLLLQVCHLQ CAASEPCRAV FREAEVLEA GGAEQEPGQA LGKVFMGCPG 60
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPFSKR ILRRHKRDWV VAPISVPENG 120
 KGFPFQRLNQ LKSNKDRDTK IPYSITGPGA DSPPEGVFAV EKETGMLLIAN KPLDREBIAX 180
 YELFGHAYSE NGASVEDPMN ISIIIVTDQND HKPKPTQDTF RGSVLEGVLP GTSVMQVTAT 240
 50 DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRTGTIS VISSGLDREK VPEYTLTIQA 300
 TDMDDGGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEP AVGHEVQRLT VTDLDAFNPS 360
 AWRATYLYMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLMDF DSGQVTAAGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLLTLD 540
 55 VNDHGVPEVP RQITICNQSP VRHVLNITDK DLSPTSPFPQ AQLTDDSDIY WTAEVNNEGD 600
 TVVLSLKKFL KQDTYDVHLS LSDHGKNEQL TVIRATVDCD HGHVETCPGP WKGGFILEVL 660
 GAVLALLPLL LVLLLLVREK RKIKEPLLLP EDDTRDNVPY YGEBGGGEED QDYDITQLHR 720
 GLBARPEVVL RNDVAPITIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
 DYEAGSGSDAA SLSSLTSSAS DQDQDYDYLA EWGSRPFKLA DMYGGGEDD

A179 DNA SEQUENCE

60 Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
 Unigene number: Hs.258583
 Probeset Accession #: NM_012152
 Nucleic Acid Accession #: NM_012152
 65 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
 CTCTCTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
 GACAAGCACA TGAATTTTTT TTATAATAGG AGCAACACTG ATACTGTGGA TGACTGGACA 120
 GGAACAAGAC TTGTGATTGT TTGTGTGTTT GGCAGCTTTT TCTGCTGTTT TATTTTTTTT 180
 TCTAATTCTC TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATT CCCTTCTAC 240
 75 TACCTGTTGG CTAATTTAGC TGCTGCGGAT TTCTTGTCTG GAATGCTTA TGTATTCTCT 300
 ATGTTTAAAC CAGGCCCAGT TTCAAAAACT TTAGCTGTCA ACCGCTGGTT TCTCCGTGAG 360
 GGCCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCGTGGAG 420
 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480
 CTGCTCATTT CTCTTGTCTG GGCCATGCCC ATTTTATGAG GGGCGGTCCC CACACTGGGC 540
 80 TGGAAATGCC TCTGCAACAT CTCTGCTGCT TCTTCCCTGG CCCCATTATA CAGCAGGAGT 600
 TACCTTGTGT TCTGGACAGT GTCCAACTTC ATGGCTTCC TCATCATGGT TGTGGTGTAC 660
 CTGCGGATCT CCGGTACGCT CAAGAGGAAA ACCAAAGTCT TGTCTCCGCA TACAAGTGGG 720
 TCCATCAGCC GCGCGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780

		GCCTTTGTGG	TATGCTGGAC	CCCGGGCCTG	GTGGTTCTGC	TCCTCGACGG	CCTGAACTGC	840
		AGGCAGTGTG	GCCTGCAGCA	TGTGAAAAG	TGGTTCCTGC	TGCTGGCGCT	GCTCAACTCC	900
		GTGCTGAACC	CCATCATCTA	CTCCTACAAG	GACGAGGACA	TGTATGGCAC	CATGAAGAAG	960
5		ATGATCTGCT	GCTTCTCTCA	GGAGAACCCA	GAGAGGGCTC	CCTCTCGCAT	CCCTCCACA	1020
		GTCTCGACGA	GGAGTGACAC	AGGCAGCCAG	TACATAGAGG	ATAGTATTAG	CCAAGGTGCA	1080
		GTCTGCAATA	AAAGCACCTC	CTAAACTCTG	GATGCCTCTC	GGCCACCCA	GGTGATGACT	1140
		GTCTTAGG						
10		<u>A180 Protein sequence:</u>						
		Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7						
		Unigene number: Hs.258583						
		Probeset Accession #: NM_012152						
15		Protein Accession #: NP_036284						
		Signal sequence: none found						
		Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295						
		Cellular Localization: plasma membrane						
20		1	11	21	31	41	51	
		MNECHYDKHM	DFPYNRSNTD	TVDDWTGTKL	VIVLCVGTFF	CLFIFFSNSL	VIAAVIKNRK	60
		FHFPPFYLLA	NLAAADFFAG	IAYVFLMFNT	GPVSKTLTVN	RWFLRQGLLD	SSLTASLTNL	120
25		LVIAVERHMS	IMRMVHNSL	TKKRVTLIL	LVWAIAlFMG	AVPTLGNWCL	CNISACSSLA	180
		PIYSRSYLVF	WTVSNLMAFL	IMVVVYLRIY	VYVKRKTNVL	SPHTSGSISR	RRTPMKLMKT	240
		VMTVLGAFVV	CWTPGLVLL	LDGLNCRQCG	VQHVKNFLL	LALLNSVVNP	IISYKDEDM	300
		YGTMKIMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK	STS	
30		<u>A181 DNA SEQUENCE</u>						
		Gene name: ESTs						
		Unigene number: Hs.162859						
		Probeset Accession #: AA569531						
		Nucleic Acid Accession #: AA569531						
35		Coding sequence: 1-504 (underlined sequences correspond to start and stop codons)						
		1	11	21	31	41	51	
		<u>ATGACCTACA</u>	<u>GTTACTCATT</u>	<u>TTTCAGGCCT</u>	<u>GAGTTGATCG</u>	<u>TTAATCATCT</u>	<u>TAATTATGTT</u>	60
		CATTCTGAAG	CCACACAGGAG	AACCAAGACC	AAAACCTTTAT	TGCTCTGCT	TTCAATTTCTT	120
40		GATGAAACCT	CTGGACATAAG	CACACATCTT	CCTTGTATTAT	CTCTCTCAAA	GGAGTGTGGA	180
		GTGCTTCATC	TGGACATCCA	CGGGAAGAAG	GAAACATGTA	GAATCACCCA	ACAGTCTTCC	240
		CAGCTATACC	TGTGGGACAT	GGGTGTTT	ACAATATTTA	AGAACCTGTG	GATGAGCCTC	300
		ATACCCAGAG	GGAAACAAAG	CTCCCCAAA	AGAGTTACAG	AAACCATCCT	GAGAGATTTT	360
		AAGCAGAAGC	AAAGTTCAAA	GATCCAAGAG	GAGAGACGAA	GAGAGTCTGC	AGGACCAAAC	420
45		CTCTCTTAT	TCTGTTTGT	GGGGAATGCT	GGAAGAGGAG	ACAGGCCCCA	GATTTGGGCA	480
		GGAAAGTAAAC	AGTTTTCAGG	CTGAGGCCAA	TCTGAGCAGG	AACATTCCAA	TATTTCTTCA	540
		GCTACGTTGT	CCCAGCATT	CACCTGGTTAA	CCTTTTATGT	CCACCATTTG	TGGATTTCAC	600
		AGCTACTTGT	CAATGGTGAA	TATTGATCAT	CATCATTATC	TACTGAGCTG	CTACCATATC	660
		CCAGCTACTC	CTTGATGTT	GTTCAATTAT	TTCTCAACAC	TCAGCATATT	TGCAATATGT	720
50		TATGTAATAT	CACAGCAAG	GAAACTGAAC	GCAGAAATGT	TTTATTCTT	GCCAAACATC	780
		ACATGAGGAT	GAACAATGAA	ACCGATTGTA	AACCGAGATT	GTCTGATTCC	AACATCTCTG	840
		GGTCTCTTTT	CACCTGATA	TGCTGCAATT	AAAAAGCCAT	TTCTAAGACT	GT	
55		<u>A182 Protein sequence:</u>						
		Gene name: ESTs						
		Unigene number: Hs.162859						
		Probeset Accession #: AA569531						
60		Protein Accession #: none found						
		Signal sequence: 1-46						
		Transmembrane domains: none found						
		Cellular Localization: not determined						
65		1	11	21	31	41	51	
		MTYSYSFFRP	ELIVNHLNYV	HSEANRRRTKT	KTLLSLLSFL	DETSGLSTHL	PCLSLSKECG	60
		VLHLDIHGKK	EDMRITQSS	QLYLWDMGGF	TIFKNLWMSL	IPRGNKRSPK	RVETILRDF	120
70		KQKQSSKIQE	ERRRESAGFN	LSSFVFGVNA	GRGDRPQIWA	GSKQPSG		
		<u>A183 DNA SEQUENCE</u>						
		Gene name: ESTs						
		Unigene number: Hs.179809						
		Probeset Accession #: N95796						
75		Nucleic Acid Accession #: XM_050197						
		Coding sequence: 310-1971 (underlined sequences correspond to start and stop codons)						
		1	11	21	31	41	51	
80		TCACACGTGC	CAAGGGGGCTG	GCTCAGCGGA	ACCAGCCTGC	ACGCGCTGGC	TCGGGGTGAC	60
		AGCCGCGCGC	CTCGCCAGG	ATCTGAGTGA	TGAGACGTGT	CCCCACTGAG	GTGCCCCACA	120
		GCAGCAGGTG	TTGAGCATGG	GCTGAGAAGC	TGGACCGGCA	CCAAAGGGCT	GGCAGAAATG	180
		GGCGCTGGC	TGATTCTCTAG	GCAATTGGCG	GCAGCAAGGA	GGAGAGGCGG	CAGCTTCTGG	240
		AGCAGAGCCG	AGACGAAGCA	GTTCTGGAGT	GCCTGAACGG	CCCCCTGAGC	CCTACCGGCC	300

5 TGGCCCACTA TGGTCCAGAG GCTGTGGGTG AGCCGCTGCG TGCGGCACCG GAAAGCCACG 360
 CTCTGTGCTGG TCAACCTGCT AACCTTTGGC CTGGAGGTGT GTTTGGCCCG AGGCATCACC 420
 TATGTGCCCC CTCTGCTGCT GGAAGTGGGG GTAGAGGAGA AGTTTCATGAC CATGGTGCTG 480
 GGCAATTGGT CAGTGTGGGG CTGTGTCTGT GTCCCGCTCC TAGGCTCAGC CAGTGACCCAC 540
 TGGCGTGGAC GCTATGGCCG CCGCGGGCCC TTCACTCTGG CACTGTCTCT GGGCATCCTG 600
 CTGAGCCTCT TTCTCATCCC AAGGGCCGGC TGGCTAGCAG GGCTGTCTGT CCGGATCC 660
 AGGCCCTGG AGCTGGCACT GCTCATCTCG GCGTGGGGC TGCTGGACTT CTGTGGCCAG 720
 GTGTGCTTCA CTCACCTGGA GGCCCTGCTC TCTGACCTCT TCCGGGACCC GGACCACTGT 780
 10 CGCCAGGCTT ACTCTGCTTA TGCCCTCATG ATCAGTCTTG GGGGCTGCC TGGCTACCTC 840
 CTGCTCTGCA TTAGCTGGGA CACCACTGCC CTGGCCCCCT ACCTGGGCAC CCAGGAGGAG 900
 TGCCCTCTTG GCTGCTCAC CCTCATCTTC CTCACCTGCG TAGCAGCCAC ACTGCTGGTG 960
 GCTGAGGAGG CAGGCTGGG CCCCACCGAG CCAGCAGAAG GGCTGTCCGC CCCCTCCTTG 1020
 TGCCGCCACT GCTGTCCATG CCGGGCCCCG TTGGCTTTCC GGAACCTGGG GCGCTGCTT 1080
 15 CCGCGGCTGC ACCAGCTGTG CTGCGCATG CCGCGACCC TGCGCGGCT CTTCGTGGCT 1140
 GAGCTGTGCA GCTGGATGGC ACTCATGACC TTCACTGTGT TTTACACGGA TTTCTGGGGC 1200
 GAGGGGCTGT ACCAGGGCGT GCCCAGAGCT GAGCCGGGCA CCGAGGCCCG GAGACACTAT 1260
 GATGAAGGCG TCGCATGGA GAGCCTGGGG CTGTTCTTGC AGTGCGCCAT CTCCCTGGTC 1320
 TTCTCTCTGG TCATGGACCG GCTGGTGAGC CGATTCCGGA CTCGAGCAGT CTATTGGGCC 1380
 20 AGTGTGGCAG CTTTCCCTGT GGCTGCGGT GCCACATGCC TGTCCACAG TGTGGCCGTG 1440
 GTGACAGCTT CAGCGGCCCT CACCGGGTTC ACCTTCTCAG CCCTGCAGAT CCTGCCCTAC 1500
 ACACTGGCCT CCTCTACCA CCGGAGAGA CAGGTGTTCC TGCCCAATA CCGAGGGGAC 1560
 ACTGGAGGTG CTAGCATGGA GGACAGCCTG ATGACCACTT TCCTGCCAGG CCTTAAGCCT 1620
 GGAGCTCCTT TCCTTAATGG ACACTGGGT GCTGGAGGCA GTGGCCTGCT CCCACCTCCA 1680
 25 CCGCGCTCT CCGGGGCTCT TGCTGTGAT GTCTCGTAC GTGTGGTGGT GGGTGAGCCC 1740
 ACCGAGGCCA GGGTGGTTCC GGGCCGGGCG ATCTGCTCGG ACCTCGCCAT CCTGGATAGT 1800
 GCCTTCTGCG TGTCCAGGT GGGCCCATCC CTGTTTATGG GCTCCATTGT CCAGCTCAGC 1860
 CAGTCTGTCA CTGCTATAT GGTGTCTGCC GCAGGCTGG GTCTGTGCG CATTTACTTT 1920
 30 GCTACACAGG TAGTATTGA CAAGAGCGAC TTGGCCAAAT ACTCAGCGTA GAAACCTTCC 1980
 AGCACAATGG GGTGAGGGC CTGCTCACT GGGTCCAGC TCCCGCTCC TGTTAGCCCC 2040
 ATGGGGCTGC CCGGCTGGCC GCCAGTTTCT GTTGTGCCA AAGTAATGTG GCTCTCTGCT 2100
 GCCACCTGCT GCTGTGAGG TGCGTAGCTG CACAGCTGGG GGCTGGGGCG TCCCTCTCCT 2160
 CTCTCCCGAG TCTCTAGGCG TGCTGACTG GAGGCTTCC AAGGGGTTT CAGTCTGGAC 2220
 35 TTATACAGGG AGGCCAGAG GGTCCATGC ACTGGAATGC GGGGACTCTG CAGGTGGATT 2280
 ACCCAGGCTC AGGTTAACA GCTAGCCTCC TAGTTGAGAC ACACCTAGAG AAGGGTTTTT 2340
 GGGAGCTGAA TAACTCAGT CACTGGTGT CCATCTCTA AGCCCTTAA CCGTCAAGCTT 2400
 CGTTTAATGT AGCTCTTGA TGGAGTTTC TAGGATGAAA CACTCCTCCA TGGGATTTGA 2460
 40 ACATATGAAA GTTATTGTA GGGGAAGAGT CTTGAGGGGC AACACACAAG AACCAAGTCC 2520
 CCTCAGCCCC ACAGGCACTG GTCTTTTTTG CTNGANTCCA CCCCCCCTT CTTTACCCTT 2580
 TT

A184 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.179809
 45 Probeset Accession #: N95796
 Protein Accession #: XP_050197
 Signal sequence: none
 Transmembrane domains: 21-43, 53-75, 90-112, 125-147, 160-182, 199-221, 323-345, 350-372, 379-401
 50 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 55 MVQLRWVSR LRRHKAQLLL VLLTFGLEV CLAAGITYVP PLLLEVGVVE KFMTMVLGIG 60
 PVLGLVCPPL LGSASDHWRG RYGRRRPFIW ALSLGILLSL FLIPRAGWLA GLLCPDFRPL 120
 ELALLILGVG LLDPCGVQCF TPLEALLSDL FRDPDHCRQA YSVYAFMISL GGCLGYLLPA 180
 IDWDTSALAP YLGTQEECLF GLTLTIFLTC VAATLLVASE AALOPTPEAP GLSAPSLSPH 240
 CPCRARLAP RNLGALLPRL HQLCCRPRT LRRLFVAELC SWMALMTFTL FYTDFVGEGL 300
 60 YQGVPRAPFG TBSRRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFQ TRAVYLASVA 360
 AFPVAAGATC LSHSVAVVTA SAALTGTFPS ALQILPYTLA SLYHREKQVF LFKYRGDTGG 420
 ASSEDSLMTS FLPGPKPGAP FPNHVGAGG SGLLPPFPAL CGASACDVSF RVVVGEPTEA 480
 RVVPGRGICL DLAILDSAPL LSQVAPSLFM GSVIQLSQSV TAYMVAAGL GLVAIYPATQ 540
 VVFDKSLIAK YSA

A185 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.11260
 Probeset Accession #: R73640
 70 Nucleic Acid Accession #: AK002126
 Coding sequence: 1-1593 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 75 ATGGTTGCCG GGGGGCTGCT TGCGTGGATT TCCCGGGTGG TGGTTTGTCT GGTGCTCCTC 60
 TGCTGTGCTA TCTCTGTCTT GTACATGTTG GCCTGCACCC CAAAGGTGTA CGAGGAGCAG 120
 CTGGCACTGC CCAGGGCCAA CAGCCCCACG GGGAGGAGG GGTACCAGGC CGTCTTCTAG 180
 GAGTGGGAGG AGCAGCACCG CAACTACGTG AGCAGCCTGA AGCGGCAGAT CGCAGCCTC 240
 80 AAGGAGGAGC TGCAGGAGAG GAGTGAGCAG CTCAGGAATG GGCAGTACCA AGCCAGCGAT 300
 GCTGTCTGCC TGGGTCTGGA CAGGAGCCCC CCAGAGAAAA CCGAGGCCGA CTCTCTGGCC 360
 TTCTGCACT CGCAGGTGGA CAAGGCAGAG GTGAATGCTG GCGTCAAGCT GCCACAGAG 420
 TATGCAGCAG TGCCCTTCTG TAGCTTTACT CTACAGAAGG TGTACCAGCT GGAGACTGGC 480
 CTTACCGCCG AGCCCGAGGA GAAGCCTGTG AGGAGGACA AGCGGATGA GTTGTGGGAA 540
 GCCATTGAAT CAGCCTTGGA GACCCTGAAC AATCTGCAG AGAACAGCCC CAATCAGCT 600

5 CCTTACACGG CCTCTGATT CATAGAAGGG ATCTACCGAA CAGAAAGGGA CAAAGGGACA 660
 TTGTATGAGC TCACCTTCAA AGGGGACCAC AAACAAGAAAT TCAACCGCT CATCTTATTT 720
 CGACCATTCG GCCCATCAT GAAAGTGAAA AATGAAAAGC TCAACATGGC CAACACGCTT 780
 ATCAATGTTA TCGTGCTCT AGCAAAAAGG GTGGACAAGT TCCGCGAGTT CATGCAGAAAT 840
 TTCAGGAGGA TGTGCATTGA GCAGGATGGG AGAGTCCATC TCACTGTGTGTTTACTTTGGG 900
 AAAGAAGAAA TAAATGAAGT CAAAGGAATA CTGAAAACA CTTCCAAAGC TGCCAACTTC 960
 AGGAACCTTA CCTTCATCCA GCTGAATGGA GAATTTTCTC GGGGAAAAGG ACTTGATGTT 1020
 GGAGCCCGCT TCTGGAAGGG AAGCAACGTC CTCTCTCTTT TCTGTGATGT GGACATCTAC 1080
 10 TTACATCTG AATTCCTCAA TACGTGTAGG CTGAATACAC AGCCAGGGAA GAAGGTATTT 1140
 TATCCAGTTC TTTTCAGTCA GTACAATCCT GGCATAATAT ACGGCCACCA TGATGCAGTC 1200
 CCTCCCTTGG AACAGCAGCT GGTCAATAAG AAGGAACTG GATTTTGGAG AGACTTTGGA 1260
 TTTGGGATGA CGTGTGAGTA TCGGTGAGAC TTCAATCAATA TAGGTGGGTT TGATCTGGAC 1320
 ATCAAAGGCT GGGGCGGAGA GGATGTGCAC CTTTATGCGA AGTATCTCCA CAGCAACCTC 1380
 15 ATAGTGGTAC GGACGCTGT GCGAGGACTC TTCCACTCT GGCATGAGAA GCGCTGCATG 1440
 GACGAGCTGA CCCCGAGCA GTACAAGATG TGCATGCAGT CCAAGGCCAT GAACGAGGCA 1500
 TCCCACGGCC AGCTGGGCAT GCTGGTGTTC AGGCACGAGA TAGAGGCTCA CCTTCGCAAA 1560
 CAGAACAGAG AGACAAGTAG CAAAAAACA TGA

20 A186 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.11260
 Probeset Accession #: R73640
 Protein Accession #: NP_060841
 25 Signal sequence: 1-26
 Transmembrane domains: none found
 Cellular Localization: not determined

30 1 11 21 31 41 51
 | | | | |
 MVRRGLLAWI SRVVLVLLV CCAISVLYML ACTPKGDEEQ LALPRANSPT GKEGYQAVLQ 60
 EWEEQHRYNV SSLKRRQIAQL KEELQERSEQ LRNGQYQASD AAGLGLDRSP PEKTQADLLA 120
 FLHSQVDKAE VNAGVKLATE YAAVPFDSFT LQKVYQLETG LTRHEPEKPV RDKRDELVE 180
 35 AIESALETLN NPAENSPNHR PYTASDFIEG IYRTERDKGT LYELTFKGDH KHEFKRLILF 240
 RPFPIIMKVK NEKLANMANTL INVIVPLAKR VDKFRQFMQN FREMCIEQDG RVHLTVVYFG 300
 KEELINEVGI LENTSKAAMF RNFTFIQLNG EFSRGRGLDV GARFWKGSNV LLFPDVEDIY 360
 FTSEPLNTCR LNTQPGKKVF YPVLFSQYNP GIIYGHDAV FPLEQQLVIK KETGFWRDFG 420
 FGMTQYRSD FINIGGFDDL IKGWGGEDVH LYRKYLSHNL IIVRTIPVRGL FHLWHEKRCM 480
 40 DELTPEQYKM CMQSKAMNEA SHGQLGMLVF RHEIEAHLRK QRKQTSKKT

A187 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 45 Nucleic Acid Accession #: AF189723
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 | | | | |
 ATGATTCCTG TATTGACATC AAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
 ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
 TTTCAATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
 55 TCTCAGTTTA AAAATCCCTT TATTATGCTG CTCTGGCTT CTGAGTCAT CAGTGTITTA 240
 ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300
 GCCTTTGTTT AGGAATATCG TTCAGAAAAA TCTCTGAAG AATTGAGTAA ACTTGTGCCA 360
 CCAGAATGCC ATTGTGTGGG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420
 CAGGTGTGATA CAGTTTGCTT TCTGTGTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTGT 480
 60 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTCTT 540
 AAGGTGACAG CTCTCAGCC AGCTGCAACT AATGAGATC TTGCATCGAG AAGTAACATT 600
 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTCTAT TGGAACAGGA 660
 GAAAATCTG AATTGGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
 CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTACTC CTTTGGTATA 780
 65 ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAA ATATCTGTGA AATGTTTACT 840
 ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCCATTGT GGTCAAGTGT 900
 AOGCTAGCTC TTGGTGTAT GAGAAATGGT AAGAAAAGGG CCATTGTGAA AAGACTGCCT 960
 ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTCG AACACTGAOG 1020
 AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGATGTC TGAGGTTACT 1080
 70 GGAGTTGGCT ATAATCAAIT TGGGGAAGTG ATTGTGATG GTGATGTTGT TCATGGATTC 1140
 TATAACCCAG CTGTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
 AGAAACATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260
 ATGGGCTCTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320
 GAGCAAAAGT GGAATGGCTG TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
 75 TGTTTATAGA AAGGTGCTTA CGAACAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
 GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAGA GAAGGCACCG 1500
 ATGGGCTCAG CGGAGACTCAG AGTCTTGTCT TTGGCTTCTG GTCTGTAAGT GGGACAGCTG 1560
 ACATTTCTTG GCTTGTGGG AATCATGTAT CCACETAGAA CTGCTGTGAA AGAAGCTGTT 1620
 ACACACATCA TTGCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTG ACAGGAGACT 1680
 80 GCAGTTGCAG TCGCCAGTCT TCTGGGATG TATTCCAAAA CTTCAGATC AGTCTCAGGA 1740
 GAGGAAATAG ATGCAATGGA TGTTCAGCAG CTTCACAAA TAGTACCAAA GGTTCAGTA 1800
 TTTTACAGAG CCGGACCAAG GCACAAGATG AAAATTATTA AGTCCTACA GAAGAAGCGT 1860
 TCAGTTGTAG CCATGACAGG AGATGGAATA AATGATGCAG TTGCTCTGAA GGTGTCAGAG 1920
 ATTGAGATTG OGATGGGCCA GACTGGTACA GATGTTTACA AAGAGGCAGC AGACATGATC 1980
 CTAGTGGATG ATGATTTTCA AACCAATAAT TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040

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AATAACATTA AAAATTCGT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACCTTA 2100
ATCTCATTGG CTACATTAAT GAACCTTCCT AATCCTCTCA ATGCCATGCA GATTTTGTTG 2160
ATCAATATTA TTATGGATGG ACCCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
GATGTATTAC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTGATA 2280
CTTAAATATC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTGT CTTCTGGCGT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
TTTTTTGACA TGTTCAATGC ACTAAGTTC AGATCCAGA CCAAGTCTGT GTTTGAGATT 2460
GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTTCCTG GATCCATCAT GGGACAATTA 2520
CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTGTT TTCTTTTGGG TCTCACTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTGA GTTCGACATC ATCATCTTTT 2700
CTTGAAGTAT GA

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A188 Protein sequence:
Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: N51919
Protein Accession #: AAF27813
Signal sequence: none found
Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
Cellular Localization: not determined

1 11 21 31 41 51
MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FHGWNEDFIS EDEPLWKKYI 60
SQFKNPLIML LLASAVISVL MQQDDDAVSI TVAILIVTV AFVQYERSEK SLRELSKLV 120
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSIDES SLTGETTPCS 180
KVTAPQPAAT NGDLASRSNI AFMGTLVRCG KAGGVVIGTG ENSEFGEVFK MMQAEAPKT 240
PLQKSMDLG KQLSFYSFGI IGIIMLVGWL LGKDILEMPT ISVSLAVAAI PEGPLIVTV 300
TLALGVNRMV KIRAIIVKKLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAETV 360
GVGVNQFGEV IVDGDIVHGF YNPAVSRIE AGCVNDVAI RNNTLMGKPT EGALIALAMK 420
MGLDGLQDY IRKAEYPPSS EQKNMAVKCV HRTQQRPEI CFMKGAYEQV IKYCTTYQSK 480
GQTLTLTQQQ RDVYQEKAR MGSAGLRVLA LASGPELGQL TFLGLVGIID PPRTGVKEAV 540
TLIASGVSI KMITGDSQET AVAIA SRLGL YSKTSQSVSG EEDIDAMDVQQ LSQIVPKVAV 600
FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVMAGTGT DVCKEADMI 660
LVDDDFQTIM SAIEEGGIY MNINKFVRPQ LSTSI AALTL ISLATLMNFP NPLNAMQILW 720
INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFNW 780
ELRDNVITPR DTTMTFTCFV FDDMFNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIINGQL 840
LVIYFPPLQK VFQTESLSIL DLLFLGLTSL SVCIVAEIHK KVERSREKIQ KHSSTSSSF 900
LEV

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A189 DNA SEQUENCE
Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Nucleic Acid Accession #: N62096
Coding sequence: 1-1284 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGGGCTACC AGAGGCAGGA GCCTGTCTC COGCCGAGA GAGGATTGCC TTATTCAATG 60
AAGCAAGCTG GGTTCCTCTT GGAATATTG CTTTATCTT GGGTTTCATA TGTTACAGAC 120
TTTCCCTTG TTTTATTGAT AAAAGGAGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180
TTGGTCAATA AAACCTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTTCT TCAGTTTGTG 240
TATCCTTTTA TAGCAATGAT AAGTTACAT ATAATAGCTG GAGATACTTT GAGCAAAGTT 300
TTTCAAAGAA TCCAGGAGT TGATCTCTGAA AACGTGTTTA TTGGTCGCCA CTTCAATTAT 360
GGACTTTCCA CAGTTACCTT TACTCTGCTT TTATCCTTGT ACOGAAATAT AGCAAAGCTT 420
GGAAAGGTCT CCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGGAAAT TGTAATGGCA 480
AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAGG 540
CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTATTGGCCA CCATAACTCC 600
TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTATCCAT 660
ATGTCCATCG TGATTTCTGT ATTTATCTGT ATATTCTTGT CTACATGTGG ATACTTGACA 720
TTTACTGGCT TCAOCCAAAG GGACTTATTT GAAAATTAAT GCAGAAATGA TGACCTGGTA 780
ACATTTGGAA GATTTTGTTA TGGTGTCACT GTCAATTTGA CATACCTTAT GGAATGCTTT 840
GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTTCATC GGTTTTCCAC 900
ATTGTTGTAA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCATTGCT GATTGATTGC 960
CTCGGGATAG TTCTAGAACT CAATGGGTGT CTCTGTGCAA CTCCCTCAT TTTTATCATT 1020
CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG 1080
TCTTGTGTCA TGCTTCCCAT TGGTGTCTGT GTGATGGTTT TTGGATTGCT CATGGCTATT 1140
ACAAATHTC AAGACTGCAC CCATGGGCAG GAAATGTCT ACTGCTTCC TGACAAATTC 1200
TCTCTCAA AATCCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260
ATTAGTATCT TTCAACTCGA GTA

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A190 Protein sequence:
Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Protein Accession #: none found
Signal sequence: none found
Transmembrane domains: 28-50, 66-88-112-134, 142-164, 217-239, 260-282, 298-320, 327-348, 359-381

Cellular Localization: plasma membrane

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1 11 21 31 41 51
| | | | | |
MGYQRQEPVI PPQRGLPYSM KQAGFPLGIL LLFWVSIVTD FSLVLLIKGG ALSGTDITYQS 60
LVNKTFFGPPG YLLLSVQLFL YPFIAMISYN IIAGDTLSKV FQRIPGVDPE NVFIGRHFII 120
GLSTVTFTLP LSLYRNIAKL GKVSILSTGL TTLILGIVMA RAISLGHPIH KTEDAWVPAK 180
10 FNAIQAVGVM SFAFICHENS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT 240
FTGFTQGDLF ENYCRNDDLIV TFGRFCYGVV VILTYPMCEP VTREIVANVF FGGNLSVVFH 300
IVVTVMVITV ATLVSLLDIC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM 360
SCVMLPIGAV VMVFGFVMAI TNTQDCTHQ EMPYCFPDNF SLTNTSESHV QQTQLSTLN 420
ISIFQLE

15 A191 DNA SEQUENCE
Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Nucleic Acid Accession #: N62096
20 Coding sequence: 1-1203 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
| | | | | |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CGGCCGCGAGT TTTCCCTTGT TTTATTGATA 60
AAAGGAGGGG CCCTCTCTCG AACAGATACC TACCAGTCTT TGTCATATAA AACTTTCGGC 120
TTTCCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180
AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAAGTTT TCAAGAAGAT CCCAGGAGTT 240
30 GATCCTGAAA ACGTGTTTAT TGGTCGCCAC TTCATTATTG GACTTTCAC AGTTACCTTT 300
ACTCTGCCTT TATCCTTTGA CCGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT 360
ACAGGTTTAA CAATCTGAT TCTTGGAAAT GTAATGGCAA GGGCAATTTC ACTGGGTCCA 420
CACATACCAA AACAGAAGA CGCTTGGGTA TTGCAAAAGC CCAATGCCAT TCAAGCGGTC 480
GGGGTTATGT CTTTTCGATT TATTGTCAC CATAACTCCT TCTTAGTTTA CAGTCTCTTA 540
35 GAAGAACCAC CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCATCGT GATTTCGTGA 600
TTTATCTGTA TATTCTTTGC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG 660
GACTTATTGG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTGGAAG ATTTTGTAT 720
GGTGCTACTG TCATTTTGAC ATACCCTATG GAATGCTTTG TGACAAGAGA GGTAATTGCC 780
AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTTCCACA TTGTTGTAAC AGTGATGGTC 840
ATCAGTGTAG CCACGCTTGT GTCAATTGCTG ATTGATTGCC TCGGGATAGT TCTAGAACTC 900
40 AATGGTGTGC TCTGTGCAAC TCCCTCAATT TTTATCATTC CATCAGCCTG TTATCTGAAA 960
CTGTCTGAAG AACCAAGGAC ACACCTCGAT AAGATTATGT CTTGTGTCAT GCTTCCCAT 1020
GGTGCTGTGG TGATGGTTTT TGGATTGGTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080
CATGGGCAGG AAATGTTCTA CTGCTTTCTT GACAAATTTT CTCTCACAAA TACCTCAGAG 1140
45 TCTCATGTTC AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200
TAA

50 A192 Protein sequence:
Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Protein Accession #: none found
Signal sequence: 1-26
55 Transmembrane domains: 45-61, 92-108, 117-132, 191-207, 274-290, 297-313, 335-351
Cellular Localization: plasma membrane

60 1 11 21 31 41 51
| | | | | |
MGYQRQEPVI PPQPSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QFLYPFIAMI 60
SYNIIAGDTL SKVPQRIPGV DPENVFIGRH FIIGLSTVTF TLFLSLYRNI AKLGKVSLS 120
TGLTTLILGI VMARAIISLP HIPKTEDAWV FAKPNAIQAV GVMSPAFICH HNSFLVYSSL 180
EEPTVAKWSR LIHMSIVISV FICIFFATCG YLFTGTGFTQG DLFPENYCRND DLVTFGRFCY 240
65 GVTVILTYPM ECFVTREIVIA NVFPNGNLSS VPHIVVTVMV ITVATLVSLI IDCLGIVLEL 300
NGVLCAFLPI FIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360
HGQEMFYCFP DNPSLTNTSE SHVQQTQLS TLNISIFQLE

70 A193 DNA SEQUENCE
Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Nucleic Acid Accession #: N62096
75 Coding sequence: 1-1140 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
| | | | | |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CGGCCGCGAG TCAATAAAAC TTTCCGCTTT 60
CCAGGCTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTATATAG AATGATAAGT 120
TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTC AAAGAATCCC AGGAGTTGAT 180
CCTGAAAACG TGTTTATTGG TGGCCACTTC ATTATTGGAC TTCCACAGT TACCTTTACT 240
CTGCCCTTAT CCTGTATCCG AAATATAGCA AAGCTTGGAA AGGCTCCCT CATCTCTACA 300
GTTTAAACAA CTCTGATTCT TGGAAATGTA ATGGCAAGGG CAATTTCAT GGGTCCACAC 360
ATACCAAAAA CAGAAGACGC TTGGGTATT TGGCAAGCCA ATGCCATTCA AGCGGTGGGG 420

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GTTATGCTCT TTGCATTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
 GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540
 ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
 TTATTTGAAA ATACTGACAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660
 GTCACGTGCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
 GTGTTTTTGT GTGGGAATCT TTCATCGGTT TTCCACATG TTGAACAGT GATGGTCAATC 780
 ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840
 GGTGTGCTCT GTGCAACTCC CCTCATTTTT ATCAITCCAT CAGCCTGTTA TCTGAAACTG 900
 TCTGAAGAAC CAAGGACACA CTCGATAAG ATTATGCTT GTGTCATGCT TCCCATTGGT 960
 GCTGTGGTGA TGGTTTTTGG ATTGTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020
 GGGCAGGAAA TGTCTACTG CTTTCCTGAC AATTCTCTC TCACAAATAC CTCAGAGTCT 1080
 CATGTTCAAG AGACAACACA ACTTCTTACT TTAATATTA GTATCTTTCA ACTCGAGTAA

A194 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 24-40, 70-86, 95-111, 171-186, 253-269, 276-292, 314-330
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MG YQRQEPVI PPQVNKTPGF PGYLLLSVLQ FLYPPFIAMIS YNIIAGDTLS KVFQRI PGVD 60
 PENVPIGRHF IIGLSTVTFT LPLSLYRNIA KLKQVSLIST GLTTLILGIV MARAISLGPH 120
 IPKTEDAWVF AKPNAIQAVG VMSFAPICHH NSFVLYSLE EPTVAKWSRL IHMSIVISVF 180
 ICIFPATOGY LFTFGFTQGD LFENYCRNDD LVTFGRP CYG VTVILTYPM ECFVTREVIAN 240
 VFFGNLSSV FHVIVTVMVI TVATLVSLLI DCLGIVLELN GVLCAFLIF IIPSACYLKL 300
 SEEPRTSDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLTNTSES 360
 HVQQTQLST LNIISIFQLE

A195 DNA SEQUENCE:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Nucleic Acid Accession #: N62096
 Coding sequence: 1-1389 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGA GAGATTAGA TGACAGAGAA 60
 ACCCTTGTTT CTGAACATGA GTATAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120
 GTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT 180
 GGGTTTCTCT TGGGAATATT GCTTTTATTC TGGSTTTTCA ATGTACAGA CTTTCCCTT 240
 GTTTTATTGA TAAAGGAGG GGCCTCTCTT GGAACAGATA CCTACCAGTC TTGGTCAAT 300
 AAAACCTTTC GCTTTCAGG GTATCTGCTC CTCTCTGTTT TFCAGTTTTT GTATCCTTTT 360
 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAGT TTTTCAAGAA 420
 ATCCAGGAG TTGATCCTGA AAAAGTGTTC ATTGGTCCGC ACTTCATTAT TGGACTTTCC 480
 ACAGTTACCT TTAATCTGCC TTTATCCTTG TACCGAAATA TAGCAAAGCT TGGAAAGGTC 540
 TCCCTCATCT CTACAGGTTT AACAACTCTG ATCTCTGGAA TTGTAATGGC AAGGGCAATT 600
 TCAGTGGGTC CACACATACC AAAAACAGAA GACGCTTGGG TATTGCAAAA GCCCAATGCC 660
 ATCAAGCGG TCGGGGTTAT GTCTTTTGCA TTTATTGCCC ACCATAATCT CTCTTAGATT 720
 TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780
 GTGATTCTCT TATTATCTG TATATTCTTT GCTACATGTG GATACTTGAC ATTTACTGGC 840
 TTCACCAAG GGGACTTATT TGAAATTTAC TGCAGAAATG ATGACCTGGT AACATTGGA 900
 AGATTTTGTT ATGGTGTGAC TGTCAATTTG ACATAACCTA TGGAAATGCT TGTGACAAGA 960
 GAGGTAATTG CCAATGRTT TTTTGGTGGG AATCTTTCAT CGGTTTTCCT CATGTTGTA 1020
 ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCAATGC TGATTGATTG CCTCGGATA 1080
 GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATCAT TCCATCAGCC 1140
 TGTATCTGTA AACTGTCTGA AGAACCAAGG ACACACTCOG ATAAGATTAT GTCTTGTGTC 1200
 ATGCTTCCCA TTGGTGTCTG GGTGATGGTT TTTGGATTCT TCAATGGCTAT TACAAATACT 1260
 CAAGACTGCA CCCATGGGCA GGAAATGTTT TACTGCTTTC CTGACAAATT CTCTCTACA 1320
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAAA TATTAGTATC 1380
 TTTCAATGA

A196 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 37-53, 66-82, 109-125, 155-172, 180-196, 255-271, 338-354, 361-377, 399-415
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MG YQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMRQA 60

GFPLGILLIF WVSVYVDFSL VLLIKGGALS GTDTYQSLVN KTFGPPGVLL LSVLQFLYFF 120
 IAMISYNIIA GDTLSKVQQR IPGVDPENVF IGRHFIIGLS TVTFTPLPLSL YRNIARKLKV 180
 SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVPAKFNA IQAVGVMSFA FICHHSFLV 240
 YSSLEPTVA KWSRLIHMSI VISVPICIFF ATCGYLTFTG FTQGDLFENY CRNDLVTFG 300
 RFCYGVTVIL TYRMECFVTR EVIANVFFGG NLSSVFHIVV TVMVTIVATL VSLLDICLGI 360
 VLELNGVLCA TPLIFIIPSA CYLKLSEPR THSDKIMSCV MLPIGAVVMV FGFVMAITNT 420
 QDCTHQEMF YCFPDNFSLT NTSSEHVQQT TQLSTLNISI FQ

A197 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.31608
 Probeset Accession #: H18836
 Nucleic Acid Accession #: NM_017636
 Coding sequence: 1-3501 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 20 ATGGAGGATG CCTTCGGGGC AGCCGTGGTG ACCGTGTGGG ACAGCGATGC ACACACCACG 60
 GAGAAGCCCA CGATGCTGA CGAGAGAGCTG GACTTCACGG GGGCGGCGCG CAAGCACAGC 120
 AATTTCCTCC GGCTCTCTGA CGGAACGGAT CCAGCTGCAG TTTATAGTCT GGTCACACGC 180
 ACATGGGGCT TCGGTGCCCC GAACCTGGTG GTGTCACTGC TGGGGGGATC GGGGGGCCCC 240
 GTCTCCAGA CCTGGCTGCA GGACCTGCTG CGTCGTGGGC TGGTGCGGGC TGCCACAGAC 300
 25 ACAGGAGCCT GGATTGTAC TGGGGGTCTG CACACGGGCA TCGGCGGCA TGTGTGTGTG 360
 GCTGTACGGG ACCATCAGAT GGCCAGCACT GGGGGCACC AAGTGTGTGC CATGGGTGTG 420
 GCCCCTCGGG GTGTGTCCG GAATAGAGAC ACCCTCATCA ACCCCAAGGG CTGTTCCCT 480
 GCGAGGTACC GTGTGGCGGG TGACCCGGAG GACGGGTCC AGTTTCCCT GGACTACAAC 540
 TACTCGCCT TCTTCTGTG GGAACGAGC ACACACGGCT GCCTGGGGG CAGAACCGC 600
 TTCCGCTTGC GGCTGGAGTC CTACATCTCA CAGCAGAAGA CGGCGGTGGG AGGGACTGGA 660
 30 ATTGACATCC CTGTCTGTG CTCTCTGATT GATGGTGATG AGAAGATGTT GACGCGAATA 720
 GAGAACGCCA CCGAGGCTCA GCTCCCATGT CTCTCTGTG CTGGCTCAGG GGGAGCTGCG 780
 GACTGCCTGG CCGAGACCTT GGAAGACACT CTGGCCCCAG GAGATGGGG AGCCAGGCAA 840
 GGCGAAGCCC GAGATCGAAT CAGGCGTTTC TTTCCCAAG GGGACCTTGA GGTCTGCGAG 900
 35 GCCCAGGTGG AGAGGATTAT GACCCGGAAG GAGCTCTGTA CAGTCTATT TTTCTAGGAT 960
 GGGTCTAGGG AATTCTGAGC CATAGTTTTC AAGGCCCTTG TGAAGGCTTG TGGGAGCTCG 1020
 GAGGCTCTAG CCTACCTGGA TGAGCTGCGT TTGGCTGTGG CTTGGAACCG CGTGGACATT 1080
 GCCCAGAGTG AACTCTTTG GGGGACATC CAATGGCGGT CCTTCCATCT CAGAGCTTCC 1140
 CTCATGGAGC CCTCTGTAAG TGACCGGCTT GAGTTGTGTC GCTTGCTCAT TTCCACGGC 1200
 40 CTCAGCCTGG GCCATCTTCT GACCCCGATG GGCCTGGCCC AACTCTACAG CGCGGCGCCC 1260
 TCCAACTGCG TCATCCGCAA CTTTGTGGAC CAGCGCTCC ACAGCGCAGG CACCAAGGCC 1320
 CCAGCCCTAA AAGGGGAGC TGCGGAGCTC CGGCCCTCG ACCTGGGCA TGTGCTGAGG 1380
 ATGTCTGTGG GGAAGATGTG CGCGCGAGG TACCCCTCG GGGCGGCTG GGACCTCTAC 1440
 CCAGGCCAGG GCTTCGGGGA GAGCATGTAT CTGCTCTGG ACAAGGCCAC CTCGCGGCTC 1500
 45 TGCTGTGATG CTGGCTCGG GCAGGCCCC TGGAGCGACC TGCTTCTTT GGCACGTGTG 1560
 CTGAACAGGG CACAGATGGC CATGTACTTC TGGGAGATGG GTTCCAATGC AGTTTCTCTA 1620
 GCTCTTGGGG CCGTTTGTCT GCTCCGGGTG ATGGCACGCC TGGAGCTTGA CGCTGAGGAG 1680
 GCAGCACGGA GGAAGACCTT GCGGTTCAAG TTTGAGGGGA TGGGOGTTGA CCTCTTTGGC 1740
 GAGTGTATC GCAGCAGTGA GGTGAGGGCT GCCGCGCTCC TCCTCGCTG CTGCGCGCTC 1800
 50 TGGGGGATG CCACTTGCTT CCAGCTGGCC ATGCAAGCTG ACGCCGCTG CTCTTTGCC 1860
 CAGGATGGGG TACAGTCTCT GCTGACACAG AAGTGTGTGG GAGATATGGC CAGCATACA 1920
 CCCATCTGGG CCTCTGTTCT CGCCTTCTTT TGCCCTCCAC TCATCTACAC CGCCTCATC 1980
 ACCTTCAGGA AATCAGAAGA GGAGCCACCA CGGAGGAGC TAGAGTTTGA CATGGATAGT 2040
 GTCATTAATG GGGAAAGGCC GTTCGGGAGC GCGGACCCAG CCGAGAAGAC GCCGCTGGGG 2100
 55 GTCCCGCGCC AGTCGGGCGG TCGGGTTGTC TGCGGGGCG GCTGCGGGG GCGCGGCTG 2160
 CTAAGCCGCT GGTTCACATT CTGGGGCGCG CCGGTGACCA TCTTCATGG CAACGTGGTC 2220
 AGCTACCTGC TGTTCCTGCT GCTTTCTCG CGGTGTCTGC TCGTGGATTI CCAGCCGGCG 2280
 CGCGCCGCT CCTCTGAGCT GCTGCTCTAT TTCTGGGCTT TCACTGTCT GTGCGAGGAA 2340
 60 CTGCGCCAGG GCTCTGAGCG AGCGGGGGG AGCCTGSCCA GCGGGGGGCC CGGCTGTGG 2400
 CATGCTCAG TGAGCCAGCG CCTGCGCTC TACCTGCGG ACAGCTGGAA CCACTGCGAC 2460
 CTAGTGGCTC TCACCTGCTT CCTCTGGGCG GTGGGCTGCC GGCTGACCCC GGGTTTGTAC 2520
 CACCTGGGCC GCACTGTCTT CTGCATCGAC TTCATGGTTT TCACGGTGGC GCTGCTTAC 2580
 ATCTTCACGG TCAACAAACA GCTGGGCCCC AAGATCGTCA TCGTGAGCAA GATGATGAAG 2640
 65 GACGTGTCTT TCTTCTCTT CTCTCTGGG GTGTGGCTGG TAGCCTATGG GTGGCCACG 2700
 GAGGGGCTCC TGAGGCCACG GACACGTGAC TTCCCAAGTA TCCTGCGCGG CGTCTTCTAC 2760
 CGTCCCTACC TGCAATCTT CGGCGAGATT CCCCAGGAGG ACATGGAGCT GGGCCTCATG 2820
 GAGCACAGCA ACTGCTGGT GGAGCCCGGC TTCTGGSCAC ACCCTCTGG GGGCCAGGCG 2880
 GGCACTGCG CTCTCCAGTA TGCCAACTGG CTGGTGGTGC TGCTCTCTGT CATCTTCTG 2940
 70 CTGCTGGCCA ACATCTGCTT GGTCAACTTG CTCATTGCCA TGTTCAGTGA CACATTGGC 3000
 AAGTACAGG GCAACAGCGA TCTCTACTGG AAGGCGCAGC GTTACCGCTT CATCGGGAA 3060
 TTCCACTCTC GGGCCGCGCT GGGCCCGCCC TTTATCGTCA TCTCCACTT GGGCCTCTG 3120
 CTCAGGCAAT TGTGCAAGGG ACCCGGAGC CCCCAGCGGT CCTCCCGGC CTCGAGCAT 3180
 75 TTCCGGTTT ACCTTTCTAA GGAAGCGAG CGGAAGCTGC TAACTGGGA ATCGGTGCAT 3240
 AAGGAGAACT TTCTGCTGGC ACGCGCTAGG GACAAGCGG AGAGCGACTC CGAGCGTCTG 3300
 AAGCGCAGT CCAAGAAAGT GGACTTGGCA CTGAAACAGC TGGGACACAT CGCGAGTAC 3360
 GAACAGCGCC TGAAGTGTCT GGAGCGGGAG GTCCAGCAGT GTAGCGCGT CTGGGGTGG 3420
 GTGGCCGAGG CCTTGAGCG CTCTGCTTG CTGCCCCAG GTGGGCGCC ACCCCCTGAC 3480
 CTGCTGGGT CCAAGACTG A

A198 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.31608
 Probeset Accession #: H18836
 Protein Accession #: none found

Signal sequence: none found
 Transmembrane domains: 214-230, 537-556, 642-662, 730-752, 760-782, 815-837, 842-864, 877-899, 973-995
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MEDAFGAAVV TVWDSDAHTT EKPTDAYGEL DFTGAGRKHS NFLRLSDRTD PAAVYSLVTR 60
TWGFRAPNLV VSVLGGSGGP VLQTLWLQDLL RRLVLRRAQS TGAWIVTGGL HTGIGRHVGV 120
AVRDHQMAST GGTQKVAMGV APWGVVRNRD TLINPKGSFP ARYRWRGDPE DGVQPFPLDYN 180
YSAPFLVDDG THGCLGGENR FRLRLLESYIS QKTGVGGTG IDIPVLLLI DGDEKMLTRI 240
ENATQAQLPC LLVAGSGGAA DCLABTLEDL LAPGSGGARQ GEARDRIRRP FPKGLDLEVLQ 300
AQVERIMTRK ELLTVYSSSD GSEEFETIVL KALVKACGSS EASAYLDELRL LAVANNRVDI 360
AQSELFGRDI QWRSFHLEAS LMDALLNDRP EFVRLLIHQ LSLGHFLTFM RLAQLYSAAP 420
SNSLRNLND QASHSAGTKA PALKGGAABL RPPDVGHVLR MLLGKMCAPR YPSGGAWDPH 480
PGQGFESMY LLSKATSPSL SLDAGLGQAP WSDLLWLALL LNRAQMAMYF WEMGSNAVSS 540
ALGACLLLRV MARLEPDABE AARRKDLAFK FEGMGVDLFG ECVRSSEVRA ARLLLRRCPL 600
WGATCLQLA MQADARAFFA QDGVQSLLTQ KWWGDMASTT PIWALVLAFF CPPLIYTRLI 660
TFRKSEEEPT REELEFDMDS VINGEGPVGT ADPAEKTPLG VPRQSGRPGC CGGRCGRRRC 720
LRRWFHFWGA PVTIPMGNVV SYLLFLLLF S RVLVDFQPA PPGSLLELLY FWAFTLLCEE 780
LRQLSGGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY 840
HLGRTPVLCID FMVPTVRLH IFTVNKQLGP KIVIVSKMMK DVEFFLFFLG VMLVAYGVAT 900
EGLLRPRSD PPSILRRVVFY RPYLQIFCQI PQEDMDVALM EHSNCSSEPG FWAHPGAQA 960
GTCVSQYANW LVVLLLVIFL LVANILLVNL LIAMPSYTFG KVQGNSDLYW KAQRYRLRE 1020
PHSRPALAPP FIVISHLRLL LRQLCRRPRS PQSSPALEH FRVYLSKEAE RKLLTWESVH 1080
KENFLARAR DKRESDSERL KRTSQKVDLA LKQLGHIREY EQRLKVLERE VQCCSRVLGW 1140
VAELSRSA LPPGGPPPPD LPSKD

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A199 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.40808
 Probeset Accession #: AA054237
 Nucleic Acid Accession #: AA054237
 Coding sequence: 1-894 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGAGCGCG GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCCTGTG CTCCCTGGGG 60
CTGCTCGTCA CGGCCATCTT CACCGACACC TGGTACGAGA CCGACCCCGG GCGCCACAAG 120
GAGAGCTGGG AGCGCAGCGG CGCGGGCGCC GACCCCGCGG ACCAGAAGAA CCGCTGATG 180
CCGCTGTGCG ACCTGCGGCT GCGGGACTCG CCCCCTGCGG GCGCCCGGCT GCTCCCGGGC 240
GGCCCGGGGG GCGCGACACC CGAGTCTCTG CGCTCGCTCC TGGGGCTCGG CCGGCTGGAC 300
GCCGAGTGGG GCCGCGCCCT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
CTGGGCGATG ACCCGGACAT OGACACCCCT ATCCTGAAAG GTATTGCGCA GCGATGCACG 420
GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGCGAA ACATTCCTTT TAATTAAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCATTATA GAAGAATCAC TGCTGGCTTC 540
CTGGGATAGG CCGTAGCCGT CCTTCTCTGC GGCTGCATIG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGACTCCTGT TCCTCATGAC AGGGATATTT 660
TGCAACATTT CCTCTGTAC TTATGCGCCG AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
AAGCTAATTT ATAGCTCGCC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC 780
GCCTGCTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATGCG TTATCCGTTT 840
ATTACCGGGA CCAAGATTGC ACAGCTAAAG TCTGGCAGAG ACTCCACGGT ATGA

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A200 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.40808
 Probeset Accession #: AA054237
 Protein Accession #: none found
 Signal sequence: 1-18
 Transmembrane domains: 179-201, 209-231, 257-279
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DFPDQKNRLM 60
PLSHLPLRDS PPLGRRLLP GPGRADPESW RSLGLGLD ABOGRPLPAT YSGLWRKCYF 120
LGIDRDIDL ILKGIAQRCT AIKYHFSQPI RLRLNIPNLK RTIQDDEWEL LHLRRITAGF 180
LGMNAVAVLC GCIVATVSFF WEESLTQHVA GLLPLMTGIF CTISLCTYAA SISYDLNRLP 240
KLILYSLPADV EHGYSWSIFC ANCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV

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A201 DNA SEQUENCE

Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Nucleic Acid Accession #: NM_016570
 Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
ATGAGGCGAC TGAATCGGAA AAAAACTTTA AGTTTGGTAA AAGAGTTGGA TGCCTTTCCG 60
AAGGTTCCCTG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120

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5 TTTACAACCTA TGGCTTTATT AACCATAATG GAATTCCTCAG TATATCAAGA TACATGGATG 180
 AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAT TAAGAATTAA TATAGATATT 240
 ACTGTTGCCA TGAAGTGTC AATATGTTGA GCGGATGTAT TGGATTTAGC AGAAACAATG 300
 GTTGCACTCG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
 AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACCT 420
 CAAGATGTGA TATTTAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480
 GATGATTCAT CACAGTCTCC AATGTCATGC AGAATTCATG GCCATCTATA TGTCAATAAA 540
 GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCTCTG TGGTCATGCA 600
 10 CATTGGGCAG CACTGTGCAA CCATGAATCT TACAATTTT CTCTAGAAAT AGATCATTGT 660
 TCTTTGGAG AGCTGTCTCC AGCAATTAIT AATCCTTTAG ATGGAACCTGA AAAAATTGCT 720
 ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780
 TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAAC 840
 CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTATGA AATATGATCT CAGTTCTCTT 900
 15 ATGGTGACAG TTACTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTAAAG ACTCTGTGGT 960
 ATTGTTGGAG GAATCTTTTC AACACAGGC ATGTTACATG GAATTGGAAG ATTTATAGTT 1020
 GAAATAATTT GCTGTGTTT CAGACTTGGG TCCTATAAAC CTGTCAATTC TGTTCCTTTT 1080
 GAGGATGGCC ACACAGACAA CCACCTACCT CTTTGTAGAA ATAATACACA TTGA

20 A202 Protein sequence:
 Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Protein Accession #: NP_057654
 25 Signal sequence: none found
 Transmembrane domains: none found
 Cellular Localization: nuclear

30 1 11 21 31 41 51
 | | | | |
 MRRLNRKKTLL SLVKELDAFF KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60
 KYEYEVVDKDF SSKLRINIDI TVAMKCOYVG ADVLDLAETM VASADGLVYE PTVFDLSPQQ 120
 35 KEWQRLQLI QSRLQEEHSL QDVIFKSAFK STSTALPPRE DDSSQSPNAC RIHGHLYVNK 180
 VAGNFHIVG KAIPIPRGHA HLAALVNHEH YNFSHRIDHL SFGLVPAII NPLDGTEDIA 240
 IDHNMQFYF ITVVPKLTHT YKISADTHQF SVTERERIIIN HAAGSHGVSG IFMKYDLSSL 300
 MVTVEEHMP FWQFFVRLCG IVGGIFSTTG MLHGIGKPIV EIICCRFLRG SYKPVNSVFP 360
 EDGHTDNHLP LLENTH

40 A203 DNA SEQUENCE
 Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
 Unigene number: Hs.44926
 Probeset Accession #: S79876
 45 Nucleic Acid Accession #: NM_001935.1
 Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 | | | | |
 CGCGGCTCTC CGCGGCGCCG GTGACTTCTG CCGGCTCTCC TTCTCTGAAC GCTCACTTCC 60
 GAGGAGACGC CGACGATGAA GACACCGTGG AAGATTCTTC TGGAGCTGCT GGGTCTGCT 120
 CGCGTTGTCA CCATCATCAC CGTGCCCGTG GTTCTGCTGA ACAAGGCAC AGATGATGCT 180
 ACAGCTGACA GTGCGAAAC TTACACTCTA ACTGATTACT TAAAAATAC TTATAGACTG 240
 55 AAGTTATACT CCTTAAGATG GATTTCAGAT CATGAATATC TCTACAACA AGAAAAATAAT 300
 ATCTTGGTAT TCAATGCTGA ATATGGAAC AGCTCAGTTT TCTTGGAGAA CAGTACATTT 360
 GATGAGTTTG GACATCTCAT CAATGATTAT TCAATATCTC CTGATGGGCA GTTTATTCTC 420
 TTAGAATACA ACTACGTGAA GCAATGGAGG CATTCTTACA CAGCTTCATA TGACATTTAT 480
 GATTTAAATA AAAGGCAGCT GATTACAGAA GAGAGGATTC CAAACAACAC ACAGTGGGTC 540
 60 ACATGGTCAC CAGTGGGTCA TAAATTGGCA TATGTTTGA ACAATGACAT TTATGTTAAA 600
 ATTGAACCAA ATTTACCAAG TTACAGAAAT ACATGGACGG GGAAGAAGA TATAATATAT 660
 AATGGAATAA CTGACTGGGT TTATGAAGAG GAAGTCITCA GTGCCCTACT TGCTCTGTGG 720
 TGGTCTCCAA ACGGCACCTT TTAGCATAT GCCCAATTTA ACGACACAGA AGTCCCACTT 780
 65 ATTGAATACT CCTTCTACTC TGATGAGTCA CTGCACTACC CAAAGACTGT ACGGGTTCCA 840
 TATCCAAAGG CAGGAGCTGT GAATCCAACT GTAAAGTTCT TTGTTGTAAT TACAGACTCT 900
 CTCAGCTCAG TCACCAATGC AACTTCCATA CAAATCACTG CTCTGCTTTC TATGTTGATA 960
 GGGGATCACT ACTTGTGTGA TGTGACATGG GCAACACAAG AAGAATTTTC TTGTCAGTGG 1020
 CTCAGGAGGA TTCAGAACTA TTCGGTCATG GATATTGTG ACTATGATGA ATCCAGTGGG 1080
 70 AGATGGAATC GCTTAGTGGC ACGGCAACAC ATTGAAATGA GTACTACTGG CTGGGTTGGA 1140
 AGATTTAGGC CTTCAAGAAC TCAATTTTACC CTTGATGGTA ATAGCTTCTA CAAGATCATC 1200
 AGCAATGAAG AAGGTTACAG ACACATTTCG TATTTCCAAA TAGATAAAAA AGACTGCACA 1260
 TTTATTACAA AAGGCACCTG GGAAGTCATC GGGATAGAAG CTCTAACCAAG TGATATCTA 1320
 TACTACATTA GTAATGAATA TAAAGGAATG CCAGGAGGAA GGAATCTTTA TAAAAATCAA 1380
 75 CTTATTGACT ATACAAAAGT GACATGCCTC AGTGTGTAGC TGAATCCGGA AAGGTGTGAG 1440
 TACTATTCTG TGTCATTTCG TAAAGAGGCG AAGTATTATC AGCTGAGATG TTCCGGTCTC 1500
 GGTCGCCCCC TCTATCTCTC ACACAGCAGC GTGAATGATA AAGGGCTGAG AGTCTCGGAA 1560
 GACAATTCAG CTTTGGATAA AATGCTGCAG AATGTCCAGA TGCCCTCCAA AAAAATGGAC 1620
 80 TTCAATTTT TGAATGAAAC AAAATTTTGG TATCAGATGA TCTTGCTCTC TCAATTTGAT 1680
 AAATCCAGA AATATCTCTC ACTATTAGAT GTGTATGCAG GCCCATGTAG TCAAAAAGCA 1740
 GACACTGTCT TCAGACTGAA CTGGGCCACT TACCTTGCAA GCACAGAAAA CATTATAGTA 1800
 GCTAGCTTTG ATGGCAGAGG AAGTGGTTAC CAAGGAGATA AGATCATGCA TGCAATCAAC 1860
 AGAAGACTGG GAACATTGGA AGTGAAGAT CAAATTGAAG CAGCCAGACA ATTTTCAAAA 1920
 ATGGGATTGT TGACAACAA ACGAATTGCA ATTTGGGGCT GTTCATATGG AGGGTACGTA 1980
 ACCTCAATGG TCCTGGGATC GGAAGTGGC GTGTTCAAGT GTGGAATAGC CGTGGCGCCT 2040

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GTATCCCGGT GGGAGTACTA TGACTCAGTG TACACAGAAC GTTACATGGG TCTCCCAACT 2100
CCAGAAGACA ACCTTGACCA TTACAGAAAT TCAACAGTCA TGAGCAGAGC TGAATAATTTT 2160
AAACAAGTTG AGTACCTCCT TATTCATGGA ACAGCAGATG ATAACGTTCA CTTTCAGCAG 2220
TCAGCTCAGA TCTCCAAAGC CCTGGTCGAT GTTGGAGTGG ATTTCCAGGC AATGTGGTAT 2280
ACTGATGAAG ACCATGGAAT AGCTAGCAGC ACAGCACACC AACATATATA TACCCACATG 2340
AGCCACTTCA TAAACAATG TTTCTCTTTA CCTTAGCACC TCAAAATACC ATGCCATTTA 2400
AAGCTTATTA AAACCTATT TTGTTTTCAT TATCTCAAAA CTGCACTGTC AAGATGATGA 2460
TGATCTTTAA AATACACACT CAAATCAAGA AACTTAAGGT TACCTTTGTT CCCAAATTTT 2520
ATACCTTACA TCTTAAGTAG GGACTTCTGT CTTCAACAAC GATTATTACC TTACAGAAGT 2580
TTGAATTATC CGTCGGGTT TATTGTGTTA AAATCATTTT TGCATCAGCT GCTGAAACAA 2640
CAATAGGAA TTGTTTTTAT GGAGGCTTTG CATAGATTCC CTGAGCAGGA TTTTAATCTT 2700
TTTCTAACTG GACTGGTTCA AATGTTGTTT TCTTCTTTAA AGGGATGGCA AGATGTGGGC 2760
AGTGATGTCA CTAGGGCAGG GACAGGATAA GAGGGATTAG GGAGAGAAGA TAGCAGGGCA 2820
TGGCTGGGAA CCCAAGTCCA AGCATACCAA CACGAGCAGG CTACTGTGAG CTCCCCTCGG 2880
AGAAGAGCTG TTCACCAAGA GACTGGCACA GTTTTCTGAG AAAGACTATT CAAACAGTCT 2940
CAGGAAATCA AATATCGAAA GCACGTGACT CTAAGTAAAC CACAGCAGTT GAAAGACTCC 3000
AAAGAAATGT AAGGGAATCT GCCAGCAAAC CAGCCCCCAG GTGCCAGTTA TGGCTATAGG 3060
TGCTACAAAA ACACAGCAAG GGTGATGGGA AAGCATTTGA AATGTGCTTT TAAAAAATAA 3120
TACTGATGTT CCTAGTGAAG GAGGCAGCTT GAAACTGAGA TGTGAACACA TCAGCTTGCC 3180
CTGTTAAAG ATGAAAATAT TTGTATCACA AATCTTAACT TGAAGGACTC CTGTCATCAA 3240
TTTTTCTTAT TTCATTCTTT TGAGTGCTTT AATTAAAGA ATATTTTAACT TTCCTTGGAC 3300
TCATTTTAAA AATGGAACA TAAATACAA TGTATGTAT TATTATCCCT ATTCTACATA 3360
CTATGGAATT TCTCCAGTCT ATTTAATAAA TGTGCCTTCA TTTTTC
  
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A204 Protein sequence:

Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
 Unigene number: Hs.44926
 Probeset Accession #: S79876
 Protein Accession #: NP_001926.1
 Signal sequence: none found
 Transmembrane domains: 6-28
 DPPIV_N_term domain: 43-557
 Peptidase_S9 domain: 558-635
 Cellular Localization: plasma membrane

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1 11 21 31 41 51
| | | | |
MKTFWKILLG LLGAALVTI ITVPVVLINL GTDDATADSR KTYTLTDYKL NTYRLKLYSL 60
RWISDHEYLY KQENNILVFN AEYGNSSVFL ENSTFDEFHG SINDYSISPD GQFILLEVNY 120
VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVTWSFV GHKLAYVWNN DIYVKIEPNL 180
PSYRITWTGK EDIIYNGITD WVYEEVFPFA YSALWNSPFG TFLAYAQFND TEVPLIEYSF 240
YSDSLQYYPK TVRPVYPRAG AVNPTVKFFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300
CDVTWATQER ISLQWLRRIO NYSVMDICDY DESSGRWNCL VARQHIEMST TGWVGRFRPS 360
EPHFTLDGNS FYKIIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYYISN 420
EYKGMPPGRRN LYKIQLLIDYT KVTCLSCELN PERQVYVSFS FSKEAKYVQL RCGSPGLPLY 480
TLHSSVNDKG LRVLEDNSAL DKMLQNVQMP SKKLDPIILN ETKFWYQML PPHFDKSKKY 540
PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIVASFDG RSGSYQGDKI MHAINRRLGT 600
FEVEDQIEAA RQFSKMGFVD NKRIALNGWS YGGYVTSMLV GSGSGVFKCG IAVAFVSRWE 660
YYDSVYTERY MGLPTFPEDNL DHYRNTVMS RAENFKQVEY LLIHGTADDN VHFQQAQIS 720
KALVDVGVD FQAMWYDDEH GIASSTARQH IYTHMSHPK QCPSLP
  
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A205 DNA SEQUENCE

Gene name: predicted exon
 Unigene number: none found
 Probeset Accession #: none found
 Nucleic Acid Accession #: none found
 Coding sequence: 1-261 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
ATGGCTCTGG CGAAGGTGAG GGAGCCAAAC GCAAATGACA ATGCCATCAG AGTTGACAAC 60
AGAAAGTGTA TTAAGGTGCG TGCTAACCGA TGTTCCCTGC ATGAGGCAGA AAGTGAATCC 120
AGAAACCCTC AGGAGCTCTG GATGGGCTCG CTCTCTTGA TGGGGGTCCT AGAAGCATGT 180
GTGGAATAGA GGCTCTGTCT AGTCTGGTCC CTGAGAGATG ACAAGGAGCA GAGCCCCAC 240
CAGCCACAC TGGATGTCTA A
  
```

A206 Protein sequence:

Gene name: predicted exon
 Unigene number: none found
 Probeset Accession #: none found
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 46-68
 Cellular Localization: not determined

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1 11 21 31 41 51
| | | | |
MALAKVREFN ANDNAIRVDN RSVIKVRANQ CSLHEAESES RNPQELNMGL LLLMGVLEAC 60
VEMRPLSVWS LRDDKEQSPH QPTLDV
  
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A207 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.222886
 Probeset Accession #: AI672225
 Nucleic Acid Accession #: none found
 Coding sequence: 1-462 (underlined sequences correspond to start and stop codons)

```

10      1      11      21      31      41      51
      |      |      |      |      |      |
      ATGCCAAATG CTGAGTTAGA AGCAAAGAGC CTTGGAAGCA GTAAATGTTT AAAAACTGCT 60
      CTCATACTTG CTGTATGTTG TGGATCAGCA AATATAGTCA GCCCTCTACT TGAGCAAAAT 120
      ATTGATGTAT CTCTCAAGA TCTGGACAGA CGGCCAGAGA GTATGCTGTT TCTAGTCATC 180
15      ATCATGTGGA CCAGTTTGTG GGAAGACAAT CTTTCCATGG GCTGGGGGAA GCTAGAAGAT 240
      TTTATGGCTA TTGAAGAAGA AATGAAGAAG CACGGAAGTA CTCATGTGGG ATTCCAGAA 300
      AACCTGACTA ATGGTGCCGC TGCTGGCAAT GGTGATGATG GATTAATTCC TCCAAGGAAG 360
      AGCAGAACAC CTGAAAGCCA GCAATTTCCT GACACTGAGA ATGAAGAGTA TCACAGGTTT 420
      GTCAAAGATC AGATAGTTGT AGATATGCGG CGTTATTCTT GA
  
```

A208 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.222886
 Probeset Accession #: AI672225
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 16-38
 Cellular Localization: not determined

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30      1      11      21      31      41      51
      |      |      |      |      |      |
      MPNAELEAKS LGSSKCLKTA LILAVCCGSA NIVSPILLEQN IDVSSQDLDR RPESMLFLVI 60
      IMWTSFVEDN LSMGWGKLED FMAIBEEMKK HGSTHVGFPE NLINGAAAGN GDDGLIPPRK 120
35      SRTPEQQFP DTENEYHRF VKDQIVVDMR RYF
  
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A209 DNA SEQUENCE

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1
 Unigene number: Hs.23796
 Probeset Accession #: NM_014253
 Nucleic Acid Accession #: NM_014253
 Coding sequence: 65-8242 (underlined sequences correspond to start and stop codons)

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45      1      11      21      31      41      51
      |      |      |      |      |      |
      GACTGCTGTC ATTTAAAGGAC TTCCTCATCC TTTTTCATCAT GAAACTGAGC TTGCTTAATC 60
      AGAGATGGAG CAAACTGACT GCAAACCCCTA CCAGCCTCTA CCAAAGTCA AGCATGAAAT 120
      GGATCTAGCT TACACAGTT CTCTGATGA GAGTGAAGAT GGAAGAAAC CAAGACAGTC 180
50      ATACAAGTCC AGGGAGACCC TGCAAGAGTA TAACCCAGGAG CTGAGGATGA ATTACAATAG 240
      CCAGAGTAGA AAGAGGAAAG AAGTAGAAAA ATCTACTCAA GAGATGGAAT TCTGTGAAC 300
      CTCTCACACT CTGTGCTCTG GCTACCAAAC AGACATGCAC AGCGTTTCTC GGCATGGCTA 360
      CCAGCTAGAG ATGGGATCTG ATGTGGACAC AGAGACAGAA GGTGCTGCCT CACCTGACCA 420
      TGCACTAAGA ATGTGGATAA GGGGAATGAA ATCAGAGCAT AGTTCTCTGT TGTCCAGCCG 480
55      GGCCAACCTC GCATTATCCT TGACTGACAC TGACCATGAA AGGAAGTCTG ATGGGGAAAA 540
      TGGTTTCAAA TTCTCTCTG TTTGTTGTGA CATGGAGGCT CAAGCTGGGT CTACTCAAGA 600
      TGTGAGAGC AGCCACACCA ACCAGTTCAC CTTCAGACCC CTCGCCCGC CACCTCGGCC 660
      TCTCATGCC TGCACTGTG CCAGGAAGCC ACCCCCTGCA GCGGACTCTC TTCAGAGGAG 720
      ATCAATGACT ACCCGAGCC AGCCAGCCC AGCTGCTCCA GCTCCCCAA CCAGCAAGCA 780
60      GGATTCAGTC CATCTGCATA ACAGCTGGGT CCTGAACAGC AACATACCAT TGGAGACCAG 840
      GCATTCCCTG TTCMAACATG GATCTGGTTC CTCTGCGATC TTCAGTGCAG CCAATCAGAA 900
      CTACCCCTCG ACATCCAATA CCGTGTACTC GCCCCCTGCC AGGCTCTCTC CTCGAAGCAC 960
      CTTTCCCGA CCTGCCTTTA CCTTTAACAA ACCTTACAGG TGCTGCAACT GGAAGTGCAC 1020
      AGCATTTAGC GCCATGCAA TCACAGTGAC TTTGGCCCTG TACTAGCCT ATGTGATTGC 1080
65      AGTGCAATTG TTGGGCTGTA CTGGCAGTT GCAACCAATT GAAGGAGAGC TGATGCAAA 1140
      TGGAGTTAGC AAAGGGAACA GGGGAGACGA GTCCATGGAC ACTACTTACT CTCCAATTGG 1200
      AGGAAAGATT TCTGATAAAT CAGAGAAAAA AGTGTTCAG AAGGAGCGG CGATAGACAC 1260
      TGGAGAAGTT GACATTGGTG CACAGGTCAT GCAGACCAAT CCACCTGGTT TATTCTGGG 1320
      TTTCCAGATT ACTATCCACC ATCCAATATA TCTGAAGTTC AATATTCTT TAGCCAAAGGA 1380
70      CTCTCTGCTG GGAATTTATG GCAGAAGAAA CATTCACCT ACACATACTC AGTTTGATTT 1440
      TGTAAACTTA ATGGATGGCA AACAGCTGGT CAAGCAGGAC TCCAGGGCT CTGATGATAC 1500
      ACAGCACTCC CCTCGGAACC TGATCTTAAC TTGCTTCAG GAGACAGGTT TCATAGAGTA 1560
      TATGGATCAA GGAACCTTGT ATCTGGGCTT TTACAATGAT GGAAGAAAGA TGGAGCAAGT 1620
      ATTGCTGTTA ACTACAGCAA TTGAAATAT GGTGACTGT TCAACCAATT GCAATGGAAA 1680
75      TGGAGAGTGT ATCTCTGGCC ATTGTCATTG TTTCCAGGA TTCTTGGAC CTGACTGTGC 1740
      TAGAGATTCC TGCCCTGTGC TGTGTGTG TGATGGAGAA TACGAGAAAG GACACTGTGT 1800
      CTGCCGCACT GGTGGAAGG GGCCAGAGTG TGACGTTCCG GAAGAACCAAT GCATTGATCC 1860
      AACATGCTTT GGCCAGGCA CCTGCATCAT GGGAGTCTGC ATCTGTGTGC CAGGATACAA 1920
      AGGAGAAATA TGGAGGAAG AGGACTGCCT AGACCCCAAT TGTTCCAACC ATGGCATCTG 1980
      TGTAAAGAGA GAATGTCACT GTTCTACTGG CTGGGGAGGA GTTAAGTGTG AAACACCACT 2040
      TCCTGTATGT CAAGAGCAGT GCTCAGGACA CGGAACCTTT CTCTGGAGC CTGGAGTATG 2100
      CAGCTGTGAT CCCAAGTGGG CAGGATCTGA CTGCTCAACA GAGCTGTGTA CCATGGAGTG 2160
80      TGGTAGCCAT GGAATCTGCT CAAGAGGAAT TTGCCAGTGT GAAGAGGCT GGGTAGGACC 2220
      AACATGTGAG GAACGCTCCT GTCAATTCTCA TTGTACTGAG CATGGCCCAAT GCAAAGATGG 2280
  
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	AAAAATGTGAG	TGTAGCCCTG	GATGGGAGGG	CGACCACTGC	ACAAATGCTC	ACTACTTAGA	2340
	TGCTGTCCGA	GATGGCTGCC	CAGGGCTCTG	CTTTGGAAAT	GGACGATGTA	CCCTGGATCA	2400
	AAATGGTTGG	CAGTGTGTGT	GTGAGGTGGG	TGGAGTGGG	ACAGGCTGCA	ATGTTGTCTAT	2460
5	GGAAATGCTT	TGTGAGATA	ACTTGGACAA	TGATGGAGAT	GGTTTAAACG	ACTGTGTGGA	2520
	TCCTGACTGT	TGTCAACAAA	GCAACTGTTA	TATAAGTCCT	CTCTGCCAGG	GCTCACCAGA	2580
	TCCTCTTGAC	CTCATTCAGC	AAAGCCAAAC	TCTCTTCTCT	CAGCACACTT	CAAGACTTTT	2640
	TTATGATCGA	ATCAAAATCC	TCATTGGCAA	GGACAGTACT	CATGTCAATC	CTCCTGAGGT	2700
	GTCAATTTGAC	AGCAGGCGTG	CCTGTGTGAT	TCGAGGCCAA	GTGGTGGCCA	TAGATGGAAC	2760
10	TCCTCTAGTG	GGAGTGAATG	TCAGTTTCTT	GCACCCAGAT	GATTATGGGT	TTACCATCAG	2820
	CCGGCAAGAT	GGAGCTTTTG	ACCTCGTGGC	CATCGGTGGC	ATCTCTGTCA	TCTTAATCTT	2880
	CGACCGATCC	CCTTTCTCTG	CTGAGAAGAG	AACACTCTGG	TGCGCTTGGA	ATCAGTTTAT	2940
	TGTGTGTAGG	AAAGTCACCA	TGCAGAGAGT	TGTATCAGAC	CCGCCATCCT	GCGATATCTC	3000
	CAACTTTATC	AGCCCAAAAC	CTATTGTGCT	TCCTTCACCG	CTCACATCAT	TTGGAGGGTC	3060
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15	TCCTCCAGAG	TTTGTGAGGC	TGAGTTACCT	GAGCAGCCGC	ACCCCTGGGT	ATAAAACCTT	3180
	GCTACGGATC	CTTCTGACAC	ATTCAACGAT	TCCCGTAGGC	ATGATAAAAG	TACACCTCAC	3240
	AGTAGCTGTG	GAAGGGCGAC	TCACACAGAA	GTGGTTTCCC	GCCGCAATTA	ATCTTGCTTA	3300
	CACATTTGCT	TGGAAACAAGA	COGATATCTA	TGGACAGAAG	GTTTGGGGCC	TGGCAGAGGC	3360
20	TTTGGTATCT	GTGGGATATG	AATATGAAAC	GTGCCCTGAC	TTTATTTCTCT	GGGAGCAAAG	3420
	GACAGTGTGT	TTACAAGGTT	TTGAGATGGA	TGCTTCTAAG	CTAGGAGACT	GGTCTTTGAA	3480
	TAAGCATCAC	ATTTTGAATC	CTCAAGTGG	AATCATACAT	AAAGGGAATG	GAGAAAATAT	3540
	GTTCAATTTCC	CAGCAGCCCC	CAGTCATATC	ARCCATAATG	GGTAATGGAC	ACCAAAGGAG	3600
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	AGTCTACAAG	TGTAATATCTC	TTGTGGAGAC	GAAAGATCTG	TCCAAGAAAT	TTGAAGTGGT	3900
	GGCAGGAATC	GGTGTACAGT	GCCTTCCCTT	TGACCAGAGT	CATTGTGGAG	ATGGTGGGAG	3960
30	AGCATCGGAA	GCTTCACTGA	ATAGCCCTCG	AGGCATCACA	GTTGATAGGC	ATGGATTTAT	4020
	TTACTTTGTG	GATGGGACTA	GATTTCGCAA	AATTGATGAG	AATGCTGTGA	TCACAAGTGT	4080
	AATCGGCTCA	AATGGTCTGA	CTTCCACACA	ACCACTGAGC	TGTGACTCAG	GAATGGACAT	4140
	CACCTAGGTT	CGATTAGAGT	GGCCAAACAGA	CCTTGCAGTA	AATCTATGAG	ACAATTCATT	4200
	GTATGCTCTG	GATAACAACA	TTGTGCTGCA	AATTTCTGAG	AACAGGCGTG	TTCCGATCAT	4260
35	CGCAGGACCG	CCCATTCACT	GCCAGGTGCC	AGGCATCGAT	CATTTCCTGG	TCAGCAAGGT	4320
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40	CTTAGCAGTG	TGCGCTGATG	GAACCCCTCTA	TGTGGCAGAC	CTCGGAAATG	TTGGAATTCG	4620
	TACCATCAGC	AGGAAACCAAG	CCCACCTGAA	TGACATGAAC	ATTTATGAGA	TTGCTTCACC	4680
	CGCTGATCAG	GAACCTGACC	AGTTCACTGT	AAATGGAACC	CACCTACACA	CCCTGAACCT	4740
	GATAACAAGG	GACTATGTTT	ATAACTTCAC	CTACAATTCT	GAAGGTGACT	TGGGCGCGAT	4800
	TACCAGCAGC	AATGCAATTT	CAGTGCACAT	TGCGGTGAT	GCAGGCGGAA	TGCCGCTATG	4860
45	GCTTGTGGTG	CCTGGCGGAC	AAGTATACTG	GCTGACTATA	AGCAGCAATG	GAGTCTGTAA	4920
	AAGAGTGTCA	GGCCAAAGGT	ATAATCCCGG	CTTAATGACC	TATCCAGGAA	ACACAGGGCT	4980
	TCTGGCTACC	AAAAGTAAAG	AAAATGGATG	GACAACCGTT	TATGAGTATG	ACCCGAGGGG	5040
	ACACCTGACC	AATGCAACGT	TTCCCACTGG	AGAGGTGACG	AGCTTCCACA	GTGACCTGGA	5100
	GAAGCTGACA	AAAGTGAAGC	TAGATACTTC	CAACCGTGAA	AATGTCCTCA	TGTCAACCAA	5160
50	CTTGACGGCA	ACTAGTACCA	TATATATTTT	AAAAACAAGAA	AATACTCAAA	GTACCTATCG	5220
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	ATTGCCCCGA	GAGCACAATG	CAAACTCAT	CGAGTGGCGG	CAGAGGAAGG	AGCAAAACAA	5400
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55	AGATTTTGAT	CATATAACCC	GCACAGGAAA	GATCTATGAT	GACCATCGAA	AAATCACCCT	5520
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	GAATGAATAA	ATGGAATATG	ACCAAGTGGG	GAAATTAATT	TCAAGAACTT	GGGCTGATGG	5700
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60	GGTTACATCT	TTTGAATATG	ACCAATCAGA	TTGCCCTGCTG	TCAGTTACCA	TGCCTAGCAT	5820
	GGTGCGCCAC	AGCTTACAAA	CCATGCTTTC	AGTGGGCTAC	TACCGTAATA	TCTACACCCC	5880
	ACCGGACAGT	AGCACTTCTT	TTATCCAAGA	CTATAGTCTG	GATGGCCGAT	TGCTACAGAC	5940
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	TTTGCTTATA	GATCTTTACC	GATATGTTGA	TGCTCTGTGC	AGAACAGAGC	AGTTTGGAAA	6300
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	GGTAGGAGTA	GATGCCAATA	TAACAAGGTA	CTTCTATGAA	TACGATGCTG	ATGGGCAACT	6540
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	AGTTACTCAT	TTGTACAACC	ACACAAGCTC	GGAGATTACA	TCTCTGTATT	ATGATCTCCA	6960
80	AGGTACCTTT	TTTGCCATGG	AGTTAAGCAG	TGGTGAAGAA	TATTATGTAG	CCTGTGATAA	7020
	TACAGGTACC	CCACTAGCTG	TGTTGAGCAG	CCGAGGTCAG	GTCAATAAAG	AGATACTATA	7080
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	TGTTGTGTCT	GGCAGATGGA	CAACGGCCTA	TCATCACATA	TGGAAACAGT	TGAACCTCCT	7260
	TCCTAAACCA	TTCAACCTCT	ACTCCTTTGA	AAATAACTAC	CCAGTTGGCA	AAATTCAGAA	7320

	TGTTGCAAG	TATACCACAG	ACATCAGAAG	TTGGTTGGAG	CTATTTGGTT	TCCAATTACA	7380
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	TCTACGGCTT	CAGACAAAAA	CTCAAGAGTG	GGATCCTGGA	AAGACTATCC	TGGGCATTCA	7500
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5	CCGATACAAT	GATGGACGGT	GCCTTGAAGG	AGGGAAGCAA	CCAAGGTTTG	CTGCTGTCCC	7620
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15	GTCTGTGGAG	CAGTATTTAG	AACTTTCTGA	CAGTGCCAAT	AATATTCAC	TTATGAGACA	8220
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	AAATATGGAG	GAATAACATA	TCCAACCTGCC	TTTCAATGTG	ACGGAAGATG	GTATTTTAAT	8400
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25	TCTGTATAG	GAACCTTAAA	AACAGGTGTA	AAATGTCTTC	AGCCACCATC	TCCTAGAGTG	8760
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30	GCTGTATTGG	TATCATGTAA	ACATAGCTTT	TATTAACCTG	GGTAGGAATT	TCTCATTTAT	9060
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	CACAAAGGAA	AGCAAGGGAA	AGGAAATGAC	CCTGGCAAAC	AGTAGGGAAG	GGTGTATTCA	10080
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	AGTATTTATT	CAGAAATGAA	TTCTAAAATT	ACTAACAAAC	TTGTTGAAAA	TTTGAATAAC	10320
	TCCACACCAA	CCTAAAATG	GACCTTAAGT	TCTAGAAC	TCTGATGTTT	TTTTAAATTA	10380
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	GGAAATGCAC	TTTTTATTAC	TTACAGCTGT	GGTTTTAATA	CTGCTTGAA	CTATTATTAT	10740
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	ATATATAATA	TATACAACT	AGCCAAATGT	ATGAAAACCT	GACAAATGTAT	AATTTGGAA	11520
	TCACATGCTA	CCTATGTAGA	CAGGTATGAA	ATTAAGTTAT	AATTTTCATG	AGACATTTTC	11580
	ATCACTGTTG	ACACAGTTTC	AAGGCATTC	ATCATGTTAT	TTTGACTCTT	TTTCTTTTTT	11640
	TTTTCTTTAA	AAATATATTT	TTAACTAGAC	CAGGCCCCAC	TATAATATCA	CTTAAGAGAG	11700
75	TCAGGGCAAA	GTTTTTCAT	TTATGAAGAT	GTGTTCAATG	AAGGGTGATT	GTAATGGAGT	11760
	TCATTGTGTA	TAGAAGCAAA	AGTACAGTAA	CGAAGTATTG	AAAAGAAAA	TTTGGAGACA	11820
	TTGGAGCAT	TTATATATAG	CTTGTGGAAA	GACATAAGGC	TACAGATGGA	ATGGAACATT	11880
	CCTGTTTTCT	TGAAGAAATT	CACATACACA	TAGCTGACCT	GACTAGTACT	TCAGCTCTTC	11940
	CACAGCCTTC	TATAAAGGTT	CTTCTCTCTG	CAAGAAAAAC	AAAAACAAAC	AAAAACAAAC	12000
80	AAAAAAACAA	AAAAAAGCG	CAAAAAACAA	AAAAACAAA	AAAAACAAAG	TAAAAATTA	12060
	AAATACAGAA	AACAAACAC	AAAAAAGAA	TCAACCAATA	ATAGTGACTA	TTATTTTCAG	12120
	TGTTCTCTTC	ATGTGAAAGC	TATTAAGGAC	CAAAATATACT	ACTGTTTCTA	AGAAGAAATT	12180
	ACTTTCTAAA	CAGTAACCTA	AAATACCTAG	AGTTAAACCT	GCTGTGGATT	TTGCTTGGC	12240
	AGTTGTCTAT	TTACATTAAT	TGTCAAAGGA	AATGTGTTTG	GCAGTTAAAA	ATCTTCTCTT	12300
	AGATTTAGTG	GTGGACCTTA	ACCTCTTAAA	TAAATGTTAG	TATATCAGAT	TGTGTCCTTG	12360

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AAAAATATT TACTTGATG AATCATGACA ACGTCTAAAT CTTTACTATT CTTCTGGCAA 12420
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TGCTGTAATA ATTTAAAGTT AAACATTATG TGTGTATATT TGAAAGAAAA GTACTTTTGA 12840
TATTTTCATT TTAATAAATA AAATTGCCAA TGAAAAAATA

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A210 Protein sequence:

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1
 Unigene number: Hs.23796
 Probeset Accession #: NM_014253
 Protein Accession #: NP_055068
 Signal sequence: none found
 Transmembrane domains: 318-340
 Cellular Localization: plasma membrane

1 11 21 31 41 51

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LRMWIRGMKS EHSSCLSSRA NSALSITDIT HERKSDGENG FKFSFVCCDM EAQAGSTQDV 180
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SVHLHNSWVL NSNIPLETRH SLFKHSGSSS AIFSAASQNY PLTSNTVYSF PPRPLPRSTF 300
SRPAETFNKP YRCNWKCTA LSATAITVTL ALLLAYVIAV HLFGLTLWQL PVEGELYANG 360
VSKGNRGTES MDTTYSPIGG KVSDKSEKKV FQKGRADITG EVDIGAQVMQ TIPPGLFWRF 420
QITTHPIYIL KFNISLAKDS LLGIYGRNNI PPTHTQFDFV KLMDGKQLVK QDSKGSDDTQ 480
HSPRNLIITS LQETGFI EYM DQGPWYLAFF NDGKMEQVF VLTTAIBIMD DCSTNCNGNG 540
ECISGHCHCF PGFLGPDCAE DSCFVLCCGN GEYKKGHCVC RHGKNGPECD VPEBQCIDPT 600
CFHGHTCIMG VCICVPGYKG EICEEDCLD PMCSNHGICV KGECHCSTGW GGVNCEPLP 660
VCQEQCSGHG TFLLDAGVCS CDFKWTGSDC STELCTMECG SHGVCSRIGC QCESGWVGPT 720
CEERSCHSHC TEHGQCKDGK CECSPGWEDG HCTIAHYLDA VRDGCPLGCF GNGRCTLQDN 780
GNHCVCQVWG SGTGQNVVME MLCGDNLND GDGLTDCVDP DCCQGSNCYI SFLCQGSFDP 840
LDLIQSSQTS FLSQHTSRLEF DRIKFLIGKD STHVIPPEVS FDSRRACVIR GQVVAIDGTP 900
LVGVNVSLFH HSDYGFITISR QDGSFDLVAI GGISVILIPD RSPFLPEKRT LMLPWNQPIV 960
VEKVTMQRVV SDPPSCDISN PISPNPIVLP SPLTSPGGSC PERGTTIVPEL QVVQEEIPIP 1020
SSPFLVLSYS SRTPGYKTLI RILLTHSTIP VGMKIVHLTV AVEGRLTQKW FPAAINLVYT 1080
FAWNKIDYQ QKWNGLAEL VSVGYEYEC PDFILMBQRT VVLQGFEMDA SNLGDWLNK 1140
HHLILPQSGI IHKNGENMFP ISQPPVIST IMGNGHQRVS ACTNCGPAH NNKLEFAPVAL 1200
ASGPDGVSYY GDPNFVRRI FSGNSVSILE LSTSPARKYY LAMPVSESL YLSDTNTRKV 1260
YKLKSLVETK LSKNFVVA GTGDQCLPFD QSHOGDGGRA SEASLNSPRG ITVDREHFTY 1320
FVDGTMIRKI DENAVITTVI GSNGLTSTQF LSCDSGMDIT QVRLEWPTDL AVNPMONSLY 1380
VLDNNIVLQI SEMRRVRIIA GRPIHCQVPG IDHFLVSKVA IHSTLESARA ISVSHSGLLF 1440
IAETDERKVN RIQQVTINGE IYIIAGAPTD CCKIDFNCD CFSGDGGYAK DAKMKAPSSL 1500
AVSPDGTLYV ADLGNVRIIT ISRNQAHND MNIYELASPA DQELYQFTVN GTHLHTLNLI 1560
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LTKVELDTSN RENVLMSTNL TATSTIYILK QENTQSTYRV NPDGSLRVTF ASGMEIGLSS 1740
EPHILAGAVN PTLGKCNISL PGEHNANLIE WRQRKEQNGK NVSAFERRLR AHNRMLLSID 1800
FDHITRTGKI YDHRKFTLR ILYDQGTGRPI LWSFVSRYNE VNITYSPSGL VTFIQRGTWN 1860
EKMEYDQSK IISRTWADGK INSYTYLEKS VMLLLHSQRR YIFEYDQSDC LLSVTMPSMV 1920
RHSGLQMLSV GYRYNIYTPF DSSTSFIDY SRDGRLLQTL HLGTRRVLY KYTKQARLSE 1980
VLXDITQVTL TYEESGVIK TIHLMDGFI CTIRYRQTGP LIGRQIPRPS EBLVNRARFD 2040
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IFSANGQVIE VQVEILKATA YWMTIQYDNV GRHGNMCIHV GVDANITRYF YEYDADGQLQ 2160
TVSVNDKQW RYSYDLNGDI NLLSHGKSAR LTPRLYDLRD RITRLGELIY KMEDEGFLRQ 2220
RGNDIFEVNS NGLLQKAYNK ASGNTVQYYY DGLGRRVASK SSLGQHLQFF VDATANPIRV 2280
THLYNHTSSE ITSLEYDLQG HLIAMELSSG BEYVACDNT GTPLAVPSSR GQVIKEILYT 2340
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KPNLYSPEN NYPVKGIDV AKYTTDIRSW LELPGFQLEN VLPGPPEL ENLELTVELL 2460
RLQTKTQEW DPGKTLGIQC ELQKQLRNFI SLDQLPMTPR YNDGRCLGEG KQPRFAAVPS 2520
VFGKGIKFAI KDGIIVTADII GVANEDSRRL AAILANAHYL ENLHFTIEGR DTHYPIKLSG 2580
LEEDLVLIEN TGGRRILENG VNVTVSQMIS LLNGRTRRFA DIQLQHGALC FNIRYGTIVE 2640
EERNHVLEIA RQRAVAQAWT KEQRRLQEGE EGIRAWTEGE KQQLLSTGRV QGYDGYFVLS 2700
VEQYLELSDS ANNHFMQRQS EIGRR

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A211 DNA SEQUENCE:

Gene name: Solute carrier family 26, member 4
 Unigene number: Hs.159275
 Probeset Accession #: AF030880
 Nucleic Acid Accession #: NM_000441
 Coding sequence: 225-2567 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

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CTCAGCCTTC CCGGTTCCGG AAAGGGGAAG AATGCAGGAG GGGTAGGATT TCTTCTCTGA 60
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TTGCTCCGTA ATAAACGCT CCACCTGCCT TCTGAGAGCG CTATAAAGGC AGCGGAAGGG 180
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GCAGGTCGGA CCGCCCGCAG CTCCCGAGT ACAGCTGCAG CTACATGTTG TCGCGGCGCG 300
TCTACAGCGA GCTCGCTTTC CAGCAACAGC ACGAGCGGCG CTTGACAGGAG CGCAAGACGC 360

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5 TGCGGGAGAG CCTGGCCAAG TGCTGCAGTT GTTCAAGAAA GAGAGCCTTT GGTGTGCTAA 420
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 CCTACTAGC TGCAATTCTT GTCGGATATG GTCTCTACTC TGCTTTTTTC CCTATCCTGA 600
 CATACTTTAT CTTTGGAAACA TCAAGACATA TCTCAGTTGG AOCCTTTCCA GTGGTGAGTT 660
 TAATGGTGGG ATCTGTTGTT CTGAGCATGG CCCCOCAGCA ACACITTTCTC GTATCCAGCA 720
 GCAATGGAAAC TGTATTAAAT ACTACTATGA TAGACACTGC AGCTAGAGAT ACAGCTAGAG 780
 TCCTGATTGC CAGTGCCTCG ACTCTGCTGG TTGGAATTAT ACAGTTGATA TTTGGTGGCT 840
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 15 TGACGATAAT TGCTACTGCC ATTTTCATATG GAGCCAACCT GGAATAAAT TACATGCTG 1200
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 CAGTAGGAAA GGTGCTGGT ACCAAGTATG ATTAACCAT CGATGGGAAC CAGGAATTCA 1380
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 20 CTCCTTCCCG CACGGCCGTC CAGGAGAGCA CTGGAGGAAA GACACAGGTT GCTGGCATCA 1500
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 25 TGTGACTGT GGTCTGAGA GTTCAGTTTC CTCTCTGAA TGCCCTTGA AGCATCCCTA 1800
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 30 GTGATGCTGT TTCAACAAAT AATGCTTTTG AGCCTGATGA GGATATTGAA GATCTGGAGG 2100
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 CTGAACAAAA

A212 Protein sequence:

Gene name: Solute carrier family 26, member 4
 Unigene number: Hs.159275
 Probeset Accession #: AF030880
 Protein Accession #: O43511
 Signal sequence: none found

Transmembrane domains: 81-103, 109-131, 136-158, 185-207, 221-243, 245-267, 270-291, 295-317,
347-369, 386-408, 420-442, 448-470, 486-508
Cellular Localization: plasma membrane

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AFGVKTLVLP ILEWLPKVRV KEWLLSDVIS GVSTGLVATL QGMAYALLAA VPVGYGLYSA 120
FFPILTYFIF GTSRHSVSGP FVVVSLMVG S VVLSMAPDEM FLVSSSNGTV LNTTMTDTAA 180
RDTARVLIAS ALTLVLGIIQ LIFGGLQIGF IVRYLADPLV GGFTTAAAFQ VLVSQKLKIVL 240
NVSTKNYNGV LSIIYTLVEI FQNIQDNLIA DFTAGLLTIV VCMVAVKELND RPRHKIPVPI 300
PIEVIVTIIA TAISYGANLE KNYNAGIVKS IPRGFLPPEL PVSLSFSEML AASFISIAVVA 360
YAIASVSGKV YATKYDYTID GNQEFIAFGI SNIPSGFPSC FVATTALSRT AVQESTGGKT 420
QVAGIISAAI VMIAILALGK LLEPLQKSVL AAVVIANLKG MFMQLCDIPR LWRQNKIDAV 480
IWFVTCIVSI IIGLDLGLLA GLIFGLLTVV LRVPFSPWNG LGSIPSTDYI KSTKNYKNIE 540
EPQGVKILRF SSPIFYGNVD GPKKCIKSTV GFDAIRVYNK RLKALRKIQK LIKSGQLRAT 600
KNGIISDAVS TNNAFEPDED IEDLEELDIP TKSIEIQVDW NSELVPVKVNV PKVPIHSLVL 660
DCGAISFLDV VGVRSRLRVIV KEFQRIDVNV YFASLQDYVI EKLEQCGPFD DNIRKDTFFL 720
TVHDAILYLQ NQVKSQEGQG SILETITLIQ DCKDTLELIE TELTEEBLDV QDEAMRTLAS 780
QDEAMRTLAS

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25 A213 DNA SEQUENCE:

Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]
Unigene number: Hs.98280
Probeset Accession #: AA418000
Nucleic Acid Accession #: NM_021614
Coding sequence: 458-2197 (underlined sequences correspond to start and stop codons)

30

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1      11      21      31      41      51
|      |      |      |      |      |
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CCGGGGCAGC CAGCTCAATG TGAGCGAGCT GAGCGCGTCC AGCCATGCCA GTGCGCTCCG 240
GCAGCAGTAC GCGCAGCAGT CCGCGCAGCA GTCGGGTCTC GCCTCCCACT ACCACCACTG 300
CCACAGCCTG CAGCCCGCGC CCGCCGCCAC GGGCAGCCTC GGCAGTCTGG GCTCCGCGCC 360
CCGCTCTCG CACCCACACC ACCACCCGCA CCGCGGCGAC CACCAGCACC ACCAGCCCA 420
GGCGCGCGCG GAGAGCAACC CCTTCACCGA AATAGCCATG AGCAGCTGCA GGTACAACGG 480
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CTCAGCTGGG CAGCCCGTGC AGCCCCCGCG GTCTGTGCGA GGAGGTGGCG GCGCGTCCCT 600
CCGCTCTGCA CAGCTGCGCG CCGCGCGCGC TGTGTGCTCC TCAGCCCGCG AGATCGTGGT 660
GTCTAAGCCC GAGCACAACA ACTCCAACAA CCTGGGCTCT TATGGAACCG GCGCGGAGG 720
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CATGACTTAT GAGCGTATTT TCTTCATCTG CTTGGAATA CTGGTGTGTG CTATTCATCC 1140
CATACAGGGG AATTATACAT TCACATGGAC GGCCCGGCTT GCCTTCTCCT ATGCCCATC 1200
CACAAACACC GCTGATGTGG ATATTATTTT ATCTATACCA ATGTTCTTAA GACTCTATCT 1260
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GCAGAGGAAA CTGAATGACC AAGCAACAC TTTGGTGGAC TTGGCAAGA CCCAGAACAT 1920
CATGTATGAT ATGATTCTG ACTTAAACGA AAGGAGTGAA GACTTCGAGA AGAGGATTGT 1980
TACCCGGAAC ACAAACTAG AGACTTTGAT TGGTAGCATC CACGCCCTCC CTGGGCTCAT 2040
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CTAATCAGCG TTATCCGGGT TCTGATGTCA GAATCCTGGG AACCTGAACA CTAAGTTTAA 2340
GGCCAAAATG AGTGAACACT CTTTTTTTTT CTTTCAGATG CACAGGGAAT GCACCTATTA 2400
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AACTTTACTA CTACATTATA TGATATATAA TAAAAAAGT TAATTTCGGA

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80 A214 Protein sequence:

Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]
Unigene number: Hs.98280
Probeset Accession #: AA418000
Protein Accession #: NP_067627
Signal sequence: none found
Transmembrane domains: 135-157, 168-190, 208-230, 254-276, 306-328, 342-364, 373-394

Calmodulin binding domain: 412-488
Cellular Localization: plasma membrane

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LGHRRALFEK RKRLSDYALI FGMFGIVVMV IETELSWGAY DKASLYSLAL KCLISLSTII 180
10    LLGLIIVYHA REIQLFMVDN GADDWRIAMT YERIFPICLE ILVCAIHPIP GNYTFTWTAR 240
LAFSYAPSTT TADVDIILSI PMFLRLYLIA RVMLLHSLKF TDASSRSIGA LNKINFNTRF 300
VMKTLMTICP GTVLLVPSIS LWIIAAWTVR ACERYHDQDD VTSNPLGAMW LISITPLSIG 360
YGDMPVNTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVENFM MDTQLTKRVK 420
15    NAAANVLRET WLIYKNTKLV KKDIDHAKVRK HQRKFLQAIH QLRSVIMEQR KLNDQANTLV 480
DLAKTQNMVY DMISDLNERS EDPEKRIVTL ETKLETIGS IHALPGLISQ TIRQQQRDFI 540
EAQMESYDKH VTYNASRSRS SSRRRRSST APPTSSESS

```

A215 DNA SEQUENCE:

Gene name: CGI-86 protein
Unigene number: Hs.109201
Probeset Accession #: AW161450
Nucleic Acid Accession #: NM_016029
Coding sequence: 228-1097 (underlined sequences correspond to start and stop codons)

```

25      1      11      21      31      41      51
      |      |      |      |      |      |
CTGCGATCCC GCAGGGCAGC GACGCGACTC TGGTGC GGCG CGTCTTCTTC CCCCCGAGCT 60
GGGCGTGCGC GGCOCGCAATG AACTGGGAGC TGCTGCTGTG GCTGCTGGTG CTGTGCGCGC 120
30    TGCTCCTGCT CTGTGGTGCA GCTGCTGCGCT TCCTGAGGGC TGAAGGGGAC CTGACGCTAC 180
TATGGGCGGA GTGGCAGGGA CGACGCCAGC AATGGGAGCT GACTGATATG GTGGTGTGGG 240
TGACTGGAGC CTGGAGTGGA ATTGGTGAGG AGCTGGCTTA CCAGTTGTCT AAACCTAGGAG 300
TTTCTCTTGT GCTGTCCAGC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAA AGAAGATGCC 360
TAGAGAAATGG CAATTTAAAA GAAAAAGATA TACTTGTGTT GCCCTTGAC CTGACCGACA 420
35    CTGGTTCCCA TGAAGCGGCT ACCAAAGCTG TTCTCCAGGA GTTTGGTAGA ATCGACATTC 480
TGGTCAACAA TGGTGGAATG TCCACGCGTT CTCTGTGCAT GGATACCAGC TTGGATGTCT 540
ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGTGTC CTTGACAAAA TGTGTTCTGC 600
CTCACATGAT CGAGAGGAAG CAAGGAAAGA TTGTTACTGT GAATAGCATC CTGGGTATCA 660
TATCTGTACC TCTTCCATT GGATACTGTG CTAGCAAGCA TGCTCTCCGG GGTTTTTTTA 720
40    ATGGCCTTCG AACAGAACTT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTTGCCGAG 780
GACCTGTGCA ATCAATATT GTGGAAGATT CCCTAGCTGG AGAAGTCACA AAGACTATAG 840
GCAATAATGG AGACCACTCC CACAAGATGA CAACCACTCG TTGTGTGCGG CTGATGTTAA 900
TCAGCATGGC CAATGATTG AAAGAAGTTT GGATCTCAGA ACAACCTTTC TTGTTAGTAA 960
45    CATATTGTG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCAACAAG ATGGGGAAGA 1020
AAAGGATTGA GAATTTAAG AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTTA 1080
AGACAAACA TGAAGTAAA GAGCACCTGT ACTTTTCAAG CCACTGGAGG GAGAAATGGA 1140
AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200
ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260
50    AGATTGCCAT GAATCTTGCA AA

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A216 Protein sequence:

Gene name: CGI-86 protein
Unigene number: Hs.109201
Probeset Accession #: AW161450
Protein Accession #: NP_057113
Signal sequence: 1-26
Transmembrane domains: 183-206, 221-243
Cellular Localization: plasma membrane

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65      1      11      21      31      41      51
      |      |      |      |      |      |
MNWELLWLWL VLCALLLLLV QLLRFLRADG DLTLLEAEWQ GRRPEWELTD MVMVVTGASS 60
GIGEEIAYQL SKLGVSLVLV ARRVHELERV KRRCLENGNL KEKDILVLPL DLDTGTSHEA 120
ATKAVLQEFQ RIDILVNNGG MSQRSLOMDT SLDVYRKLE LNYLGTVSLT KCVLPHMIER 180
KQGKIVTVNS ILGIIIVPLS IGYCASKHAL RGFFNGLRTE LATYPGLIIVS NICPGFVQSN 240
IVENSLAGEV TKTIIGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISBQP FLVLYTLWQY 300
70    MPTWAWIWN KMGKKRIENF KSGVDADSSY FKIFKTKHD

```

A217 DNA SEQUENCE:

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
Unigene number: Hs.27373
Probeset Accession #: F13036
Nucleic Acid Accession #: AC012478
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

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80      1      11      21      31      41      51
      |      |      |      |      |      |
ATGCGCGCCG TGCGCGTGCC CGCCCGGCTC CTGCGCGTGC TGCTGCTGCG GCTCCTGGCC 60
GCTCCGCGCG CCGCGCGCAG CAGAGCCGAG TCGCTCTCCG CGCGGTGCGC CGAACCCGAG 120
CGCGAGTGGC GCGCACCGCC CGCCCGGGGG CCGCGGAACA CCACCCGCTT TGGGCTCGGG 180
GCGGCGGGCG GCAGCGGCAG CTCAGCTCC AACAGCAGTG GCGAGCCTT GGTGACCCGC 240

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ATTTCATCC TCCCTCCGGA CCTACCCACC CTCAAGGCAG CGGTGATCGT GGGTTCCGCC 300
TTTACCAACC TCCCTCATGC CTGCCCTGCTG CTGCGCGTCT TCAGGTCCGG AAAGAGGTGA 360
AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGGCCCA 420
CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
TCCCTGCGCG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCCT 540
GTGCCCCCAC CCTTCATCCT CGACATTGAC CTTCAGCAA GATGCACTGG AAGGCCTGAT 600
GGTGGAAATCA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCCTGT GGAAAGTTGG 660
TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTGCGT CGGAGGTGTT 720
GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGGGTGTC AGGCATCTGC 780
TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCAACACAA TGGAGTTGCT TCTGCCACCC 840
TTTGGGCATC CCTTTAAAGT GCCCCTACT TCTACTCCCC ATGGTTTTCG ACAAATGCG 900
CTGAATCTCA TGGAAAGCT GGATTCTCT GCCTTACGCA GAAACACCCG GGCCTCCATCT 960
GCCAGTGCT TGCACCTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCTTTTACAC ACAAACCATG 1080
AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCCGCCGAGC GGGGCACCTT TTGTGAAGAC 1140
AGAGCAGTGA CTAAGGTTCCT CCAGGCTAGC TCTTTCTCCA AACAGCTGGG CTGGAAGCCA 1200
GCCCTAGAGT GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
ACCCATCCTG TCAGTTTGGC TCGTTCAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320
AGGGGTGTTT GGGTCCCGCG GCAGTCTCTG CATGGCGGAG GGTGAGGGG TACCGCAACT 1380
TGCCCTTTGG TTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTTCTACAAA 1440
ATCTGTCTCC CTTGCTGTGC CGTGGAAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
GTCCCTTGCGT CATTTGAGCA GAGCCCAACAA AAGGCAGCTG CTGCCACCG GGAGCTGTCT 1560
AAACGAGGGC CCACTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCCACTGTA GGATGTCACT 1680
CACCCCTGGG GAGACTTGGG TGGGGTGGCA AATTCTTATT TGGAGGAAGA GGGTTTCCAG 1740
GATGACAGAT GCCAGAGAT GGTCTGTATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCTTCTCTT 1860
TCCCCCGGAC AGCCCTGTGT TCTGTCCAGG CCTTGA
  
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A218 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
 Unigene number: Hs.27373
 Probeset Accession #: F13036
 Protein Accession #: FGENESH predicted
 Signal sequence: 1-27
 Transmembrane domains: 94-115, 448-469
 Cellular Localization: not determined

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1 11 21 31 41 51
MRAVPLPAPL LPLLLALLLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTTRFGSG 60
AAGSGSSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF FTTLLIACLL LRVFRSGKRL 120
KKTAKYDIIT TPAERVEMAP LNEDEDEDED STVFDIKYRV SLPAALRRQL PGQTLTLLVP 180
VPPFPILID LPARCSGRPD GGIRPGKTCF PANWHPVBSW SAATWGVKDW TWKPCVGGV 240
ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPP FGHPPKVPPT STPHGFRQLQ 300
LNLMERLSS ALRNRTRAPS ARCLPLVLAH MAABESDLPH PWHFSAATGS PIKTLTYQTM 360
STLGLDVFVG AGQRGTFCEB RAVTKVLQGS SFSKQLRWKP ALESFPPHLL RLLRECPPLS 420
THPVRLARSD ARGQASLTGR RVFRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLLDPYK 480
ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAAGHEPV KRGPSSQLTR HTPCPGWGTH 540
ANLQTTPTDQ QGEGFPREDVT HPGGDLGVA NFYLEEBSFG DGRQKQWLM SEEGPPSLTG 600
CERLTGSHHF SSHSKWSFL SFRQPLEFLSR P
  
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A219 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

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 75
 80

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1 11 21 31 41 51
ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTA AGAGAGTGGG 60
GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
CAGCAAGGT ACACACACCT GGTGCAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180
TCCATATTGA GCTATTACCC AAGTTATTAC TGGATTGGAA TCAGAAAGT CAACAATGTG 240
TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300
GAACCCAAAC ATAGGCAAAA AGATGAGGAC TGGTGGAGA TCTACATCAA GAGAGAAAAA 360
GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
GCTGCCTGTA CCAATACATC CTGCACTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAACGTG 540
ACAGCCCTGG AATCCCTGTA GCATGGAAGC CTGGTTTGCA GTCAACCACT GGGAAACTTC 600
AGCTACAATT TTCTCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
ACCATGCACT GTATGTCTCT TGGAGAAATG AGTGCTCTTA TCCAGCCTG CAATGTGGTT 720
GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTGGTGG AATGTTTCCA AAACCTGGA 780
AGCTTCCCAT GGAACACAC CTTGATACAT GACTGTGAAG AAGGATTTGA ACTAATGGGA 840
GCCCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900
GCTGTGACAT GCAGGGCOGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
CTGCTGGGAG AGTTCACCTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
TTGCAGGGAC CAGCCAGGT TGAATGCACC ACTCAAGGGC AGTGGACACA GCNAATCCCA 1080
GTTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAAACCCG AGCGAGGCTA CATGAATTGT 1140
CTTCTAGTG CTTCTGGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTCTCT CTGTGAGCAG 1200
GGTTTGTGT TGAAGGGATC CAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAAC 1260
  
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5 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
 GTGAGGTGTG CTATTCCCC TATTGGAGAA TTCACCTACA AGTCTCTTGT TGCCTTCAGC 1380
 TGTGAGGAGG GATTTGAATT ATATGGATCA ACTCAACTTG AGTGCCATC TCAGGGACAA 1440
 TGGACAGAAG AGGTTCCTTC CTGCCAAGTG GTAAAATGTT CAAGCCTGGC AGTTCGGGA 1500
 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGCCA CTGTGTGCAA GTTCGCTGT 1560
 CCTGAAGGAT GGACGCTCAA TGGCTCTGCA GCTCGACAT GTGGAGCCAC AGGACACTGG 1620
 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
 CTTTCTGCTG CTGAGCTCTC CCTCCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740
 10 TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
 GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

A220 Protein sequence:

15 Gene name: Selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Protein Accession #: NP_000441
 Signal sequence: 1-22
 20 Transmembrane domains: 555-573
 C-lectin domain: 23-139
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51
 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRTHLVAI QNKIEIEYLN 60
 SILSYSPSY WIGIRKVN NVVWVGTQKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120
 DVGMMWDERC SKKKLALCYT AACINTSCSG HGECVETINN YTKCDPGFS GLKCEQIVNC 180
 30 TALESPHEGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIACNVV 240
 ECDAVTNPNP GFVECFQNPNG SFPWNTTCTF DCEBGFELMG AQSILQCTSSG NWDNEKPTCK 300
 AVTCRAVRQP QNGSVRCSSHS PAGEFTFKSS CNPTCEBFGM LQGPQVVECT TQGWTTQOIP 360
 VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWMDN 420
 EKPTCEAVRC DAVHQPPKGL VRCAHSPIGE FTYKSSCAFS CEBGFELYGS TQLECTSQGQ 480
 35 WTEEVFSCQV VKCSSLAVPG KINMSCSGEP VFGTVCKPAC PEGWTLNGSA ARTCGATGHW 540
 SGLLPTEAPR TESNIPLVAG LSAAGLSLLT LAPFLMLWRK CLRKAKRFVP ASSCQSLESD 600
 GSYQRPSYIL

Taxol ProstateA221 DNA SEQUENCE

40 Gene name: ESTs; Liprin A2
 Unigene number: Hs.306480
 Probeset Accession #: NS1002
 Nucleic Acid Accession #: NS1002
 45 Coding sequence: 1-3793 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 50 ATGATGTGTG AAGTGATGCC CACGATTAAT GAGGACACCC CAATGAGCCA AAGGGGTGCC 60
 CAAAGCAGTG GCTCGGACTC AGACTCCCCT TTTGAGCAGC TGATGGTGAA TATGCTAGAT 120
 GAAAGGGATC GTCTTCTAGA CACCTTCGGG GAGACCCAGS AAAGCCTCTC ACTTGCCOCAG 180
 CAAAGACTTC AGGATGTCAT CTATGACCGA GACTCACTCC AGAGACAGCT CAATTTCAGCC 240
 CTGCCACAGG ATATCGAATC CCTAACAGGA GGGCTGGCTG GTTCTAAGGG GGCTGATCCA 300
 COGGAATTGG CTGCACTGAC AAAAGAATTA AATGCCTGCA GGGAAACAAC TCTAGAAAAG 360
 55 GAAGAAGAAA TCTCTGAAC TAAAGCTGAA AGAAACAACA CAAGACTATT ACTGGAGCAT 420
 TTGGAGTGCC TTGTGTACG ACATGAAAGA TCACTAAGAA TGACGGTGGT AAAACGGCAA 480
 GCCCAGTCTC CCTCAGGAGT ATCCAGTGAA GTTGAAGTTC TCAAGGCAC TGAATCTTTG 540
 TTTGAGCACC ACAAGGCCTT GGATGAAAAG GTAAGGGAGC GACTGAGGGT TTCTTTAGAA 600
 AGAGTCTCTG CACTGGAAGA AGAACTAGCT GCTGCTAATC AGGAGATTGT TGCTTGGCT 660
 60 GAACRAAATG TTCATATACA AAGAAAATG GCATCAAGCG AGGGATCCAC AGAGTCAGAA 720
 CATCTTGAAG GGATGGAACC TGGACAGAAA GTCCATGAGA AGCGTTTGTC CAATGGTTCT 780
 ATAGACTCAA CCGATGAATC TAGTCAAATA GTTGAAC TAC TGAATGTCT TGAAGAGCAA 840
 AACTATGAAA TGGCCAGATG GAAAGAACGT TTAGCAGCCC TTCTTCCCG AGTGGGAGAG 900
 GTGGAACAGG AAGCAGAGAC AGCAAGAAAG GATCTCATT AAACAGAGA AATGAACACC 960
 65 AAGTATCAAA GGGACATTAG GGAGGCCATG GCACAAAAGG AAGATATGGA AGAAAGAATT 1020
 ACAACCCCTG AAAAGCGTTA CCTCAGTGCT CAGAGAGAAT CTACCTCCAT ACATGACATG 1080
 AATGATAAAC TAGAAAATGA GTTAGCAAAAT AAAGAAGCTA TCCTACGGCA GATGGAAGAG 1140
 AAAAACAGAC AGTTACAAGA ACGTCTTGAG CTAGCTGAAC AAAAGTTGCA GCAGACCATG 1200
 AGAAAGGCTG AAACCTTGCC TGAAGTAGAG GCTGAACTGG CTCAGAGAA TGCAGCCCTA 1260
 70 ACCAAGGCTG AAGAGAGACA TGGAAATATT GAAGAACGTA TGAGACATTT AGAGGGTCAA 1320
 CTTGAAGAGA AGAATCAAGA ACTTCAAGA GCTAGGCAAA GAGAGAAAAT GAATGAGGAG 1380
 CATACACAGA GATTATCGGA TACGGTTGAT AGACTTCTGA CTGAATCCAA TGAACGCTA 1440
 CAATCACTCT TAAAGGAAAG AATGGCTGCT CTAGAAGAAA AGAATGTTTT AATCAAGAA 1500
 TCAGAACTTT TCAGAAAGAA TCTTGAAGAA TCTTTACATG ATAAGGAAAAG ATTAGCAGAA 1560
 75 GAAATTGAAA AGCTGAGATC TGAACCTGAC CAATTGAAAA TGAGAACTGG CTCTTTAATT 1620
 GAACCCACAA TACCAAGAAC TCATCTAGAC ACCTCAGCTG AGTTGCGGTA CTCAGTGGGA 1680
 TCCTTAGTGG ACAGCCAGTC TGATTACAGA ACAAATAAAG TAATAAGAAG ACCAAGGAGA 1740
 GGCCGATGG GTGTGGAAG AGATGAGCCA AAGGTGAAAT CTCTTGGGGA TCACGAGTGG 1800
 AATAGAACTC AACAGATTGG AGTACTAAGC AGCCACCCCT TTGAAAGTGA CACTGAAATG 1860
 80 TCTGATATTG ATGATGATGA CAGAGAAACA ATTTTAGCT CAATGGATCT TCTCTCTCCA 1920
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 AACAAAGAAA TCAGGCTAAT TCAGGAAGAA AAAGAATCTA CAGAGTTGCG TGCTGAAGAA 2040
 ATTGAAAATA GAGTGGCTAG TGTGAGCCTC GAAGGCCTGA ATTTGGCAAG GGTCCACCCA 2100

5 GGTACCTCCA TTACTGCCTC TGTACAGCT TCATCGCTGG CCAGTTTCATC TCCCCCAGT 2160
 GGACACTCAA CTCCAAAGCT CACCCCTCGA AGCCCTGCCA GGGAAATGGA TCGGATGGGA 2220
 GTCATGACAC TGCCAAAGTGA TCTGAGGAAA CATCGGAGAA AGATTGCACT TGTGGAAGAA 2280
 GATGGTGGAG AGGACAAAGC AACAATTAAT TGTGAAACTT CTCTCTCTCC TACCCCTAGA 2340
 GCCCTCAGAA TGACTCACAC TCTCCCTTCT TCCTACCACA ATGATGCTCG AAGTAGTTTA 2400
 TCTGTCTCTC TTGAGCCAGA AAGCCTCGGG CTTGGTAGTG CCAACAGCAG CCAAGACTCT 2460
 CTTACACAAAG CCCCCAAGAA GAAAGGAATC AAGTCTTCAA TAGGACGTTT GTTTGGTAAA 2520
 AAAGAAAAAG CTCGACTTGG GCAGCTCCGA GGCTTTATGG AGACTGAAGC TGCAGCTCAG 2580
 10 GAGTCCCTGG GGTTAGGCAA ACTCGGAAC CAAGCTGAGA AGGATGGAAG ACTAAAGAAA 2640
 AAGCATGAAC TTCTTTGAAGA AGCTCGGAGA AAGGGAATTAC CTTTGGCCCA GTGGGATGGG 2700
 CCAACTGTGG TGCATGGCT AGAGCTTTGG TTGGGAATGC CTGCGTGGTA CGTGGCAGCC 2760
 TGCCGAGCCA ACGTGAAGAG TGGTGCCATC ATGTCTGCTT TATCTGACAC TGAGATCCAG 2820
 AGAGAAATGG GAATCAGCAA TCCACTGCAT CGCTTAAAC TTCCATTAGC AATCCAGGAG 2880
 ATGGTTTCCC TAACAAGTCC TTCAGCTCCT CCAACATCTC GAACCTCTTC AGGCAAGCTT 2940
 15 TGGGTGACTC TTCTTTGAAGA GGAAATCTTT GCAGCTCCAG CAAAAACGAA AGAATCTGAG 3000
 GAAGGAAGCT GGGCCCAAGT TCGGTTTITT CTACAGACCC TGGCTTATGG AGATATGAAT 3060
 CATGATGGTA TTGGAATGTA ATGGCTTCCC AGCTTGGGGT TACCTCAGTA CAGAAGTTAC 3120
 TTTATGGAAT GCTTGGTAGA TGCAAGAATG TTAGATCACC TAACAAAAAA AGATCTCCGT 3180
 GTCCATTATA AAATGGTGGT TAGTTTCCAT CGAACAGATT TACAATATGG AATTATGTGC 3240
 20 TTAAGAGAGT TGAATTAAGA CAGAAAAGAA CTAGAAAGAA GACGGGAAGC AAGCCACAT 3300
 GAAATAAAG AGTGTGGT GTGGAGCAAT GACCGAATTA TTCGCTGGAT ACAAGCAATT 3360
 GGACTTCGAG AATATGCAAA TAATATACTT GAGAGCGGTG TGCATGGCTC ACTTATAGCC 3420
 CTGGATGAAA ACTTTGACTA CAGCAGCTTA ACTTTATTAT TACAGATTCC AACACAGAAC 3480
 25 ACCCAGGCAA GGCAGATTCT TGAAGAGAAA TACAATAACC TCTTGGCCCT GGGAACTGAA 3540
 AGGCCACTGG ATGAAGTGA TGACAGAAGC TTCAGACGTG GATCAACCTG GAGAAGGCAG 3600
 TTCTCTCTCT GTGAAGTACA TGAATCAGC ATGATGCCTG GGTCTCAGA AACATTACCA 3660
 GCTGGATTAA GGTAAACCA ACCTCTGGG CAATCAAGAA AAATGACAA AGATGTTGCT 3720
 30 TCATCAAGAC TGCAGAGGTT AGACAACTCC ACTGTCGCA CATACTCATG TCTCGAGTAA 3780
 GCGGCCGCTT TAA

A222 Protein sequence:

35 Gene name: ESTs; Liprin A2
 Unigene number: Hs.306480
 Probeset Accession #: N51002
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: none found
 40 AAA domain: 286-539
 SAM domains: 895-964, 1017-1084, 1105-1177
 Cellular Localization: not determined

45 1 11 21 31 41 51
 MMCEVMPTIN EDTPMSQRGS QSSGSDSDSH FEQLMVNMLD ERDRLLDTRL ETQESLSLAQ 60
 QRLQDVIYDR DSLQRQLNSA LPQDIESLTG GLAGSKGADP PEFAALTKEI NACREQLLEK 120
 EEEISELKAE RNNTLRLLLEH LECIVSRHER SLRMTVVKRG AQSPSGVSSE VEVLKALKSL 180
 FEHKKALDEK VRERLRVSLR RVSALEELA AANQEIVALR EQNVHIQRKM ASSEGSTESE 240
 50 HLEGMEFQKQ VHEKRLSNGS IDSTDTSQI VELQELLEKQ NYEMAQMKER LAALSSRVGE 300
 VEQEAETARK DLIKTEEMNT KYQDIREAM AQKEDMEERI TLEKRYLSA QRESTSIHDM 360
 NDKLENELAN KESTELRQME KNRQLQERLE LAEQKLQQTM RKAETLPEVE AELAQRITAA 420
 TKAEEERHNI EERMRHLEQ LEEKNQELQR ARQREKNNEE HNKRLSDTVD RLLTESNERL 480
 QLHLKERMAA LEEKNVLIQE SETFRKNLEE SLHDKERLAE EIEKLRSELD QLMKRTGSLI 540
 55 EPTIPRTHLD TSAELRYSVG SLVDSQSDYR TTKVIRPRPR GRMGVRRDEP KVKSLGDHEW 600
 NRTQQIGVLVS SHPFESDTEM SDIDDDRET IFSSMDLLSP SGHSDAQTLA MMLQQLDAI 660
 NKEIRLIQEE KESTELRQME IENRVASVSL EGLNLRVHP GTSITASVTA SSLASSSPFS 720
 GHSTPKLTPR SPAREMDRMG VMTLPDLRK HRRKIIVVEE DGREDKATIK CETSPPPTPR 780
 ALRMTTLPS SYENDARSL SVSLEPESLG LGSANSSQDS LHKAPKKGI KSSIGRLFGK 840
 60 KEKARLQQLR GFMEETAAAG ESLGLGKLGQ QAEKDRRLKK KHELLEZARR KGLPFAQWDG 900
 PTVVAVLELW LGMPAWYVAA CRANVKSIAI MSALSDTEIQ REIGISNPLH RLKRLRLAIQE 960
 MVSLTSPSAP PSTRTPSGNV WVTHEEMENL AAPAKTKESE EGSWAQCPVP LQTLAYGDMN 1020
 HEWIGNEWLP SLGLPQYRSY PNECLVDARM LDHLTKKDLR VHLKMDVSPH RTSLQYIGIMC 1080
 LKRLNYDRKE LERRREASQH BIKDVLVWSN DRIIRWIAI GLREYANNIL ESGVHGSLIA 1140
 65 LDENFDYSSL TLLQLIPTQN TQARQILERE YNNLLALGTE RRLDESDDKN FRRGSTWRRQ 1200
 FPPREVHGIS MMPGSETLFP AGFRLTTTSG QSRKMTTIVA SSRLQRLDMS TVRTYSCLC

A223 DNA SEQUENCE

70 Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Nucleic Acid Accession #: NM_016570
 Coding sequence: 1- 1134 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
 ATGAGGCGAC TGAATCGGAA AAAAACTTTA AGTTTGGTAA AAGAGTTGGA TGCCCTTTCOG 60
 AAGGTTCTCTG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120
 80 TTTACACTA TGGCTTTATT AACCATAATG GAATCTCAG TATATCAAGA TACATGGATG 180
 AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAAT TAAGAATTAA TATAGATATT 240
 ACTGTTGCCA TGAAGTGTCA ATATGTTTGA GCGGATGTAT TGGATTAGC AGAAACAATG 300
 GTTGCACTCG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
 AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA ACATTCACTT 420
 CAAGATGTGA TATTTAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480

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GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCATATAA 540
GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600
CATTGGCAG CACTTGTCAG CCATGAATCT TACAATTTT CTGATAGAAT AGATCATTTG 660
TCTTTGGAG AGCTTGTTCC AGCAATTATT AATCCTTTAG ATGGAACCTGA AAAAAATTGCT 720
ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780
TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAA 840
CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTTATGA AATATGATCT CAGTTCTCTT 900
ATGGTGACAG TTAGTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTAAAG ACTCTGTGGT 960
ATTGTTGGAG GAATCTTTTC AACCAACAGC ATGTTACATG GAATTGGAAA ATTTATAGTT 1020
GAAATAATTT GCTGTGTTT CAGACTTGGG TCCTATAAAC CTGTCAATTC TGTTCTCTTT 1080
GAGGATGGCC ACACAGACAA CCACCTTACCT CTTTATAGAAA ATAATACACA TTTGA

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A224 Protein sequence:

Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Protein Accession #: NP_057654
 Signal sequence: none found
 Transmembrane domains: none found
 Cellular Localization: nuclear

1 11 21 31 41 51
 MRRINRKKTL SLVKELDAPP KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60
 KYEYEVKDFP SSKLRINIDI TVAMKCOYVG ADVLDLAETM VASADGLVYE PTVFDLSPQQ 120
 KEWQRMQLLI QSRLEQEHSL QDVIFKSAPK STSTALPPRE DDSSQSPNAC RIHGHLYVNK 180
 VAGNFHITVG KAIPHPRGHA HLAALVNHEH YNFSHRIDHL SFGLVFAII NPLDGTEDIA 240
 IDHNQMPQYF ITVVPTKLHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300
 MVTITEEHMP FWQPFVRLCG IVGGIFSTTG MLHGIGKFIV EIIICRFRLG SYKPVNSVPP 360
 EDGHTDNHLP LLENNTN

Uterine**A225 DNA SEQUENCE:**

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
 CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTACAG TTTCTTCCAA CCTTGCCATT 120
 GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
 ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
 ATGGTTATTC ATCACTGGA GGAATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGGCC 300
 CAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
 GAAACCACTG ATAAGAATTT ATCACTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
 GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
 TATGAGCCTC GGGATTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTCA 600
 GAAGAAAACC TCTGGCAGAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAA 660
 TTACTATTTA GTTTTITTTAA TGTGTTTGA ATAGTCTTAT TAAATATAAT GTTTTTTAAA 720
 TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

A226 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

1 11 21 31 41 51
 MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLRSGWGD DITWVQTYEE GLPYAQSKSK 60
 PLMVIHLED QYQSALKKV PAQNEBIQEM AQNKFIIMNL MHETTCKNLS PDGQYVPRIM 120
 FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

A227 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Probeset Accession #: AA460530
 Nucleic Acid Accession #: NM_003667
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GTGGCGGC	CAACACCTC	AGTCCCCGCC	GCGCTTCTCC	TGCGCGCCCA	CGCCGTGGGG	60
5	TCAGGAACGC	GGCGTCTGGC	GCTGCAGACG	CCCGCTGAGT	TGCAGAAACC	CACGGAGCGG	120
	CGCCCGGCGC	GCCACGGCCC	GTAGCAGTCC	GGTCTGCTC	TCCGCGCGCG	TCCGGCTCGT	180
	GGCCCGCTAC	TTCGGGCACC	ATGGACACCT	CCCGCTCGG	TGTGCTCTGT	TCCTTGCGCTG	240
	TGCTGCTGCA	GCTGGCGACC	GGGGGACGCT	CTCCAGGTC	TGGTGTGTG	CTGAGGGGCT	300
	GCCCCACACA	CTGTCTTTCG	GAGCCCGACG	GCAGGATGTT	GCTCAGGGTG	GACTGCTCCG	360
10	ACCTGGGGCT	CTCGGAGCTG	CCTTCCCAAC	TCAGCGTCTT	CACCTCTTAC	CTAGACCTCA	420
	GTATGAACAA	GATCAGTCAG	CTGCTCCCGA	ATCCCTCGCC	CAGTCTCCGC	TTCTGGAGGG	480
	AGTTAGCTCT	TGCGGGAAAC	GCTCTGACAT	ACATTCCCAA	GGGAGCATTC	ACTGGCCTTT	540
	ACAGTCTTAA	AGTTCTTATG	CTGCAGATA	ATCAGCTAAG	ACACGTACCC	ACAGAAGCTC	600
	TGCAGAAATT	GCGAAGCCTT	CAATCCCTGC	GTCTGGATGC	TAACCAATC	AGCTATGTGC	660
15	CCCCAAGCTG	TTTCAGTGGC	CTGCATTCCC	TGAGGCACCT	GTGGCTGGAT	GACAATGCGT	720
	TAACAGAAAT	GCTAGGCAAC	GCTTTTAGAA	GTTTATCGGC	ATTGCAAGCC	ATGACCTTGG	780
	CCCTGAACAA	AATACACCAC	ATACCAGACT	ATGCCCTTGG	AAACCTCTCC	AGCTTGTGTAG	840
	TTCTACATCT	CCATAACAAT	AGAAATCCACT	CCCTGGGAAA	GAAATGCTTT	GATGGGCTCC	900
	ACAGCCTAGA	GACTTTAGAT	TTAAATTACA	ATAACCTTGA	TGAATTCGCC	ACTGCAATTA	960
20	GGACACTCTC	CAACCTTAAA	GAACATAGGAT	TTCATAGCAA	CAATATCAGG	TCGATACCTG	1020
	AGAAAGCATT	TGTAGGCAAC	CCTTCTCTTA	TTACATACA	TTTCTATGAC	AATCCCATCC	1080
	AATTTGTGTT	GAGATCTGCT	TTTCAACATT	TACCTGAACT	AAGAACACTG	ACTCTGAATG	1140
	GTGCTCACA	AATAACTGAA	TTTCTGATT	TAACTGGAAC	TGCAAACCTG	GAGAGTCTGA	1200
	CTTTAACTGG	AGCACAGATC	TCATCTCTTC	CTCAACCGT	CTGCAATCAG	TTACCTAATC	1260
25	TCCAAGTGCT	AGATCTGTCT	TACAACCTAT	TAGAAGATT	ACCCAGTTT	TCACTCTGCC	1320
	AAAAGCTTCA	GAAATTTGAC	CTAAGACATA	ATGAAATCTA	CGAAATTA	GTTGACACTT	1380
	TCCAGCAGTT	GCTTAGCCTC	CGATGCTGTA	ATTTGGCTTG	GAACAAAATT	GCTATTATTC	1440
	ACCCCAATGC	ATTTTCCACT	TTGCCATCCC	TAATAAAGCT	GGACCTATCG	TCCAACCTCC	1500
	TGTGCTCTTT	TCCATAAAT	GGGTACATG	GTTTAACTCA	CTTAAATTA	ACAGGAAATC	1560
30	ATGCTCTTCA	GAGCTTGATA	TCATCTGAAA	ACTTCCAGA	ACTCAAGGTT	ATAGAAATGC	1620
	CTTATGCTTA	CCAGTGCTGT	GCATTTGGAG	TGTGTGAGAA	TGCCTATAAG	ATTCTAATC	1680
	AATGGAATAA	AGGTGACAAC	AGCAGTATGG	ACGACCTTCA	TAAGAAAGAT	GCTGGAATGT	1740
	TTCAAGCTCA	AGATGAACGT	GACCTTGAAG	ATTTCTGCT	TGACTTTGAG	GAAGACCTGA	1800
	AAGCCCTTCA	TTCAGTGCAG	TGTTCACTT	CCCGAGGCC	CTTCAAAACC	TGTGAACACC	1860
35	TGCTTGATGG	CTGGCTGATC	AGAATTGGAG	TGTGGAACAT	AGCAGTTCTG	GCACTTACTT	1920
	GTAATGCTTT	GGTGACTTCA	ACAGTTTTC	GATCCCTCT	GTACATTTC	CCCATTAAC	1980
	TGTTAATTGG	GGTGATCGCA	GCAGTGAACA	TGCTCACGGG	AGTCTCCAGT	CCCGTCTGG	2040
	CTGGTGTGGA	TGCGTTCACT	TTTGCGAGCT	TTGCAAGACA	TGGTGCCTGG	TGGGAGAAATG	2100
	GGGTGTGGTG	CCATGTACCT	GGTTTITTT	CCATTTTTC	TTCAGAAATCA	TCTGTTTTC	2160
40	TGCTTACTCT	GGCAGCCCTG	GAGCGTGGGT	TCTCTGTGAA	ATATTCTGCA	AAATTGTGAA	2220
	CGAAAGCTCC	ATTTTCTAGC	CTGAAAGTAA	TCATTTTGCT	CTGTGCCCTG	CTGGCCTTGA	2280
	CCATGGCCGC	TGCTCCCTCG	CTGGGTGGCA	GCAAGTATGG	CGCCTCCCT	CTCTGCTCTG	2340
	CTTTGCCCTT	TGGGAGGCC	AGCAACCATG	GCTACATGCT	CGCTCTCATC	TTGCTCAATT	2400
	CCCTTGTCTT	CCTCATGATG	ACCATGCTCT	ACACCAAGCT	CTACTGCAAT	TGGCAAAAGG	2460
45	GAGACCTGGA	GAATATTTCG	GACTGCTCTA	TGGTAAACA	CATTGCCCTG	TGTCTCTTCA	2520
	CCAACTGCAT	CCTAAACTGC	CCTGTGGCTT	TCTTGTCTT	CTCCTCTTAA	ATAAACTTAA	2580
	CATTATACAA	TCTGAAGTAA	ATTAAGTTTA	TCCTTCTGGT	GGTAGTCCCA	CTCTCTGCAT	2640
	GTCTCAATCC	CCTTCTCTAC	ATCTTGTTCA	ATCCTCACTT	TAAGGAGGAT	CTGGTGAGCC	2700
	TGAGAAAGCA	AACCAACGTC	TGGACAAGAT	CAAAACACCC	AAGCTTGATG	TCAATTAATC	2760
50	CTGATGATGT	CGAAAAACAG	TCCTGTGACT	CAACTCAAGC	CTTGGTAACC	TTTACCAGCT	2820
	CCAGCATCAT	TTATGACCTG	CCTCCAGTCT	CCGTGCCATC	ACCAGCTTAT	CCAGTGACTG	2880
	AGAGCTGCCA	TCTTCTCTCT	GTGGCATTTG	TCCCATGTCT	CTAATTAATA	TGTGAAGGAA	2940
	AATGTTTTC	AAGGTTGAGA	ACCTGAAAT	GTGAGATTGA	GTATATCAGA	GCAATTAATA	3000
	ATAAGAAGAG	CTGAGGTGAA	ACTCGGTTTA	AA			

A228 Protein sequence

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Protein Accession #: NP_003658.1
 Signal sequence: 1-22
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825
 Cellular Localization: plasma membrane

	1	11	21	31	41	51	
65	MDTSRLGVLL	SLPVLQLAT	GGSSPRSGVL	LRGCPHCHC	EPDGRMLLRV	DCSDLGLSEL	60
	PSNLSVFTSY	LDLSMNNISQ	LLPNPLPSLR	FLIELRLAGN	ALTYIPKAP	TGLYSLKVLN	120
	LQNNQLRHVP	TEALQNLRLS	QSLRLDANHI	SYVPPSCPSG	LHSLRLHLWD	DNALTEIPVQ	180
70	AFRSLALQFA	MTLALNKHII	IPDYAPGNLS	SLVVLHLENN	RIHSLGKKCF	DGLHSLLETLD	240
	LNYYNNLDEF	TAIRTLNLK	ELGFHSNNIR	SIPEKAFVGN	PSLITIHFDY	NPIQFVGRSA	300
	FQHLPELRTL	TLAGASQITE	FFDLTGTAHL	ESLTLTGAQI	SSLPTQVCNQ	LPNLQVLDLS	360
	YNLLEDLPFS	SVCQKLQKID	LRENBIYEIK	VDTFQQLLSL	RSLNLAWNKI	AIHFNPAFST	420
	LPSLIKLDLS	SNLLSFPFIT	GLHGLTHLKL	TGNHALQSLI	SEENFPPELV	TEMPYAYQCC	480
75	AFGVCSNAYK	ISNQNMKGDN	SSMDLHKKD	AGMFOAQDER	DLEDPLDPE	EDLKALHSVK	540
	CSPSPGPFKP	CEHLDDGWL	RIGVWTIAVL	ALTQNALVTS	TVFRSPLYIS	PIKLIGVIA	600
	AVNMLTGVSS	AVLAGVDAFT	FGSFARHGAH	WENGVGCHVI	GFLSIFASES	SVPLLTALAL	660
	ERGFVSKYSA	KPETKAPFSS	LKVIILLCAL	LALTMARVPL	LGGSKYGASP	LCLPLPFGEF	720
	STMGYVVALI	LLNSLCFLMM	TIAYTKLYCN	LDKGDLNLIW	DCSMVKHIAL	LLPTNCLILNC	780
80	PVAFLSFSSL	INLTPIISPEV	IKFILLVVVP	LPACLNPLLY	ILFNPHFKED	LVSLEKQTYV	840
	WTRSKHPSLM	SINSDVBEKQ	SCDSTQALVT	FTSSSITYDL	PPSSVPSPAY	PVTESCHLSS	900
	VAFVPCL						

Table 75: See Table 1

Table 76A depicts Seq ID No; UnigeneID; UnigeneTitle; PKey; Predicted Cellular Localization; and Exemplar Accession for each of the sequences in Table 78. The information in

Table 76A is linked by SeqID No to Table 78.

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Seq ID No:	PKey:	ExAccn:	UnigeneID:	Unigene Title:	Pred Subcell Loc:
Sequence ID No for sequences in table					
Unique Eos probeset identifier number					
Exemplar Accession number, Genbank accession number					
Unigene number					
Unigene gene title					
Predicted sub-cellular localization					
Seq ID No	PKey	ExAccn	UnigeneID	Unigene Title	Pred Subcell Loc
Seq ID 1 & 2	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipid	plasma membrane
Seq ID 3 & 4	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	plasma membrane
Seq ID 5 & 6	429423	AI016712	Hs.287797	Integrin, beta 1 (fibronectin receptor,	plasma membrane
Seq ID 7 & 8	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	secreted
Seq ID 9 & 10	419172	AW338625	Hs.22120	ESTs; similar to TRANSMEMBRANE 4 SUPERF	plasma membrane
Seq ID 11 & 12	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 13 & 14	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 15 & 16	407836	T79340	Hs.200272	B-cell CLL/lymphoma 6, member B, zinc fi	intracell
Seq ID 17 & 18	414577	AK56548	Hs.72116	hypothetical protein FLJ20992 similar to	secreted
Seq ID 19 & 20	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	plasma membrane
Seq ID 21 & 22	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	secreted
Seq ID 23 & 24	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	secreted
Seq ID 25 & 26	429276	AF056085	Hs.198612	G protein-coupled receptor 51	plasma membrane
Seq ID 27 & 28	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	plasma membrane
Seq ID 29 & 30	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	secreted
Seq ID 31 & 32	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	intracell
Seq ID 33 & 34	418506	AA084248	Hs.85339	G protein-coupled receptor 39	plasma membrane
Seq ID 35 & 36	423961	D13666	Hs.136348	perlestin (OSF-2os)	secreted
Seq ID 37 & 38	414812	X72755	Hs.77367	monokine induced by gamma interferon	secreted
Seq ID 39 & 40	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 41 & 42	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 43 & 44	424399	AI905687	Hs.82128	AI905687:IL-BT095-190199-019 BT095 Homo	secreted
Seq ID 45 & 46	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	secreted
Seq ID 47 & 48	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	secreted
Seq ID 49 & 50	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	secreted
Seq ID 51 & 52	439569	AW602166	Hs.222399	CEGP1 protein	secreted
Seq ID 53 & 54	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
Seq ID 55 & 56	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	plasma membrane
Seq ID 57 & 58	411789	AF245505	Hs.72157	Adican	secreted
Seq ID 59 & 60	426698	AA852773	Hs.334838	KIAA1866 protein	plasma membrane
Seq ID 61 & 62	450098	W27249	Hs.8109	hypothetical protein FLJ21080	intracell
Seq ID 63 & 64	421552	AF026892	Hs.105700	secreted fritzled-related protein 4	secreted
Seq ID 65 & 66	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	plasma membrane
Seq ID 67 & 68	415539	AI733881	Hs.72472	BMP-R1B	plasma membrane
Seq ID 69 & 70	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 71 & 72	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 73 & 74	409079	W87707	Hs.82065	Interleukin 6 signal transducer (gp130,	plasma membrane
Seq ID 75 & 76	442082	R41823	Hs.7413	ESTs	plasma membrane
Seq ID 77 & 78	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	plasma membrane
Seq ID 79 & 80	451398	AI793124	Hs.144479	ESTs	intracell
Seq ID 81 & 82	429220	AW207206	Hs.105445	ESTs	plasma membrane
Seq ID 83 & 84	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	plasma membrane
Seq ID 85 & 86	423242	AL039402	Hs.125783	DEME-6 protein	plasma membrane
Seq ID 87 & 88	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 89 & 90	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 91 & 92	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 93 & 94	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 95 & 96	325372			Phase 2 & 3 Exons	cytoplasmic
Seq ID 97 & 98	450375	AA009647		a disintegrin and metalloproteinase doma	plasma membrane
Seq ID 99 & 100	426215	AW963419	Hs.155223	stanniocalcin 2	secreted
Seq ID 101 & 102	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	secreted
Seq ID 103 & 104	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 105 & 106	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 107 & 108	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	plasma membrane
Seq ID 109 & 110	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	secreted
Seq ID 111 & 112	446163	AA026880	Hs.25252	prolactin receptor	plasma membrane
Seq ID 113 & 114	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	plasma membrane
Seq ID 115 & 116	428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-II	intracell
Seq ID 117 & 118	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	plasma membrane
Seq ID 119 & 120	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 121 & 122	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 123 & 124	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 125 & 126	115522	BE614387	Hs.333893	c-Myc target JPO1	intracell
Seq ID 127 & 128	452679	Z42387	Hs.63883	transmembrane, prostate androgen induced	plasma membrane
Seq ID 129 & 130	446051	BE048061	Hs.37054	ephrin-A3	plasma membrane
Seq ID 131 & 132	422048	NM_012445	Hs.288126	spodoin 2, extracellular matrix protein	secreted
Seq ID 133 & 134	410418	D31382	Hs.63325	transmembrane protease, serine 4	plasma membrane
Seq ID 135 & 136	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	plasma membrane
Seq ID 137 & 138	422260	AA315993	Hs.105484	regenerating gene type IV	secreted

	Seq ID 139 & 140	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 141 & 142	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 143 & 144	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
5	Seq ID 145 & 146	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 147 & 148	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 149 & 150	104888	AW939591	Hs.5940	mucin 13, epithelial transmembrane	plasma membrane
	Seq ID 151 & 152	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	plasma membrane
	Seq ID 153 & 154	422330	D30783	Hs.115263	epiregulin	plasma membrane
10	Seq ID 155 & 156	452461	N78223	Hs.108106	transcription factor	intracell
	Seq ID 157 & 158	413324	V00571	Hs.75294	coricotropin releasing hormone	secreted
	Seq ID 159 & 160	412420	AL035668	Hs.73853	bone morphogenetic protein 2	secreted
	Seq ID 161 & 162	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual ara	secreted
	Seq ID 163 & 164	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	secreted
15	Seq ID 165	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (intracell
	Seq ID 166 & 167	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (intracell
	Seq ID 168 & 169	432829	W60377	Hs.57772	ESTs	intracell
	Seq ID 170 & 171	425721	AC002115	Hs.159309	uropod 1A	plasma membrane
	Seq ID 172 & 173	420370	Y13845	Hs.97234	uropod 2	plasma membrane
20	Seq ID 174 & 175	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.s.a	plasma membrane
	Seq ID 176 & 177	402075			ENSP00000251056*Plasma membrane calcium	secreted
	Seq ID 178 & 179	421110	AJ250717	Hs.1355	cathepsin E	secreted
	Seq ID 180 & 181	451668	Z43948	Hs.326444	cartilage acidic protein 1	plasma membrane
	Seq ID 182 & 183	451668	Z43948	Hs.326444	cartilage acidic protein 1	secreted
25	Seq ID 184 & 185	451668	Z43948	Hs.326444	cartilage acidic protein 1	intracell
	Seq ID 186 & 187	408243	Y00787	Hs.624	interleukin 8	secreted
	Seq ID 188 & 189	422282	AF019225	Hs.114309	apolipoprotein L	secreted
	Seq ID 190 & 191	425852	AK001504	Hs.159551	death receptor 6, TNF superfamily member	plasma membrane
	Seq ID 192 & 193	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	plasma membrane
30	Seq ID 194 & 195	404875			NM_022819*Homo sapiens phospholipase A2	intracell
	Seq ID 196 & 197	425893	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	plasma membrane
	Seq ID 198 & 199	404977			Insulin-like growth factor 2 (somatomedi	secreted
	Seq ID 200 & 201	420876	AA918425	Hs.177744	ESTs	plasma membrane
	Seq ID 202 & 203	427747	AW411425	Hs.180655	serine/threonine kinase 12	intracell
35	Seq ID 204 & 205	420281	AI623693	Hs.323494	Predicted cation efflux pump	plasma membrane
	Seq ID 206 & 207	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	intracell
	Seq ID 208	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 209 & 210	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 211 & 212	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
40	Seq ID 213 & 214	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 215 & 216	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 217 & 218	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 219 & 220	405932			C15000305:g[3806122]gb AAC69198.1 (AF0	intracell
	Seq ID 221 & 222	405932			C15000305:g[3806122]gb AAC69198.1 (AF0	intracell
45	Seq ID 223 & 224	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 225 & 226	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 227 & 228	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 229 & 230	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	secreted
	Seq ID 231 & 232	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	secreted
50	Seq ID 233 & 234	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	secreted
	Seq ID 235 & 236	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 237 & 238	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 239 & 240	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 241 & 242	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	intracell
55	Seq ID 243 & 244	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	secreted
	Seq ID 245 & 246	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	plasma membrane
	Seq ID 247 & 248	430890	X54232	Hs.2699	glypican 1	plasma membrane
	Seq ID 249 & 250	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	plasma membrane
	Seq ID 251	429466	M85835	Hs.12827	ESTs	
60	Seq ID 252	429466	M85835	Hs.12827	ESTs	
	Seq ID 253 & 254	419721	NM_001650	Hs.288650	aquaporin 4	plasma membrane
	Seq ID 255 & 256	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	secreted
	Seq ID 257 & 258	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	plasma membrane
	Seq ID 259 & 260	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	secreted & plasma membrane
65	Seq ID 261 & 262	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	secreted
	Seq ID 263 & 264	419704	AA429104	Hs.45057	ESTs	intracell
	Seq ID 265 & 266	444471	AB020684	Hs.11217	KIAA0877 protein	plasma membrane
	Seq ID 267 & 268	409395	U46745	Hs.336578	dystrobrevin, alpha	secreted
	Seq ID 269 & 270	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	secreted
70	Seq ID 271 & 272	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	plasma membrane
	Seq ID 273	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 274	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 275 & 276	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	plasma membrane
	Seq ID 277 & 278	424998	U58515	Hs.154138	chitinase 3-like 2	secreted
	Seq ID 279 & 280	412709	AL022327	Hs.74518	KIAA0027 protein	plasma membrane
75	Seq ID 281 & 282	435615	Y15065	Hs.4975	potassium voltage-gated channel, KCOT-lik	plasma membrane
	Seq ID 283 & 284	404049			NM_018937*Homo sapiens protocadherin be	plasma membrane
	Seq ID 285 & 286	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	plasma membrane
	Seq ID 287 & 288	404029			NM_018936*Homo sapiens protocadherin be	plasma membrane
	Seq ID 289 & 290	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	intracell
80	Seq ID 291 & 292	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 293 & 294	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 295 & 296	436895	AF037335	Hs.5338	carbonic anhydrase XII	plasma membrane
	Seq ID 297 & 298	421471	U90545	Hs.327179	solute carrier family 17 (sodium phospho	plasma membrane

5	Seq ID 299 & 300	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	plasma membrane
	Seq ID 301 & 302	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	plasma membrane
	Seq ID 303 & 304	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	plasma membrane
	Seq ID 305 & 306	410407	X66839	Hs.63287	carbonic anhydrase IX	plasma membrane
	Seq ID 307 & 308	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	plasma membrane
	Seq ID 309 & 310	420737	L08096	Hs.99899	CD70 ; tumor necrosis factor (ligand) s	plasma membrane
	Seq ID 311 & 312	309931	AW341683		gb3hd13d01.x1 Soares_NFL_T_GBC_S1 Homo	plasma membrane
	Seq ID 313 & 314	412719	AW016610	Hs.816	ESTs	intracell
10	Seq ID 315 & 316	417034	NM_006183	Hs.80962	neurotensin	secreted
	Seq ID 317 & 318	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	plasma membrane
	Seq ID 319 & 320	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	secreted
	Seq ID 321 & 322	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	plasma membrane
	Seq ID 323 & 324	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	secreted
15	Seq ID 325 & 326	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 327 & 328	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 329 & 330	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	secreted
	Seq ID 331 & 332	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	plasma membrane
	Seq ID 333 & 334	431846	BE019924	Hs.271580	uroplakin 1B	plasma membrane
	Seq ID 335 & 336	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	secreted
20	Seq ID 337 & 338	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	plasma membrane
	Seq ID 339 & 340	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	plasma membrane
	Seq ID 341 & 342	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	plasma membrane
	Seq ID 343 & 344	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	plasma membrane
25	Seq ID 345 & 346	417389	BE260964	Hs.82045	midline (neurite growth-promoting factor	secreted
	Seq ID 347 & 348	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	plasma membrane
	Seq ID 349 & 350	417542	J04129	Hs.82269	progesterone-associated endometrial prote	secreted
	Seq ID 351 & 352	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	plasma membrane
	Seq ID 353 & 354	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
30	Seq ID 355 & 356	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 357 & 358	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	secreted
	Seq ID 359 & 360	418462	BE001596	Hs.85266	integrin, beta 4	plasma membrane
	Seq ID 361 & 362	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	secreted
	Seq ID 363 & 364	439606	W79123	Hs.58561	G protein-coupled receptor 87	plasma membrane
35	Seq ID 365 & 366	404877			NM_005365:Homo sapiens melanoma antigen,	intracell
	Seq ID 367 & 368	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	plasma membrane
	Seq ID 369 & 370	109424	NM_005329	Hs.85962	hyaluronan synthase 3	plasma membrane
	Seq ID 371 & 372	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
40	Seq ID 373 & 374	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 375 & 376	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 377 & 378	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 379 & 380	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 381 & 382	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
45	Seq ID 383 & 384	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 385 & 386	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 387 & 388	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 389 & 390	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalinin	secreted
	Seq ID 391 & 392	332180	AF134160	Hs.7327	claudin 1	plasma membrane
	Seq ID 393 & 394	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
50	Seq ID 395 & 396	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
	Seq ID 397 & 398	439223	AW238299	Hs.250618	UL16 binding protein 2	plasma membrane
	Seq ID 399 & 400	409757	NM_001898	Hs.123114	cystatin SN	secreted
	Seq ID 401 & 402	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 403 & 404	428969	AF120274	Hs.194689	artemin	secreted
55	Seq ID 405 & 406	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 407 & 408	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 409 & 410	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 411 & 412	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 413 & 414	414774	X02419	Hs.77274	plasminogen activator, urokinase	secreted
60	Seq ID 415 & 416	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 417 & 418	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 419 & 420	428486	AW583497	Hs.184604	pancreatic polypeptide	secreted
	Seq ID 421 & 422	457489	AI693815	Hs.127179	cryptic gene	secreted
	Seq ID 423 & 424	432874	W94322	Hs.279651	melanoma inhibitory activity	secreted
65	Seq ID 425 & 426	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 427 & 428	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 429 & 430	404682			C9001188"gi 12738842 ref NP_073725.1 p	secreted
	Seq ID 431 & 432	429547	AW009166	Hs.99376	ESTs	secreted
	Seq ID 433 & 434	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter	plasma membrane
70	Seq ID 435 & 436	407242	M18728		gbHuman nonspecific crossreacting antig	plasma membrane
	Seq ID 437 & 438	407242	M18728		gbHuman nonspecific crossreacting antig	plasma membrane
	Seq ID 439 & 440	407242	M18728		gbHuman nonspecific crossreacting antig	plasma membrane
	Seq ID 441 & 442	432596	AJ224741	Hs.278461	matrilin 3	secreted
	Seq ID 443 & 444	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	plasma membrane
75	Seq ID 445 & 446	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	intracell
	Seq ID 447 & 448	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	secreted
	Seq ID 449 & 450	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 451 & 452	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 453 & 454	422109	S73265	Hs.1473	gastrin-releasing peptide	secreted
80	Seq ID 455 & 456	419235	AW470411	Hs.288433	neurotrophin	plasma membrane
	Seq ID 457 & 458	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	plasma membrane
	Seq ID 459 & 460	427333	AF067797	Hs.176658	aquaporin 8	plasma membrane
	Seq ID 461 & 462	417931	W95642	Hs.82961	trefoil factor 3 (Intestinal)	secreted
	Seq ID 463 & 464	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	secreted

5	Seq ID 465 & 466	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	secreted
	Seq ID 467 & 468	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	secreted
	Seq ID 469 & 470	452194	AJ694413	Hs.332649	Ubiquitin-like protein FAT10777	plasma membrane
	Seq ID 471 & 472	452194	AJ694413	Hs.332649	Ubiquitin-like protein FAT10777	plasma membrane
	Seq ID 473 & 474	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	secreted
	Seq ID 475 & 476	429010	Y18198	Hs.194725	one cut domain, family member 2	intracell
	Seq ID 477 & 478	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	secreted
	Seq ID 479 & 480	448243	AW359771	Hs.52620	integrin, beta 8	plasma membrane
10	Seq ID 481 & 482	426427	M86699	Hs.169840	TTK protein kinase	intracell
	Seq ID 483 & 484	428187	AJ687303	Hs.285529	G protein-coupled receptor 49	plasma membrane
	Seq ID 485 & 486	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 487 & 488	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 489 & 490	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
15	Seq ID 491 & 492	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 493 & 494	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	secreted
	Seq ID 495 & 496	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	plasma membrane
	Seq ID 497 & 498	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com	secreted
	Seq ID 499 & 500	406400			kallikrein 8 (neurosin/ovasin) (KLK8)	secreted
20	Seq ID 501 & 502	431130	NM_006103	Hs.2719	HE4; epidiolymis-specific, whey-acidic pr	secreted
	Seq ID 503 & 504	420440	NM_002407	Hs.97644	mammaglobin 2	secreted
	Seq ID 505 & 506	428450	NM_014791	Hs.184339	KIAA0175 gene product	intracell
	Seq ID 507 & 508	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	secreted
	Seq ID 509 & 510	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	secreted
25	Seq ID 511 & 512	453392	U23752	Hs.32964	SRF (sex determining region Y)-box 11	intracell
	Seq ID 513	431989	AW972870	Hs.291069	ESTs	
	Seq ID 514	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	
	Seq ID 515 & 516	409178	BE393948	Hs.50915	kallikrein 5	secreted
	Seq ID 517 & 518	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	secreted
30	Seq ID 519 & 520	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 521 & 522	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 523 & 524	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 525 & 526	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 527 & 528	452097	AB002364	Hs.27916	a disintegrin-like and metalloprotease (secreted
35	Seq ID 529 & 530	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	secreted
	Seq ID 531 & 532	431515	NM_012152	Hs.268583	endothelial differentiation, lysophospha	plasma membrane
	Seq ID 533 & 534	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	plasma membrane
	Seq ID 535 & 536	412078	X69699	Hs.73149	paired box gene 8	intracell
	Seq ID 537 & 538	412078	X69699	Hs.73149	paired box gene 8	intracell
40	Seq ID 539 & 540	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	secreted
	Seq ID 541 & 542	407792	AJ077715	Hs.39384	putative secreted ligand homologous to f	secreted
	Seq ID 543 & 544	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	plasma membrane
	Seq ID 545 & 546	452792	AB037765	Hs.30652	KIAA1344 protein	plasma membrane
	Seq ID 547 & 548	400294	N95795	Hs.278695	Homo sapiens protein mRNA, complete cds	plasma membrane
45	Seq ID 549 & 550	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 551 & 552	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 553 & 554	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 555 & 556	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 557 & 558	400290	H18836	Hs.31608	hypothetical protein FLJ20041	plasma membrane
50	Seq ID 559 & 560	410001	AB041036	Hs.57771	kallikrein 11	secreted
	Seq ID 561 & 562	418386	AJ765805	Hs.26691	ESTs	plasma membrane
	Seq ID 563 & 564	451027	AW519204	Hs.40808	ESTs	plasma membrane
	Seq ID 565 & 566	446057	AJ420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	plasma membrane
	Seq ID 567 & 568	433466	AA508353	Hs.105314	relaxin 1 (H1)	secreted
55	Seq ID 569 & 570	453370	AJ470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 571 & 572	453370	AJ470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 573 & 574	414569	AF109298	Hs.118258	prostate cancer associated protein 1	plasma membrane
	Seq ID 575 & 576	413435	X51405	Hs.75360	carboxypeptidase E	secreted
	Seq ID 577 & 578	426501	AW043782	Hs.293616	ESTs	plasma membrane
60	Seq ID 579 & 580	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	plasma membrane
	Seq ID 581 & 582	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport	plasma membrane
	Seq ID 583 & 584	412628	AJ972402	Hs.306051	hypothetical protein MGC2648	secreted
	Seq ID 585 & 586	403047			NM_005656*:Homo sapiens transmembrane pr	plasma membrane
	Seq ID 587 & 588	403047			NM_005656*:Homo sapiens transmembrane pr	plasma membrane
65	Seq ID 589 & 590	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	plasma membrane
	Seq ID 591 & 592	445413	AA151342	Hs.12677	CGI-147 protein	secreted
	Seq ID 593 & 594	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	intracell
	Seq ID 595 & 596	427958	AA418000	Hs.98280	potassium intermediate/small conductance	plasma membrane
	Seq ID 597 & 598	421887	AW161450	Hs.109201	CGI-86 protein	plasma membrane
70	Seq ID 599 & 600	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	secreted
	Seq ID 601 & 602	432101	AJ918950	Hs.123642	EphA3	plasma membrane
	Seq ID 603 & 604	407786	AA687538	Hs.38972	tetraspan 1	plasma membrane
	Seq ID 605 & 606	416836	D54745	Hs.80247	cholecystokinin	secreted
	Seq ID 607 & 608	416539	Y07909	Hs.79368	epithelial membrane protein 1	plasma membrane
75	Seq ID 609 & 610	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 611 & 612	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 613 & 614	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 615 & 616	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 617 & 618	422424	AI186431	Hs.296638	prostate differentiation factor	secreted
80	Seq ID 619 & 620	428970	BE276891	Hs.194691	retinoic acid induced 3	plasma membrane
	Seq ID 621 & 622	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	secreted
	Seq ID 623 & 624	439018	AW300887	Hs.26538	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 625 & 626	420610	AJ683183	Hs.99348	distal-less homeo box 5	intracell
	Seq ID 627 & 628	425723	NM_014420	Hs.159311	clckkopf (Xenopus laevis) homolog 4	secreted

Seq ID 629 & 630	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (fo	intracell
Seq ID 631 & 632	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	secreted
Seq ID 633 & 634	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	intracell

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Table 76B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
424399	238961_1	AI905687 AI905624 AI905837 AI905623 AA340069 R75793 W72837 BE074512 AI905633 W72838 BE092421 AI127172 BE186013 AW070916 AI139456 AW176044 AW291950
429220	301384_1	AW207206 AW341473 AA448195 AI951341
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

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Table 76C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NT_position: Indicates nucleotide positions of predicted exons.

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Pkey	Ref	Strand	NT_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
403047	3540153	Minus	59793-59958
404029	7671252	Plus	108716-111112
404049	3688074	Minus	75765-78155
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404877	1519284	Plus	1095-2107
404977	3738341	Minus	43081-43229
405932	7767812	Minus	123525-123713
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

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Table 77 provides Pkey, Seq ID No; Disease Indications; and Preferred Utility for sequences in Table 78. Seq ID No links the information in Table 77 to Table 78.

	Seq ID No: Pkey: Disease Indications: Preferred Utility:	Sequence ID No for sequences in table Unique Eos probe/identifier number Diseases designated for coverage as described in Table 1 Preference of utility, based partly upon predicted localization (Ab is antibody; sm is small molecule target; CTL is vaccine target)		
	Seq ID No	Pkey	Disease Indications	Preferred Utility
10	Seq ID 1 & 2	425023	angiogenesis	Ab, sm, CTL, imaging
	Seq ID 3 & 4	424503	pancreas, prostate, angiogenesis, bladder, lung	Ab, sm, imaging
	Seq ID 5 & 6	429423	angiogenesis	Ab, sm
	Seq ID 7 & 8	400289	angiogenesis, bladder, lung, cervical, ovarian, head & neck	Ab, sm, CTL, diagnostic
15	Seq ID 9 & 10	419172	angiogenesis, renal	Ab, sm, CTL, imaging
	Seq ID 11 & 12	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 13 & 14	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 15 & 16	407836	angiogenesis	CTL
	Seq ID 17 & 18	414577	angiogenesis	Ab, CTL, diagnostic
20	Seq ID 19 & 20	418738	angiogenesis, lung, ovarian, bladder & stomach, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 21 & 22	428368	angiogenesis, head & neck, stomach	Ab, sm, diagnostic
	Seq ID 23 & 24	415138	angiogenesis, pancreas, stomach, lung, uterine	Ab, CTL, diagnostic
	Seq ID 25 & 26	429276	angiogenesis, bladder, glioblastoma	Ab, sm, imaging
	Seq ID 27 & 28	418994	prostate, angiogenesis	Ab, CTL, imaging
	Seq ID 29 & 30	407975	angiogenesis, renal	Ab, CTL, diagnostic
25	Seq ID 31 & 32	429113	angiogenesis, bladder and stomach	sm, CTL
	Seq ID 33 & 34	418506	angiogenesis, ovarian, glioblastoma, uterine, lung, bladder, pancreas	Ab, sm, imaging
	Seq ID 35 & 36	423961	breast, colon, bladder, lung, fibrosis, pancreas, head and neck, ovarian	Ab, sm, diagnostic
	Seq ID 37 & 38	414812	breast, bladder, lung, Fibrosis, pancreas, colon, head and neck, cervical, stomach, renal, ovarian	Ab, CTL, diagnostic
30	Seq ID 39 & 40	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
	Seq ID 41 & 42	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
	Seq ID 43 & 44	424399	breast, uterine, head & neck	Ab, CTL, diagnostic
	Seq ID 45 & 46	422867	breast, ovarian, prostate, pancreas, lung, colon, uterine	Ab, CTL, diagnostic
	Seq ID 47 & 48	428227	breast, lung, bladder, ovarian, head & neck, fibrosis, colon, stomach, cervical	Ab, CTL, diagnostic
35	Seq ID 49 & 50	444381	breast, colon, bladder, lung, pancreas, head & neck, ovarian, stomach, uterine, renal, angiogenesis	Ab, CTL, diagnostic
	Seq ID 51 & 52	439569	breast, androgen withdrawal prostate, prostate, bladder	Ab, CTL, diagnostic
	Seq ID 53 & 54	411558	pancreas, prostate, stomach, breast, uterine, cervical, ovarian	Ab, sm, imaging
	Seq ID 55 & 56	400303	breast, ovarian, pros, stomach, uterine, bladder lung head & neck	Ab, sm, CTL, imaging
	Seq ID 57 & 58	411789	pancreas, lung, breast, stomach, head & neck, ovarian, uterine	Ab, CTL, diagnostic
40	Seq ID 59 & 60	428698	breast, colon, lung, pancreas, stomach, head & neck, ovarian	Ab, sm, imaging
	Seq ID 61 & 62	450098	breast, lung, stomach, uterine	CTL
	Seq ID 63 & 64	421552	breast, ovarian, pancreas, cervical, uterine, prostate, lung, stomach, head & neck	Ab, sm, CTL, diagnostic
	Seq ID 65 & 66	452747	breast, bladder, lung, head & neck, ovarian, stomach, uterine, pancreas	Ab, imaging
	Seq ID 67 & 68	415539	breast, prostate, ovarian, cervical, uterine	Ab, sm, CTL, imaging
45	Seq ID 69 & 70	416636	breast, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 71 & 72	416636	breast, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 73 & 74	409079	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 75 & 76	442082	breast, prostate, ovarian	Ab, imaging
	Seq ID 77 & 78	400297	breast, bladder, colon, prostate	Ab, sm, CTL, imaging
50	Seq ID 79 & 80	451398	breast, ovarian	CTL
	Seq ID 81 & 82	429220	breast, prostate, benign prostatic hyperplasia	Ab, CTL, imaging
	Seq ID 83 & 84	421524	breast	Ab, sm, CTL, imaging
	Seq ID 85 & 86	423242	breast, renal, ovarian, prostate, colon	Ab, CTL, imaging
	Seq ID 87 & 88	423242	breast, renal, ovarian, prostate, colon	CTL
55	Seq ID 89 & 90	423242	breast, renal, ovarian, prostate, colon	CTL
	Seq ID 91 & 92	452190	breast, stomach, pancreas	CTL
	Seq ID 93 & 94	452190	breast, stomach, pancreas	CTL
	Seq ID 95 & 96	325372	breast	CTL
	Seq ID 97 & 98	450375	breast, ovarian, head & neck, pancreas, lung, colon	Ab, sm, CTL, imaging
60	Seq ID 99 & 100	426215	breast, lung, renal, colon, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 101 & 102	425247	breast, ovarian, lung, colon, pancreas, head & neck, stomach, uterine, cervical, bladder	Ab, sm, CTL, diagnostic
	Seq ID 103 & 104	429353	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 105 & 106	429353	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 107 & 108	432201	breast, colon, lung chemo, ovarian, stomach, pancreas, uterine, cervical	Ab, sm, CTL, imaging
65	Seq ID 109 & 110	427585	breast, lung, head & neck, pancreas, stomach, colon, ovarian, cervical	CTL
	Seq ID 111 & 112	446163	breast, cervical, uterine	Ab, sm, imaging
	Seq ID 113 & 114	442117	breast, lung, bladder, pancreas, head & neck, stomach, ovarian, prostate	Ab, CTL, imaging
	Seq ID 115 & 116	428179	breast	sm, CTL
	Seq ID 117 & 118	431211	colon, bladder, lung, pancreas, head & neck	Ab, sm, imaging
70	Seq ID 119 & 120	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 121 & 122	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 123 & 124	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 125 & 126	115522	colon, lung, bladder, pancreas	CTL
	Seq ID 127 & 128	452679	prostate, colon, pancreas, Taxol prostate	Ab, CTL, imaging
75	Seq ID 129 & 130	446051	colon, breast	Ab, sm, CTL, imaging
	Seq ID 131 & 132	422048	colon, pancreas, prostate	diagnostic
	Seq ID 133 & 134	410418	colon, bladder, lung, ovarian, pancreas, head & neck	Ab, sm, CTL, imaging
	Seq ID 135 & 136	446342	uterine, colon, prostate	Ab, sm, CTL, imaging
	Seq ID 137 & 138	422260	colon, ovarian mucinous	Ab, sm, CTL, diagnostic
80	Seq ID 139 & 140	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 141 & 142	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 143 & 144	111929	colon, breast, fibrosis	Ab, sm, imaging
	Seq ID 145 & 146	111929	colon, breast, fibrosis	Ab, sm, imaging
	Seq ID 147 & 148	111929	colon, breast, fibrosis	Ab, sm, imaging

	Seq ID 149 & 150 104888	colon, stomach, uterine	Ab, imaging
	Seq ID 151 & 152 420159	bladder, stomach	Ab, sm, CTL, imaging
	Seq ID 153 & 154 422330	pancreas, colon, bladder	Ab, sm, CTL, imaging, diagnostic
5	Seq ID 155 & 156 452461	bladder, lung, head & neck, ovarian, glioblastoma, stomach, colon, cervical	CTL
	Seq ID 157 & 158 413324	bladder	Ab, sm, CTL, diagnostic
	Seq ID 159 & 160 412420	bladder, glioblastoma, lung, stomach	Ab, diagnostic
	Seq ID 161 & 162 416658	lung, ovarian, uterine, bladder	Ab, CTL, diagnostic
	Seq ID 163 & 164 407811	bladder, pancreas, stomach, uterine, lung	Ab, sm, diagnostic
10	Seq ID 165 402230	bladder	sm, CTL
	Seq ID 166 & 167 402230	bladder	sm, CTL
	Seq ID 168 & 169 432829	bladder	CTL
	Seq ID 170 & 171 425721	bladder	Ab, imaging
	Seq ID 172 & 173 420370	bladder	Ab, CTL, imaging
15	Seq ID 174 & 175 437852	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 176 & 177 402075	bladder, lung, head & neck, cervical	diagnostic
	Seq ID 178 & 179 421110	bladder, pancreas, stomach, ovarian, lung	Ab, sm, diagnostic
	Seq ID 180 & 181 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 182 & 183 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
20	Seq ID 184 & 185 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 186 & 187 408243	bladder, stomach, head & neck, cervical	Ab, diagnostic
	Seq ID 188 & 189 422282	bladder, lung, head & neck	CTL, diagnostic
	Seq ID 190 & 191 425852	bladder, lung, head & neck	Ab, sm, CTL, imaging
	Seq ID 192 & 193 439738	bladder, lung, cervical	Ab, sm, CTL, imaging
25	Seq ID 194 & 195 404875	bladder	sm, CTL
	Seq ID 196 & 197 425883	bladder, pancreas	Ab, CTL, imaging
	Seq ID 198 & 199 404977	bladder, ovarian	Ab, sm, CTL, diagnostic
	Seq ID 200 & 201 420876	pancreas, bladder	Ab, sm, CTL, imaging
	Seq ID 202 & 203 427747	bladder, lung, ovarian, stomach	sm, CTL
30	Seq ID 204 & 205 420281	lung, bladder, ovarian, pancreas	Ab, sm, imaging
	Seq ID 206 & 207 446673	bladder	sm, CTL
	Seq ID 208 437553	bladder	Ab, CTL, imaging
	Seq ID 209 & 210 437553	bladder	Ab, CTL, imaging
	Seq ID 211 & 212 437553	bladder	Ab, CTL, imaging
35	Seq ID 213 & 214 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 215 & 216 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 217 & 218 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 219 & 220 405932	bladder, lung, head & neck, cervical	sm
	Seq ID 221 & 222 405932	bladder, lung, head & neck, cervical	sm
40	Seq ID 223 & 224 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 225 & 226 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 227 & 228 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 229 & 230 444342	hepatitis C, lung, fibrosis, bladder	Ab, CTL, diagnostic
	Seq ID 231 & 232 421379	breast, pancreas, head & neck, lung, stomach, bladder, cervical, colon	Ab, CTL, diagnostic
45	Seq ID 233 & 234 417079	bladder, lung, head & neck, cervical	Ab, diagnostic
	Seq ID 235 & 236 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 237 & 238 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 239 & 240 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 241 & 242 447072	glioblastoma, pancreas	sm, CTL
50	Seq ID 243 & 244 419723	glioblastoma	Ab, CTL, diagnostic
	Seq ID 245 & 246 419723	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 247 & 248 430890	glioblastoma, lung, cervical, bladder	Ab, CTL, imaging, diagnostic
	Seq ID 249 & 250 456759	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 251 429466	glioblastoma, uterine	
55	Seq ID 252 429466	glioblastoma, uterine	
	Seq ID 253 & 254 419721	glioblastoma, lung	Ab, sm, CTL, imaging
	Seq ID 255 & 256 407034	glioblastoma	Ab, CTL, diagnostic
	Seq ID 257 & 258 413472	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 259 & 260 438380	glioblastoma	Ab, CTL, diagnostic, imaging
60	Seq ID 261 & 262 426271	glioblastoma	Ab, CTL, diagnostic
	Seq ID 263 & 264 419704	glioblastoma	sm, CTL
	Seq ID 265 & 266 444471	glioblastoma, lung, colon	Ab, sm, CTL, imaging
	Seq ID 267 & 268 409395	glioblastoma	Ab, CTL, diagnostic
	Seq ID 269 & 270 413063	glioblastoma, ovarian, bladder, lung	Ab, CTL, diagnostic
65	Seq ID 271 & 272 433800	glioblastoma, lung	Ab, CTL, imaging
	Seq ID 273 458435	glioblastoma	
	Seq ID 274 458435	glioblastoma	
	Seq ID 275 & 276 424343	glioblastoma, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 277 & 278 424998	glioblastoma	Ab, CTL, diagnostic
70	Seq ID 279 & 280 412709	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 281 & 282 435615	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 283 & 284 404049	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 285 & 286 418932	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 287 & 288 404029	glioblastoma	Ab, sm, CTL, imaging
75	Seq ID 289 & 290 436480	glioblastoma	sm, CTL
	Seq ID 291 & 292 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 293 & 294 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 295 & 296 436895	breast, renal, ovarian, glioblastoma	Ab, sm, imaging
	Seq ID 297 & 298 421471	renal	Ab, sm, CTL, imaging
80	Seq ID 299 & 300 428295	renal	Ab, sm, CTL, imaging
	Seq ID 301 & 302 423508	renal, colon	Ab, CTL, imaging
	Seq ID 303 & 304 450001	renal, lung	Ab, sm, CTL, imaging
	Seq ID 305 & 306 410407	renal, lung, colon, stomach, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 307 & 308 453496	renal, prostate	Ab, sm, CTL, imaging

	Seq ID 309 & 310 420737	renal	Ab,sm, CTL, imaging
	Seq ID 311 & 312 309931	lung	Ab,sm, CTL, imaging
	Seq ID 313 & 314 412719	lung, head & neck, bladder, glioblastoma, cervical	CTL
5	Seq ID 315 & 316 417034	lung, head & neck, a couple cervical	Ab, CTL, diagnostic
	Seq ID 317 & 318 430486	lung, bladder, head & neck, cervical	Ab,sm, imaging
	Seq ID 319 & 320 413753	lung, bladder, head & neck, pancreas, cervical, colon	CTL, diagnostic
	Seq ID 321 & 322 425650	lung, head & neck, cervical, bladder	Ab, imaging
	Seq ID 323 & 324 423673	bladder, lung, head & neck, ovarian, pancreas, colon, stomach, uterine, cervical	Ab, CTL, diagnostic
10	Seq ID 325 & 326 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 327 & 328 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 329 & 330 428610	lung	CTL, diagnostic
	Seq ID 331 & 332 406690	lung, head & neck, pancreas, stomach, bladder, colon, cervical	Ab, imaging
	Seq ID 333 & 334 431846	lung, bladder, head & neck, uterine, cervical, stomach, ovarian	Ab, imaging
15	Seq ID 335 & 336 422158	head & neck, bladder, lung, cervical, stomach	diagnostic
	Seq ID 337 & 338 431958	lung, bladder, cervical, head & neck, ovarian, colon, prostate, pancreas, breast	Ab, CTL, imaging
	Seq ID 339 & 340 437044	head & neck, cervical, lung, bladder, breast, prostate, ovarian, stomach	Ab, imaging
	Seq ID 341 & 342 428484	lung, glioblastoma, bladder, head & neck, colon, cervical	Ab, sm, imaging
	Seq ID 343 & 344 429211	lung, bladder, head & neck, cervical, stomach	Ab, imaging
20	Seq ID 345 & 346 417389	ovarian, lung, bladder, uterine, cervical, pancreas, stomach	Ab, diagnostic
	Seq ID 347 & 348 431009	lung, bladder, head & neck	Ab, sm, imaging
	Seq ID 349 & 350 417542	lung	CTL, diagnostic
	Seq ID 351 & 352 449230	lung, cervical, head & neck, bladder, ovarian, colon	Ab, imaging
	Seq ID 353 & 354 410555	lung	Ab, sm, imaging
25	Seq ID 355 & 356 410555	lung	Ab, sm, imaging
	Seq ID 357 & 358 424687	head & neck, pancreas, lung, uterine, cervical, colon, stomach	Ab, sm, imaging
	Seq ID 359 & 360 418462	lung, bladder	Ab, sm, diagnostic
	Seq ID 361 & 362 410274	lung, renal	Ab, imaging
	Seq ID 363 & 364 439606	lung, bladder, head & neck, cervical	diagnostic
30	Seq ID 365 & 366 404877	lung, bladder	Ab,sm, imaging
	Seq ID 367 & 368 444781	lung, bladder, head & neck, cervical	CTL
	Seq ID 369 & 370 109424	bladder, lung	Ab, imaging
	Seq ID 371 & 372 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab, sm, CTL, imaging
	Seq ID 373 & 374 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
35	Seq ID 375 & 376 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 377 & 378 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 379 & 380 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 381 & 382 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 383 & 384 421817	lung, cervical, head & neck & bladder	Ab,sm, CTL, imaging
40	Seq ID 385 & 386 418678	lung, bladder, stomach, ovarian, pancreas & cervical	Ab,sm, CTL, imaging
	Seq ID 387 & 388 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL
	Seq ID 389 & 390 409420	lung, head & neck, pancreas, stomach, cervical, bladder	CTL
	Seq ID 391 & 392 332180	lung	CTL, diagnostic
	Seq ID 393 & 394 408790	lung	Ab, sm, imaging
45	Seq ID 395 & 396 408790	lung	Ab,sm, CTL, imaging
	Seq ID 397 & 398 439223	lung, head & neck, cervical, bladder & colon	Ab,sm, CTL, imaging
	Seq ID 399 & 400 409757	pancreas, stomach, lung, bladder, stomach	Ab, CTL, imaging
	Seq ID 401 & 402 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 403 & 404 428969	lung, cervical	Ab, CTL, diagnostic
50	Seq ID 405 & 406 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 407 & 408 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 409 & 410 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 411 & 412 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 413 & 414 414774	lung, bladder, head & neck, pancreas, stomach, ovarian	Ab, sm, diagnostic
55	Seq ID 415 & 416 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 417 & 418 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 419 & 420 428486	pancreas	Ab, CTL, diagnostic
	Seq ID 421 & 422 457489	pancreas, prostate, lung	Ab, CTL, diagnostic
	Seq ID 423 & 424 432874	pancreas, stomach	Ab, CTL, diagnostic
60	Seq ID 425 & 426 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 427 & 428 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 429 & 430 404682	pancreas	Ab, CTL, diagnostic
	Seq ID 431 & 432 429547	pancreas, head & neck, lung, ovarian	Ab,sm, CTL, imaging
	Seq ID 433 & 434 425921	stomach, pancreas	Ab,sm, CTL, imaging
65	Seq ID 435 & 436 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 437 & 438 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 439 & 440 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 441 & 442 432596	pancreas, breast	CTL
	Seq ID 443 & 444 444006	pancreas, colon, lung, ovarian & cervical	Ab, CTL, imaging
70	Seq ID 445 & 446 423685	pancreas, uterine, colon	CTL
	Seq ID 447 & 448 428392	pancreas	Ab, CTL, diagnostic
	Seq ID 449 & 450 429597	pancreas, colon, stomach, lung	Ab,sm, CTL, imaging
	Seq ID 451 & 452 448030	pancreas, renal and stomach,	Ab,sm, imaging
	Seq ID 453 & 454 422109	pancreas, lung, colon	Ab, CTL, diagnostic
75	Seq ID 455 & 456 419235	pancreas, fibrosis, head & neck & lung	Ab, CTL, imaging
	Seq ID 457 & 458 449048	pancreas, ovarian, uterine, glioblastoma, head & neck & lung	Ab, CTL, imaging
	Seq ID 459 & 460 427333	pancreas, colon	Ab, sm, imaging
	Seq ID 461 & 462 417931	ovarian, pancreas, stomach, colon, uterine, prostate	Ab, diagnostic
	Seq ID 463 & 464 419216	pancreas, lung, stomach, cervical, prostate, head & neck	Ab, CTL, diagnostic
80	Seq ID 465 & 466 431629	pancreas, uterine, cervical, stomach	Ab, CTL, diagnostic
	Seq ID 467 & 468 413554	pancreas, glioblastoma	Ab, CTL, diagnostic
	Seq ID 469 & 470 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 471 & 472 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 473 & 474 426322	pancreas, bladder, stomach	Ab, diagnostic

	Seq ID 475 & 476 429010	pancreas	sm, CTL
	Seq ID 477 & 478 431462	pancreas, lung, glioblastoma	Ab, diagnostic
	Seq ID 479 & 480 448243	ovarian, uterine, lung, stomach, head & neck, glioblastoma, pancreas	Ab, sm, imaging
5	Seq ID 481 & 482 426427	ovarian, lung, head & neck, cervical, colon, uterine, stomach	sm, CTL
	Seq ID 483 & 484 428187	ovarian, uterine, colon, stomach	Ab, sm, CTL, imaging
	Seq ID 485 & 486 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 487 & 488 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 489 & 490 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
10	Seq ID 491 & 492 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 493 & 494 445537	ovarian, bladder, uterine, breast, lung, head & neck, renal, fibrosis, pancreas, cervical	Ab, CTL, diagnostic
	Seq ID 495 & 496 422278	ovarian, head & neck, bladder, cervical, lung	Ab, sm, imaging
	Seq ID 497 & 498 424620	ovarian	Ab, CTL, diagnostic
	Seq ID 499 & 500 406400	ovarian, uterine	Ab, CTL, diagnostic
15	Seq ID 501 & 502 431130	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 503 & 504 420440	ovarian, uterine, cervical	Ab, CTL, diagnostic
	Seq ID 505 & 506 428450	ovarian, cervical, pancreas, lung	sm
	Seq ID 507 & 508 446619	ovarian, fibrosis, pancreas, head & neck, lung, colon	Ab, diagnostic
	Seq ID 509 & 510 436982	ovarian, fibrosis	Ab, CTL, diagnostic
20	Seq ID 511 & 512 453392	ovarian, lung, glioblastoma	CTL
	Seq ID 513 431989	ovarian	
	Seq ID 514 439820	ovarian, uterine, cervical, breast, prostate	
	Seq ID 515 & 516 409178	ovarian, breast	Ab, CTL, diagnostic
	Seq ID 517 & 518 426514	ovarian, colon, bladder, lung, cervical	Ab, CTL, diagnostic
25	Seq ID 519 & 520 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 521 & 522 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 523 & 524 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 525 & 526 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 527 & 528 452097	ovarian	Ab, sm, diagnostic
30	Seq ID 529 & 530 416530	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 531 & 532 431515	ovarian, prostate, lung	Ab, sm, CTL, imaging
	Seq ID 533 & 534 419452	ovarian, prostate, lung, breast, uterine	Ab, sm, CTL, imaging
	Seq ID 535 & 536 412078	ovarian	CTL
	Seq ID 537 & 538 412078	ovarian	CTL
35	Seq ID 539 & 540 411773	ovarian	Ab, sm, CTL, diagnostic
	Seq ID 541 & 542 407792	ovarian, uterine, cervical, pancreas	Ab, CTL, diagnostic
	Seq ID 543 & 544 431616	prostate, pancreas, colon	Ab, sm, CTL, imaging
	Seq ID 545 & 546 452792	prostate, uterine, breast	Ab, CTL, imaging
	Seq ID 547 & 548 400294	prostate, taxol prostate	Ab, sm, CTL, imaging
40	Seq ID 549 & 550 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 551 & 552 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 553 & 554 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 555 & 556 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 557 & 558 400290	prostate, colon	Ab, sm, CTL, imaging
45	Seq ID 559 & 560 410001	ovarian, prostate, uterine, cervical, lung	Ab, CTL, diagnostic
	Seq ID 561 & 562 418396	prostate	Ab, sm, CTL, imaging
	Seq ID 563 & 564 451027	prostate, uterine, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 565 & 566 446057	prostate	Ab, sm, CTL, imaging
	Seq ID 567 & 568 433466	prostate	Ab, CTL, diagnostic
50	Seq ID 569 & 570 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 571 & 572 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 573 & 574 414569	prostate	Ab, sm, CTL, imaging
	Seq ID 575 & 576 413435	prostate, glioblastoma, pancreas	Ab, sm, diagnostic
	Seq ID 577 & 578 426501	prostate, breast, glioblastoma, lung	Ab, CTL, imaging
55	Seq ID 579 & 580 448999	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 581 & 582 408369	prostate, lung, fibrosis, uterine, glioblastoma, cervical, ovarian	Ab, sm, CTL, imaging
	Seq ID 583 & 584 412628	prostate	Ab, CTL, diagnostic
	Seq ID 585 & 586 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
	Seq ID 587 & 588 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
60	Seq ID 589 & 590 408430	prostate	Ab, sm, CTL, imaging
	Seq ID 591 & 592 445413	prostate, colon, uterine, ovarian, lung, pancreas	diagnostic
	Seq ID 593 & 594 451982	prostate, bladder	CTL
	Seq ID 595 & 596 427958	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 597 & 598 421887	prostate	Ab, CTL, imaging
65	Seq ID 599 & 600 425071	prostate, colon, stomach, uterine, cervical, head & neck, pancreas	Ab, diagnostic
	Seq ID 601 & 602 432101	prostate, pancreas	Ab, sm, imaging
	Seq ID 603 & 604 407786	prostate, colon, uterine, stomach, inflammatory bowel disease, ovarian	Ab, sm, imaging
	Seq ID 605 & 606 416836	Prostate, Ewing, glioblastoma	Ab, CTL, diagnostic
	Seq ID 607 & 608 416539	ZD1839 resistant cancers, head & neck	Ab, sm, CTL, imaging
70	Seq ID 609 & 610 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 611 & 612 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 613 & 614 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 615 & 616 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 617 & 618 422424	bladder, pancreas, prostate, angiogenesis, colon, stomach, lung	Ab, CTL, diagnostic
75	Seq ID 619 & 620 428970	stomach, pancreas, colon	Ab, sm, imaging
	Seq ID 621 & 622 428330	uterine, ovarian, fibrosis, prostate, pancreas, lung, bladder, head & neck	Ab, sm, CTL, diagnostic
	Seq ID 623 & 624 439018	uterine, stomach, prostate	Ab, sm, CTL, imaging
	Seq ID 625 & 626 420610	uterine, ovarian endometrioid, lung	CTL
	Seq ID 627 & 628 425723	ovarian endometrioid, uterine, colon	Ab, CTL, diagnostic
80	Seq ID 629 & 630 456662	uterine, ovarian	CTL
	Seq ID 631 & 632 418281	uterine, ovarian	Ab, CTL, diagnostic
	Seq ID 633 & 634 429903	lung	sm

Table 78

Seq ID NO: 1 DNA sequence

Nucleic Acid Accession #: NM_001400

Coding sequence: 251..1399

	1	11	21	31	41	51	
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10	AACGCAACTT	CGCCCTGCTT	GAGCGAGGCT	GCGGTTTCCG	AGGCCCTCTC	CAGCCAAGGA	120
	AAAGCTACAC	AAAAAGCCTG	GATCACTCAT	CGAACCACCC	CTGAAGCCAG	TGAAGGCTCT	180
	CTCGCCTGSC	CCTCTAGCGT	TCGTCTGGAG	TAGCGCCACC	COGGCTTCCT	GGGGACACAG	240
	GGTTGGACCC	ATGGGGCCCA	CCAGCGTCCC	GCTGGTCAAG	GCCCAACGCA	GCTCGGTCTC	300
15	TGACTACGTC	AACTATGATA	TCATGCTCCG	GCATTACAAC	TACACGGGAA	AGCTGAATAT	360
	CAGCGCGGAC	AAGGAGAAC	GCATTAAACT	GACCTCGGTG	GTGTTTCAATC	TCATCTGCTG	420
	CTTTATATAT	CTGGAGAAC	TCTTTGTCTT	GCTGAACATT	TGGAATAACA	AGAAATTCCA	480
	CCGACCCATG	TACTATTTTA	TTGGCAATCT	GGCCCTCTCA	GACCTGTTGG	CAGGAGTAGC	540
	CTACACAGCT	AACCTGCTCT	TGCTGGGGC	CACCACTTAC	AAGCTCACTC	CCGCCAGTGT	600
20	GTTCCTGGCG	GAAGGGAGTA	TGTTTGTCGC	CCTGTGAGCC	TCGTGTTTCA	GTCTCTCGC	660
	CATGCCATT	GAGCGCTATA	TCACAATGCT	GAAAAATGAAA	CTCCACACCG	GGAGCAATAA	720
	CTTCGCGCTC	TTCTGCTTAA	TCAGCGCCTG	CTGGGTCTATC	TCCTCATCC	TGGGTGGCCT	780
	GCCTATCATG	GGCTGGAAC	GCATCAGTGC	GCTGTCCAGC	TGCTCCACCG	TGCTGCCGCT	840
	CTACACAGAG	CACATATATCC	TCTTCTGCAC	CACGGTCTTC	ACTCTGCTTC	TGCTCTCCAT	900
25	GTCTATTCTG	TACTGAGAA	TCTACTCCTT	GGTCAGGACT	CGGAGCCGCC	GCTGACGTTT	960
	CCGCAAGAAC	ATTTCCAAG	CCAGCCGAG	CTCTGAGAA	TGCTGGGCG	TGCTCAAGAC	1020
	CGTAATATAT	GTCTGAGCG	TCTTCATCGC	CTGCTGGGCA	CGCTCTTCA	TCCTGCTCCT	1080
	GCTGGATGTG	GGCTGCAAGG	TGAAGACCTG	TGACATCCTC	TTGAGAGCGG	AGTACTTCTT	1140
	GGTGTAGCT	TGCTCAACT	CCGGCACCA	CCCATCAATT	TACACTCTGA	CCAACAAGGA	1200
	GATGCGTGGG	GCCTTCATCC	GGATCATGTC	CTGCTGCAAG	TGCCGAGCGG	GAGACTCTGC	1260
30	TGGCAATTC	AAGCGACCCA	TCATGCGCG	CATGGAATTC	AGCCGACGCA	AATCGGACAA	1320
	TTCTCTCCAC	CCCCAGAAAG	ACGAAGGGGA	CAACCCAGAG	ACCATTATGT	CTTCTGGAAA	1380
	CGTCAACTCT	TCTTCTAGTA	ACTGGAAGCT	GTCCACCCAC	CGGAAGCGCT	CTTTACTTGG	1440
	TCGCTGGCCA	CCCGAGTGT	TGGAAAAAAA	TCTCTGGGCT	TCGACTGCTG	CCAGGGAGGA	1500
35	GCTGCTGCAA	GCCAGAGGGA	GGAAAGGGGA	GAATACGAAC	AGCCTGGTGG	TGTGGGTTGT	1560
	TGGTGGGTAG	AGTTAGTTCC	TGTGAACAAT	GCATGCGGAA	GGGTGGAGAT	CAGGTCCCGG	1620
	CCTGGAAATAT	ATATTCTAAC	CCCTGGAGC	TTTGATTTTG	CACCTGAGCA	AAGGTCTAGC	1680
	ATTGTCAAGC	TCCTAAGAGG	TTCATTGGCC	CCCTCCTCAA	AGACTAATGT	CCCATGTGTA	1740
40	AAGCGTCTCT	TTGTCTGGAG	CITTGAGGAG	ATGTTTTCTT	TCATTTAGT	TTCAAAACCA	1800
	AGTGAGTGTG	TGCATCTCTG	CTTCTTTAGG	GATGCCCTGT	ACATCCACCA	CCCCACCTTC	1860
	CCCTCCCTTC	ATACCCCTCC	TCAACGTTCT	TTTACTTTAT	ACTTTAACTA	CCTGAGAGTT	1920
	ATCAGAGCTG	GGGTGTGGGA	ATGATCGATC	ATCTATAGCA	AATAGGCTAT	GTGAGTACG	1980
	TAGGCTGTGG	GAGATGGAAG	ATGGTTTGGG	GGGTGAAAC	AATGTCTTTC	GCTGAGGCCA	2040
45	AAGTTTCCAT	GTAAAGCGGA	TCCGTTTTTT	GGAATTTGGT	TGAAGTCACT	TTGATTCTCT	2100
	TAAAAAACAT	CTTTTCAATG	AAATGTGTTA	CCATTTTATA	TCCATTGAAG	CCGAAATCTG	2160
	CATAAGGAAG	CCCACTTTAT	CTAATGATA	TGAGCCAGGA	TCCTTGTTGT	CCTAGGAGAA	2220
	ACAGACAAGC	AAAAACAAAG	GAAAAACGAA	TGGATTAATC	TTTGCAAAAC	AAGGGAGATT	2280
	TCTTAGCAAA	TGAGTCTAAC	AAATATGACA	TCCGCTCTTC	CCACTTTTGT	TGATGTTTAT	2340
50	TTCAAGATCT	TGTGTGATTC	ATTTCAGCA	ACAACATGTT	GTATTTTGT	GTGTTAAAG	2400
	TACTTTTCTT	GATTTTGTAA	TGTATTTGTT	TCAGGAAGAA	GTCAATTTAT	GGATTTTCTT	2460
	AACCGGTGTT	AACTTTTCTA	GAATCCACCC	TCTTGTGCCC	TTAAGCATTA	CTTTAACTGG	2520
	TAGGGAGCCG	CAGAACTTTT	AAGTCCAGCT	ATTCAATAGA	TAGTAATTGA	AGATATGTAT	2580
	AAATATTACA	AAGAATAAAA	ATATATTACT	GTCTCTTTAG	TATGTTTTC	AGTGCAATTA	2640
55	AACCGAGAGA	TGCTCTGTTT	TTTTAAAAAG	AATAGTATTT	AATAGCTTTC	TGACTTTTGT	2700
	GGATCATTTT	GCACATAGCT	TTATCAACTT	TTAAACATTA	ATAAAGCTAT	TTTTTTAAAG	

Seq ID NO: 2 Protein sequence

Protein Accession #: NP_001391

	1	11	21	31	41	51	
60	MGPTSVPLVK	AHRSSVSDYV	NYDIIVRHYN	YTGKLNISAD	KENSIKLTSV	VFILICCFII	60
	LENIFVLLTI	WMTKKFHRPM	YFIGNLALS	DLLAGVAYTA	NLLLSGATTY	KLTPAQWFLR	120
	BGSMFVALSA	SVFSLLAIAI	ERYITMLKMK	LHNGSNPNFL	FLNISACWVI	SLILGGLPIM	180
65	GWNCISALSS	CSTVLPYHK	HYILPCTTVP	TLLLLSIVIL	YCRIYSLVRT	RSRLTFRKN	240
	ISKASRSSEK	SLALLKTVII	VLSVFIACWA	PLFILLLLDV	GCKVKTCDIL	FRAEYFLVLA	300
	VLSNGTNPPI	YTLNKNEMRR	AFIRMSCK	CPSGDSAGKF	KRPILAGMEF	SRSKSDNSSH	360
	PQKDEGDNPE	TIMSSGNVNS	SS				

Seq ID NO: 3 DNA sequence

Nucleic Acid Accession #: NM_002205.1

Coding sequence: 1..3149

	1	11	21	31	41	51	
75	ATGGGGAGCC	GGACGCCAGA	GTCCCTCTC	CACGCGGTGC	AGCTGCGCTG	GGGCCCCCGG	60
	CGCCGACCCC	CGCTSSGTCC	GCTGCTGTTG	CTGCTSSGTG	CGCCGCCACC	CAGGGTCGGG	120
	GGCTTCAACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
	GGATTCTCAG	TGGAGTTTTA	COGGCCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
80	CCCAAGGCTA	ATACCAGCCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCTT	300
	TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTTG	ACAGCAAAGG	CTCTGGGCTC	360
	CTGGAGTCTT	CACTGTCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCTTGCAG	420
	TGGTTGCGGG	CAACAGTTCG	AGCCCATGGC	TCCTCCATCT	TGGCATGGCC	TCCATGTAC	480
	AGCTGGGCGA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
	GATAACTTCA	CCGGAATTCT	GGAGTATGCA	CCCTGCGGCT	CAGATTTTCA	CTGGGCGAGC	600

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GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCGGAGTTCA CCAAGACTGG CCGTGTGGTT 660
TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG 720
ATTGCAGAAAT CTTATTACCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780
CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGSC TGTGTGTGAA 840
TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAAGGGAA CCTCACTTAC 900
GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTGATCCCT TCTACAACCT CTCAGGGGAA 960
CAGATGGCCT CCTACTTTGG CTATGCAGTG GCGGCCACAG ACGTCAATGG GGACGGGCTG 1020
GATGACTTGC TGGTGGGGGC ACCCTGTGCT ATGGATCGGA CCCCTGACGG GCGGCTCTAG 1080
GAGGTGGGCA GGGTCTACGT CTAOCTGCAG CACCCAGCCG GCATAGAGCC CAGGCCACCC 1140
CTTACCCTCA CTGGCCATGA TGAGTTTGGC CGATTTGGCA GCTCCTTGAC CCCCCTGGGG 1200
GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCTTTTGG TGGGGAGACC 1260
CAGCAGGGAG TAGTGTTTGT ATTTCTGGG GGGCCAGGAG GGCTGGGCTC TAAGCCTTCC 1320
CAGGTTCTGC AGCCCTGTG GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380
CGAGGAGGCC GAGACCTGSA TGGCAATGGA TATCTGATC TGATTGTGGG GTCTTTTGGT 1440
GTGGACAAGG CTGTGTGTATA CAGGGGCGCG CCCATCGTGT CGCTAGTGC CTCCCTCACC 1500
ATCTTCCCGG CCATGTTCAA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTCTGT 1560
GCTGCGATCA GCTTAGCTT CTGCCTCAAT GCTTCTGGAA AACACGTTGC TGACTCCATT 1620
GGTTTCACAG TGGAACTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA 1680
CTGTTCTCTG CCTCCAGGCA GGCAACCCCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
CGAGAGGATT GCAGAGGATT GAAGATCTAC CTCAGGAACG AGTCAGAATT TCAGACAAA 1800
CTCTCGCCGA TTCAATGCG TCTCAACTTC TCTTGGAGCC CCCAAGCCCC AGTGGACAGC 1860
CAGGCCCTCA GGCAGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920
ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCTGT ACCTGCAGCT GGAAGTGT 1980
GGGAGAGAGA ACCATGTGTA CTTGGGTGAC AAGAATGCC TGAACCTCAC TTTCCATGCC 2040
CAGAATGTGG GTGAGGGTGG CGCTATGAG GCTGAGCTTC GGGTCACCG CCCTCCAGAG 2100
GCTGAGTACT CAGGACTCGT CAGACACCCA GGAACCTTCT CCAGCCTGAG CTGTGACTAC 2160
TTTGCCGTGA ACCAGAGCCG CTGCTGGTGT TGTGACCTGG GCAACCCAT CAAGGAGGGA 2220
GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCGGGGACAC TAAGAAARCC 2280
ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAG CGACGTGGTT 2340
TCTTTCCGCG TCTCGGTGGA GGCTCAGGCC CAGGTCAACC TGAACGGTGT CTCCAAGCCT 2400
GAGGCAGTGC TATTTCCAGT AAGCGACTGG CATCCCCGAG ACCAGCCTCA GAAGGAGGAG 2460
GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGSCCC CAGCTCCATT 2520
AGCCAGGGTG TGCTGGAATC CAGCTGTCCC CAGGCTCTGG AAGGTGAGCA GCTCCTATAT 2580
GTGACACAGG TTAAGGGATC CAATGTCACC ACCAATCACC CCATTAAACC AAAGGGCCTG 2640
GAGTTGGATC CTTTCCGTTT CCTGCAACC CAGCAAAAAC GGGAAAGCTCC AAGCCGAGC 2700
TCTGCTTCTC CGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGT 2760
TGTGAGCTCG GGGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAGTTGCA TTTCCGAGTC 2820
TGGGCCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTTA GCCTGCACTG TGAGGCTGTG 2880
TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCTCGGCG AGCTGCCCCA AAAAGAGCGT 2940
CAGGTGGCCA CTTTCTTGCA ATGGACCAAG GCAGAAGGCA GCTATGGCGT CCCACTGTGG 3000
ATCATCATCC TAGCCATCCT GTTTGGCCTC CTGCTCCTAG GTCTACTCAT CTACATCCTC 3060
TACAAGCTTG GATTCTTCAA ACCTCTCCCT CCATATGGCA CCGCATGGA AAAAGCTCAG 3120
CTCAAGCCTC CAGCCACCTC TGATGCTGTA

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Seq ID NO: 4 Protein sequence
Protein Accession #: NP_002196.1

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GFSVFYRFG TDGVSVLVGA PKANTSQPGV LQGGAVYLCF WGAAPTQCTP IEFDSKGSRL 120
LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SMRTEKEPLS DPGVGTCLST 180
DNFTRILEYA PCRSDFSMAA GQGYCQGGFS AEFTKTGRVV LGSPGSYFWQ GQILSATQEQ 240
IAESYYPEYL INLVQQQLQT RQASSIYDDS YLGYSVAVGE FSGDDTDFV AGVPKGNLTY 300
GYVTILNGSD IRLSYNFSGE QMASYFYGAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ 360
EVRGVVYVLG HPAGIEPTPT LTLTGHEDEF RFGSSLTPLG DLDQDGYNDV AIGAPFQGET 420
QQGVVVFVFG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRLDNGN YFDLIVGSFG 480
VDKAVVYRGR FIVSASASLT IFFAMFNPEE RSCSLEGNFV ACINLSFCLN ASGKHVADSI 540
GPTVELQLDW QKQKGGVRRR LPLASRQATL TQTLLIQNGA REDCREMKIY LRNESEFRDX 600
LSPHIALNPF SLDPQAPVDS HGLRPLALHY SKSRIEDKQ ILLDCGENDI CVPDLQLEVP 660
GEQNHVYLDG KNALNLTFHA QNVGEGGAYE AELRVTPAPE AEYSGLVRHP GNFFSLSCDY 720
FAVNSRLLV CDLGNPMKAG ASLNGGLRFT VPHLRDTKKT IQDFQILSK NLNNSQSDVV 780
SFRLSVEAQA QVTINGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHVY ELINQGPSSI 840
SQGVLELSCP QALBQQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGSLSH QQKREAPSR 900
SASSGPGILK CPEAECFRLR CELGPLHQOE QSLSQLHFRV WAKTFLQREH QPFSLQCEAV 960
YKALKMPYRI LPRQLPKER QVATAVQWTK ABGSGYGVPLW IILAILFLGL LLLGLLIYIL 1020
YKLGPFRSL PYGTAMEKAQ LKPPATSDA

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Seq ID NO: 5 DNA sequence
Nucleic Acid Accession #: NM_002211.1
Coding sequence: 1..2397

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GCAGGGCCAA ATTGTGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCTACT 180
TCTGCACGAT GTGATGATTT AGAAGCCTTA AAAAAGAAGG GTTGCCCTCC AGATGACATA 240
GAAATCCCA GAGGCTCCAA AGATATAAAG AAAAATAAAA ATGTAAACCA CCGTAGCAAA 300
GGAACAGCAG AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCA CAAGTTGGTT 360
TTGCGATTAA GATCAGGGGA GCCACAGACA TTATACATAA AATTCAAGAG AGCTGAAGAC 420
TATCCCATTT ACCTCTACTA CCTTATGGAC CTGTCTTACT CAATGAAAGA CAGATTGGAG 480
AATGTAAAAA GGCTTGGGAC AGATCTGATG AATGAAATGA GGAGGATTAC TTGGAGCTTC 540

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AGAATTGGAT TTGGCTCATT TGTGGAAAAG ACTGTGATGC CTTACATTAG CACAACACCA 600
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AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTTGTGG AAAACAGCGC 720
ATATCTGGAA ATTTGGATTG TCCAGAAGGT GGTTCGATG CCATCATGCA AGTTGCAGTT 780
TGTGGATCAC TGATTGGCTG GAGGAATGTT ACACGGCTGC TGGTGTTC CACAGATGCC 840
GGGTTTCACT TTGCTGGAGA TGGGAAACTT GGTGGCATTG TTTTACCAA TGATGGACAA 900
TGTCACTGG AAAATAATAT GTACACAATG AGCATTATT ATGATTATCC TTCTATTGCT 960
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TTTCAGCCTG TTTACAAGGA GCTGAAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080
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TGCAAGAACG GGGTGAATGG AACAGGGGAA AATGGAAGAA AATGTTCCAA TATTCCATT 1260
GGAGATGAGG TTCATTGTA AATTAGCATA ACTTCAAATA AGTGTCCAA AAAGGATTCT 1320
GACAGCTTTA AAATTAGGCC TCTGGGCTTT ACGGAGGAAG TAGAGGTTAT TCTTCAGTAC 1380
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GATAGATCCA ATGGCTTAAT TTGTGGAGGA AATGGTGTG GCAAGTGTG TGTGTGTGAG 1740
TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTCTT TGGATACTAG TACTTGTGAA 1800
GCCAGCAACG GACAGATGCG CAATGGCCGG GGCATCTGCG AGTGTGGTGT CTGTAAGTGT 1860
ACAGATCCGA AGTTTCAAGG GCAAACTGTG GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920
GCTGAGCATA AAGAATGTGT TCAGTGCAGA GCCTTCAATA AAGGAGAAA GAAAGACCA 1980
TGCACACAGG AATGTTCCTA TTTTAACATT ACCAAGGTAG AAAGTCGGGA CAAATTACCC 2040
CAGCCGGTCC AACCTGATCC TGTGTCCCAT TGTAAAGGAGA AGGATGTGGA CGACTGTGG 2100
TTCTATTATA CGTATTCAAT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAAT 2160
CCAGAGTGTG CCACTGGTCC AGACATCATT CCAATTGTAG CTGGTGTGGT TGCTGGAATT 2220
GTTCTTATTG GCCTTGCATT ACTGCTGATA TGAAGCTTT TAATGATAAT TCATGACAGA 2280
AGGGAGTTTG CTAAATTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAATAA 2340
CCTATTATTA AGAGTGCCGT AACAACTGTG GTCAATCCGA AGTATGAGG AAAATGA

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Seq ID NO: 6 Protein sequence
Protein Accession #: NP_002202.1

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SARCDLLEAL KKKGCPDDI ENPRGSKDIK KNNVNTNRSK GTAELKLPED ITQIQPQQLV 120
LRLRSGEPQT FTLKFKRAED YPIDLYLMD LSYSMKDDLE NVKSLGTDLM NEMRRITSDF 180
RIGFGSFEVK TVMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKG E VFNELVGQR 240
ISGNLDSPEG GGDALMQVAV CGSLIGWRNV TRLLVFSFDA GFHFAGDGKL GGVILPNDGQ 300
CHLENNMYTM SHYDYPSIA HLQKLSENN IQTIFAVTEE PQPVYKELN LIPKSAVGL 360
SANSNNVQL IIDAYNSLSS EVILENGKLS EGVITISYKSY CKNGVNGTGE NGRKCSNISI 420
GDEVQFEISI TSNKCPKDS DSPKIRPLGF TEEVEVILQY ICECECQSBG IPSPFKCHBS 480
NGTFECGACR CNEGRVGRHC ECSTDEVNSE DMDAYCRKEN SSEICSNNGE CVCQCVCVRK 540
RDNTHIYSG KPCECNFNC DRNGLICGG MGVCCKRVE CNPNYTGSA DCSLDSTCE 600
ASNGIQNGR GICEGVCCK TDPKFQGTQ EMCQTCGLVC AEHKECVQCR AFNKGKKDT 660
CTQECSEYFNI TKVESRDKLP QVQPDVPSH CKEKDVDDCN FYPTYSVNGN NEVMVHVVEN 720
PECPTGPDI PIVAGVVAGI VLIGLALLLI WKLMIIDHR REFAPKFEKE MNAKWDGTGEN 780
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Seq ID NO: 7 DNA sequence
Nucleic Acid Accession #: NM_002425
Coding sequence: 26..1453

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TGCCCAAGCA TACCTAGAAA AGTACTACAA CCTOGAAAAG GATGTGAAAC AGTTTGAAG 180
AAAGACAGT AATCTCATG TTAATAAAT CCAAGGAATG CAGAAGTTC TTGGGTTGGA 240
GGTGACAGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCTGACGTT GTTCACTTCA GCTCCTTCC TGGCATGCG AGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCGTCAT 420
TGAGAAAGCT CTGAAAGTCT GGAAGAGGT GACTCCACT ACATTCPCA GGCTGTATGA 480
AGGAGAGCT GATATAATGA TCTCTTCCG AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
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TTGATGTGAC CCACTCTACA ACTCAITCAC AGAGCTCGCC CAGTTCGCCC TTTGCAAGA 780
TGATGTGAAT GGCATTCACT CTCTCTACGG ACCTCCCCCT GCCTCTACTG AGGAACCCCT 840
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ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCCTGCATG TTCTGTGACT 1560

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GAAGAAGATG AGCCTTGCAG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTCCTC 1620
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 CTT

5

Seq ID NO: 8 Protein sequence
 Protein Accession #: NP_002416

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 KIQGMQKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTIRIVNYT 120
 PDLPRDAVDS AIEKALKVWE EVTPLTFSRL YEGEADIMIS FAVKEHGFY SFDGPGHSLA 180
 HAYPPGPGLY GDHFPDDDEK WTEDASGTNL FLVAHELGH SLGLFHSANT EALMYPLYNS 240
 15 FTELAQFRLS QDDVNGIQSL YGPPPPASTEE PLVPTKSVPS GSEMPAKCOP ALSFDAISTL 300
 RGEYLPFKDR YFWRSSHWNP EPEPHLISAF WPSLPSYLD AYEVSNRDVT FIFKGNEFWA 360
 IRGNEVQAGY PRGIHTLGFPP PTIRKIDAAV SDKEKKKTYF PAADKYWRFD ENSQSMEOGF 420
 PRLIADDFPG VEPKVDVAVLQ AFGFFYFPPSG SSQFEEDPNA RMVTHILKSN SWLHC

20

Seq ID NO: 9 DNA sequence
 Nucleic Acid Accession #: XM_058189.2
 Coding sequence: 169..774

25 1 11 21 31 41 51
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 GAAGACCAGC TCAGCTCTTC AGTTGTGTGAT CATGTCTAT TGTCTCCAA ACAGTAAACC 60
 AGTATTTCAC ACTGAGATTG TCGGCTGCGG GTATATTCCA ATCCCGCTG TCCTCATGAA 120
 TATGAAGTGA AGGGCTCTGA CCCTGGAAGT GGTCTAAGC AGGGCAAAAT GGGGTCTCGG 180
 AAGTGTGGAG GCTGCTCAAG TTGTTTGTCTG ATTCCGCTTG CACTTTGGAG TATAATCGTG 240
 30 AACATATTAT TGTATTTCOC GAATGGGCAA ACTTCCTATG CATCCAGCAA TAAACTCACC 300
 AACTACGTGT GGTATTTTGA AGGAATCTGT TTCTCAGGCA TCATGATGCT TATAGTAACA 360
 ACAGTTCTTC TGGTACTGGA GAATAATAAC AACTATAAAT GTTGCCAGAG TGAAACTGCG 420
 AGCAAAAAAT ATGTGACACT GCTGTCAATT ATCTTTTCTT CCCTCGGAAT TGCTTTTCTT 480
 GGATACGTCC TGGTCACTTC TGCTTGGGTG CTTGTCCAAG GGCCATATTG CCGCACCTCT 540
 35 GATGGCTGGG AGTATGCTTT TGAAGGCACT GCTGGACGTT TCCTTACAGA TTCTAGCATA 600
 TGGATTCACT GCCTGGAACC TGCAATGTTT GTGGAGTGA ACATCATTTT ATTTTCCATT 660
 CTCATAACCC TCAGTGGGCT TCAAGTGATC ATCTGCCTCA TCAGAGTAGT CATGCAACTA 720
 TCCAAGATAC TGTGTGGGAG CTATTCACTG ATCTTCCAGC CTGGAATCAT TTGAATAAGG 780
 40 ACAAAATGTT TTCCATTATC AAGACATGGC CATCTATCTA AATATTATAT CAACTGTGTA 840
 GACTTGAGGG CAATATTGAA ATGATGGTGC TTTCTGCATT TGGTGTATT TGTAAAAA 900
 TTTGCAGTCC TCACTGCACA TGCAAGTATA CCACCTCTCC ATTTAGTATG TTTTAAAGT 960
 AATATGCATC AGAACTTCA GAAATACCTC TGCCCTTTGA TCAAACAAA CCATTTCCTAA 1020
 GAATCTGTAC TAGGGAAGTA AATAAGAATA TGAGAGAAAC CTTTATGCAA ATATGTATAT 1080
 45 TGCAACATTA TTTAATATTC TGGAAAATG GAAACACCCC AAAATTCTAA ACTCAGAGGA 1140
 AGGATTAAAT AAAGAGTGGT ACATCTGTGA AATGTTTTCT GATATTAATA AAAAAATTAA 1200
 AAAAAAATA AAGAGTACTA CATGGTTGTA AAA

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Seq ID NO: 10 Protein sequence
 Protein Accession #: XP_058189.1

55 1 11 21 31 41 51
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 MGSRRKCGCL SCILLIPLALW SIIVNILLYF PNGQTSYASS NKLTNYVWYF EGICFSGIMM 60
 LIVTTVLVLV ENNMNMYKCCQ SENCSSKKYVT LLSIIPSSLG IAFSGYCLVI SALGLVQGPY 120
 CRTLDGWEYA FEGTAGRPLT DSSIWIQCLE PAHVVEWNII LFSILITLSG LQVIICLIRV 180
 VMQLSKILCG SYSVIFQPGI I

60

Seq ID NO: 11 DNA sequence
 Nucleic Acid Accession #: NM_002421.2
 Coding sequence: 1..1409

65 1 11 21 31 41 51
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 ATGCACAGCT TTCCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTG ACACAGCTTC 60
 CCAGCGACTC TAGAAACACA AGAGCAGAGT GTGGACTTAG TCAGAAATA CCTGGAAAAA 120
 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCAGTG 180
 GTTGAATAAT TGAAGCAAT GCAGGAATTC TTTGGGCTGA AAGTGAAGTG GAAACCAAGT 240
 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCGTGATG GGTCTCAGTT 300
 70 GTCCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAAT 360
 TACAGCCAGC ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC 420
 TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGAAC TGGAGGAAAT 540
 CTGTCTCATG CTTTTCAACC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 75 GAAAGTGGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGGGCG TCATGAAGCTC 660
 GGCCATTCTC TTGGACTCTC CCAATTCTACT GATATCGGGG CTTTGATGTA CCTAGCTAC 720
 ACCTTCAGTG GTGAGTTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGACGTTCOC AAAATCTGT CCAGCCCATC GGCCCAAAA CCCCAGAGC ATGTGACAGT 840
 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAGG TGATGTTCTT TAAAGACAGA 900
 80 TTCTACATCG GCACAAATCC CTCTACCCG GAAGTTGAGC TCAATTTTCA TTCTGTTTTC 960
 TGGCCACAAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
 CGGTTTCTCA AAGGGAAATA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
 GATGAATATA AAGGATCTAT GGATCCAGGT TATCCAAAAA TGATAGCACA TGACTTTCTC 1260

GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTTA TTCTTTTCAT 1320
 GGAACAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCACTGCAG GAAAAATTAG

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Seq ID NO: 12 Protein sequence
 Protein Accession #: NP_002412.1

	1	11	21	31	41	51	
10	MHSFPPLLLL	LFWGVVSHSF	PATLETQEQD	VDLVQKYLEK	YYNLKNDGRQ	VEKRRNSGPV	60
	VEKLKMQQEF	FGLKVTGKPD	AETLKVMKQP	RCGVDPVAQF	VLTEGNPRWE	QTHLTIRIEN	120
	YTPDLPRADV	DHAIEKAPOL	WSNVTPLTFT	KVSEGGADIM	ISFVRGDHRD	NSPFDGPGGN	180
	LAHAFQPGPG	IGGDAHFDDE	ERWTNNFREY	NLHRVAAHEL	GHSGLSLHST	DIGALMYPGY	240
15	TFSGDVQLAQ	DDIDGIQAIY	GRSQNPVQPI	GPQTPKACDS	KLTFDAITTI	RGEVMPFKDR	300
	FYMRNTFFYP	EVELNPFISV	WPQLPNGLEA	AYEFADRDEV	RPFKGNKYWA	VQQQNVLHGY	360
	PKDIYSSFGF	PRTVKHIDAA	LSEENTGKTY	FFVANKYWRY	DEYKRSMDPG	YPKMIAHDFP	420
	GIGHKVDVAV	MKDGFFYPFH	GTRQYKDPK	TKRILTQKA	NSWFNCRKN		

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Seq ID NO: 13 DNA sequence
 Nucleic Acid Accession #: NM_002421.2
 Coding sequence: 1..1409

	1	11	21	31	41	51	
25	ATGCACAGCT	TTCCTCCACT	GCTGCTGCTG	CTGTTCTGGG	GTGTGGTGTC	ACACAGCTTC	60
	CCAGCGACTC	TAGAAACACA	AGAGCAAGAT	GTGGACTTAG	TCCAGAAATA	CCTGGAAAAA	120
	TACTACAACC	TGAAGAAATG	TGGGAGGCAA	GTTGAAAAGC	GGAGAAATAG	TGGCCCAAGT	180
	GTTGAAAAAT	TGAGGCAAAAT	GCAGGAATTC	TTTGGGCTGA	AAGTGACTGG	GAAACCAGAT	240
30	GCTGAAACCC	TGAAGGTGAT	GAAGCAGCCC	AGATGTGGAG	TGCCTGATGT	GGCTCAGTTT	300
	GCTCTCACTG	AGGGGAAACCC	TGCTGGGAG	CAACACATC	TGACCTACAG	GATTGAAAAAT	360
	TACACGCCAG	ATTTGCCAAG	AGCAGATGTG	GACCATGCCA	TTGAGAAAGC	CTTCCAACCT	420
	TGGAGTAATG	TCACACCTCT	GACATTCACC	AAGGTCTCTG	AGGGTCAAGC	AGACATCATG	480
	ATATCTTTTG	TCAGGGGAGA	TCATCGGGAC	AACCTCCTCT	TTGATGGAGC	TGGAGGAAAT	540
	CTTGCTCATG	CTTTTCAACC	AGGCCCAAGT	ATTGGAGGGG	ATGCTCATTT	TGATGAAGAT	600
35	GAAAGGTGGA	CAACAATTT	CAGAGAGTAC	AACCTACATC	GTGTGCGGCG	TCATGCCCTC	660
	GGCCATTCTC	TTGGACTCTC	CCATTCTACT	GATATCGGGG	CTTTGATGTA	CCCTAGCTAC	720
	ACCTTCAGTG	GATGATGTCA	GCTAGCTCAG	GATGACATTG	ATGGCATCCA	AGCCATATAT	780
	GGACGTTCCC	AAAATCCTGT	CCAGCCCATC	GGCCCAAAA	CCCCAAAAGC	ATGTGACAGT	840
	AAGCTAAACT	TGATGTCTAT	AACCTACGAT	CGGGGAGAG	TGATGTTCTT	TAAAGACAGA	900
40	TTCTACATGC	GCACAAATCC	CTTCTACCGG	GAAGTTGAGC	TCAATTTTCA	TTCTGTTTTT	960
	TGGCCACAAC	TGCCAAATGG	GCTTGAAGCT	GCTTACGAAT	TTGCCGACAG	AGATGAAGTC	1020
	CGGTTTTTCA	AAGGGAAATA	GTACTGGGCT	GTTCAGGGAC	AGAATGTGCT	ACACGGATAC	1080
	CCCAAGGACA	TCTACAGCTC	CTTTGGCTTC	CCTAGAACTG	TGAAGCATAT	CGATGCTGCT	1140
45	CTTTCTGAGG	AAAACACTGG	AAAAOCTTAC	TTCTTTGTTG	CTAACAAATA	CTGAGGATAT	1200
	GATGAATATA	AACGATCTAT	GGATCCAGGT	TATCCCAAAA	TGATAGCACA	TGACTTTTCT	1260
	GGAATTGGCC	ACAAAGTTGA	TGCAGTTTTC	ATGAAAGATG	GATTTTCTTA	TTTCTTTTCAT	1320
	GGAACAGAC	AATACAAATT	TGATCCTAAA	ACGAAGAGAA	TTTTGACTCT	CCAGAAAGCT	1380
	AATAGCTGGT	TCACTGCAG	GAAAAATTAG				

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Seq ID NO: 14 Protein sequence
 Protein Accession #: NP_002412.1

	1	11	21	31	41	51	
55	MHSFPPLLLL	LFWGVVSHSF	PATLETQEQD	VDLVQKYLEK	YYNLKNDGRQ	VEKRRNSGPV	60
	VEKLKMQQEF	FGLKVTGKPD	AETLKVMKQP	RCGVDPVAQF	VLTEGNPRWE	QTHLTIRIEN	120
	YTPDLPRADV	DHAIEKAPOL	WSNVTPLTFT	KVSEGGADIM	ISFVRGDHRD	NSPFDGPGGN	180
	LAHAFQPGPG	IGGDAHFDDE	ERWTNNFREY	NLHRVAAHAL	GHSGLSLHST	DIGALMYPGY	240
60	TFSGDVQLAQ	DDIDGIQAIY	GRSQNPVQPI	GPQTPKACDS	KLTFDAITTI	RGEVMPFKDR	300
	FYMRNTFFYP	EVELNPFISV	WPQLPNGLEA	AYEFADRDEV	RPFKGNKYWA	VQQQNVLHGY	360
	PKDIYSSFGF	PRTVKHIDAA	LSEENTGKTY	FFVANKYWRY	DEYKRSMDPG	YPKMIAHDFP	420
	GIGHKVDVAV	MKDGFFYPFH	GTRQYKDPK	TKRILTQKA	NSWFNCRKN		

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Seq ID NO: 15 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 141..1580

	1	11	21	31	41	51	
70	TCTGCGTGTG	CCGGGGCTAG	GGGCTGGAAG	TCCTGGCTCT	AGTTGCACCT	OGGAAGGAAA	60
	AGGCAACAG	AGGAGGGAAG	GCGTCTTAGG	ACTGCCTGGA	TCCAGAGCAC	TTTCTCTGGC	120
	CTCTACAGGC	CTGTGTGCT	ATGGGTTCCC	CCGCGGCCCC	GGAGGGAGCG	CTGGGCTACG	180
75	TCGCGAGTT	CACCTGCGAC	TCCTCCGACG	TGCTGGGCAA	CCTCAACGAG	CTGCGCCTGC	240
	GCGGGATCCT	CACCTAGCTC	ACGCTGCTGG	TTGGGGGCGA	ACCCCTCAGA	GCACACAAGG	300
	CAGTTCTCAT	CGCTGCTCAGT	GGCTTCTTCT	ATTCAATTTT	CCGGGGCGGT	GCGGGAGTGG	360
	GGGTGGACGT	GCTCTCTCTG	CCGGGGGGTC	CCGAAGGAGG	AGGCTTGGCC	CCTCTATTGG	420
	ACTTCATGTA	CACCTCGGCG	CTGCGCCTCT	CTCCAGCCAC	TGCACCAAGA	GTCTTAGCGG	480
80	CCGCCACCTA	TTTCAGATG	GAGCACGTGG	TCCAGGCATG	CCACCGCTTC	ATCCAGGCCA	540
	GCTATGAACC	TTGGGCGATC	TCCCTGGGCC	CCCTGGAAGC	AGAACCOCOA	ACACCCOCAA	600
	CGGCCCTTCC	ACCAGGTAGT	CCCAGGCGCT	CCGAAGGACA	CCCAGACCCA	CCTACTGAAT	660
	CTCGAAGCTG	CAGTCAAGGC	CCCCCAGTCT	CAGCCAGCCC	TGACCCCAAG	AGCTGCAACT	720
	GGAAAAAGTA	CAAGTACATC	GTGCTAAACT	CTCAGGCTCT	CCAAGCAGGG	AGCCTGGTGG	780

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GGGAGAGAAG TTCTGGTCAA CCTTGCCCCC AAGCCAGGCT CCCAGTGGG GACGAGGCCT 840
CCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GTGAAGAAGG ACCCATTCCT GGTCCCCAGA 900
GCAGGCTCTC TCCAACTGCT GCCACTGTGC AGTTCAAATG TGGGGCTCCA GCCAGTACCC 960
CCTACCTCCT CCATCCCCAG GCTCAAGACA CCTCTGGATC ACCCTCTGAA CGGGCTCGTC 1020
CACTACCGGG AAGTGAATTT TTCAAGTGCCT AGAACTGTGA GGCTGTGGCA GGGTGCCTCAT 1080
CGGGCTGGGA CTCCTTGGTT CCTGGGGAGC AAGACAAACC CTATAAGTGT CAGCTGTGCC 1140
GGTCTTGGTT CGCTACAAG GGCAACCTTG CCAGTCATCG TACAGTGCAC ACAGGGGAAA 1200
AGCCTTACCA CTGCTCAATC TGGGAGCCCC GTTTTAAACG GCCAGCAAA CTAAGAAACG 1260
ACAGCCGCAT CCATTCGGGA GAGAAGCCGT ATAAGTGTGA GACGTGCGGC TOGCGCTTTG 1320
TACAGGTGGC ACATCTGGCG GCGCACGTGC TGATCCACAC CGGGGAGAAG CCTACCCCTT 1380
GCCCTACCTG CGGAACCCGC TTCCGCCACC TGACAGCCCT CAAGAGCCAC GTTCGCATCC 1440
ACACCGGAGA GAAGCCTTAC CACTGCGACC CCTGTGGCCT GCATTTCCGG CACAAGATC 1500
AACTGCGGCT GCATCTGCGC CAGAAACAG GAGCTGCTAC CAACACCAA GTGCACTACC 1560
ACATTTCTGG GGGGCCCTAG CTGAGCGCAG GCCCAGGCC CACTTGCTTC CTGCGGTGG 1620
GAAAGCTGCA CCTTGGGGG TTGCTTCCCT ATCAGGCTTG GGCATAGGGG TGTGCCAGG 1680
CACTTTGGTA TCAGAAATTT CCACCTCTCT AATTTCTCAC TGGGGAGAGC AGGGGTGGCA 1740
GATCTCTGCT AGATCTGCTT CTGTTTGTCT GGTCAAAACC TCTTCCCCA AAGCCAGATT 1800
GTTTCTGAGG AGAGAGCTAG CTAGGGGCTG GGAAGGGGA GAGATTGGAG TCCTGGTCTC 1860
CCTAAGGGAA TAGCCCTCCA CCTGTGGGCC CCATTCGATT CAGTTTATCT GTAAATATAA 1920
TTTATTGAGG CCTTTGGGTG GCACCGGGGC CTTTATTGCA TTGCATTTC CACTCCCTC 1980
TTCCACAAGT GTGATTAAAA GTGACAGAA ACACAGAAG TGAGATCACA GCTCTGCTG 2040
CAGAGATTAC TAGCCCTTGG CTCTCTCGTT TGGCTTGGGT ATTTTATATT ATTTCTGTCA 2100
TAACTTTAT CTTAGAATT GTTCTTCTC CTGTTTGTG GCTTGTAGT TTGTTTAAAA 2160
TGGAAAAAGG GGTCTCTGT GTTCTGCCCT TGTAATTTCTA GGTCTGGAAC CTTTATTGT 2220
TCTAGGGCAG CTCCTGGGAC ATGCGGGATT GTGGAATTGG GTCAGGAACC CTCTCTGGA 2280
TTCTGGATGT TGTAGGTTCT CTAGCAGTCT AGAAATGGAT ACAGACATTT CTCTGTCTT 2340
CAAGGGTGT AGGAACCAT ATGTTGAGCC CAAAATGGAA GTAATAATAA ATGCCTCCTG 2400
GAGGCTGTGG GTGTGGGGGA TTCTGTATCT GGATTCCGTA TCACTCCAAC TGGAGGCTGT 2460
GGGTGTGGGG GATTCTGTAT CTGGATTCCG TATCACTCCA AGTGGAGGCT GGCAGGTTT 2520
TCTGCAAGT GGTCCAGAA CTAAATGTG CCATTAATCT GGTCACTTGG GTTGGCTCT 2580
GCTGTATCCA TCTATAGTGG TAGAGACCCA CCAGGGCTCA AGTGGAGTCC ATCATCCTCC 2640
CACGGGGGCC TGTCTTAGC ACTGAGTTGA TCGCTCCATG GGGGAGAGAT CAGACATTCC 2700
TTATCAGAGA TGTGTGACCC TTTCTGACT CTGCCAGTC TCTATGAATG TTATGGCCTA 2760
GGGAAGAATC ATGAATCTT TTAGCTTGAT TAGATGGTAA ACAGTGTAA CCATCCTTT 2820
ACTACAGAG CATATGGGT TGAATGTTAC CTGGGGTCT CTCTATTGAG TTGAGCCCT 2880
TCTTCTTTA GTGGGTTTG GACATCTTCT GGCAAGTGT CAGATGCCAG AACCTTCTTT 2940
TCCTCTAGAA GGGATGGTGC TTGTTAACT TACCTTTTAA AAGCTGGGTG TGTGACCTGG 3000
TCTTCCATC CCTGTGATC TGTCTGGAAC CAGTGAATGC ATTAGAACC TCCATAGGAA 3060
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TTCAAGTAGG ATTAAGAGGT TGGTTAGGG GTGCAGTTTC TGGTGTAGGC CAGGTAGGTA 3240
GAAAGTAGG AACAGGGTTG CCTCTGGCT GGGTGGAGTC TCTGAAATGT TAGAAGAAGC 3300
GCTGAAGCCT TGATTGATAG TTCTGCCCT TGTGCGCTG GGGCTTATCT GATTATGGGA 3360
CGAGGGTAGA AAGTAAGAAG CACTTTTGA TTTGTGGGT AGAACTTCAA CAATAAGTCA 3420
GTTCTAGTGG CTGTGCGCTG GGGACTAGT AGAAAGCTAC TCTTCTCCTT CTTCCCTCTT 3480
TCTCCCATTG GCCCACTCG AGAATTAAAG AAGGAAGAAG GGAAGGCGGA GGAGTCTATA 3540
AGAAGGAATC ATGATTCTA TTAGCAGAT TGGATGGCA GGTGAGAAT GCCTGGGGT 3600
AGAAATGTTA GATCTTGCAA CATCAGATCC TTGGAATAA GAAGCCTCTC TGYGWRAAA 3660
AAAAAAAAA AAAAA

Seq ID NO: 16 Protein sequence
Protein Accession #: FGENESH predicted

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1 11 21 31 41 51
MGSPAAPEGA LGYVREPTRH SSDVLGNLNE LRLRGILTDV TLLVGGQPLR AHKAVLIACS 60
GFPYSLFRGR AGVGVDLVSL PGGPEARGFA PLLDFMYTSR LRLSPATAPA VLAAATYLM 120
EHVVQACHRF IQASYEPLGI SLRPLEAEP PPPTAPPFGS PRRSEGHDP PTERSCSQG 180
PPSPASPDPK ACNWKYKYI VLNSQASQAG SLVGERSSGQ PCPQARLPSG DEASSSSSSS 240
SSSSEBPIP GPQSRLSPTA ATVPFKCGAP ASTPYLLTSQ AQDTSGSPSE RARPLPGSEF 300
FSCQNCBAVA GCSSGLDSL PVGDEKPYKC QLCRSSFRYK GNLSHRTVH TGEKPYHCSI 360
CGARFNRPAN LKTHSRILHS EKPYKCTCG SRFVQVAHLR AHVLIHTGEK PYPCTGTR 420
FRHLQTLKSH VRIHTGEKPY HCDPGLHFR HKSQRLHLR QKHGAATNTK VHYHILGGP

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: XM_039209
Coding sequence: 1..2049

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ATGCTGAAGA TGCTCTCCTT TAAGCTGCTG CTGCTGCGCG TGGCTCTGGG CTCTTTGAA 60
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AATGGGAACC CCCCGAAGCG CCTGAAAAGG AGAGACAGGA GGATGATGTC CCAGCTGGAG 180
CTGCTGAGTG GGGGAGAGAT GCTGTGCGGT GGCTTCTACC CTCGGCTGTC CTGCTGCTG 240
CGGAGTGACA GCGCGGGGCT AGGGGCGCTG GAGAATAAGA TATTTTCTGT TACCAACAA 300
ACAGAAATGT GGAAGTTACT GGAGGAAATC AAATGTGCAC TTTGCTCTCC ACATTCTCA 360
AGCCTGTTC ACTCACCTGA GAGAGAAGTC TTGAAAGAG ACCTAGTACT TCCTCTGCTC 420
TGCAAGACT ATTGCAAGA ATTCTTTTAC ACTTGCAGAG GCCATATTCC AGGTTCCTTT 480
CAACAAGCT GAGATGAGTT TTGCTTTTAC TATGCAAGAA AAGATGGTGG GTTGTGCTTT 540
CCAGATTTTC CAAGAAACA AGTCAGAGGA CCAGCATCTA ACTACTTGA CCAGATGGAA 600
GAATATGACA AAGTGGAGA GATCAGCAGA AAGCACAAAC ACACTGCTT CTGATTCTAG 660
GAGGTTGTGA GTGGGCTGCG GCAGCCCGTT GGTGCCCTGC ATAGTGGGGA TGGCTGCA 720
CGTCTCTTCA TTTGGGAAA AGAAGGTTAT GTGAAGATAC TTACCCCTGA AGGAGAAATT 780
TTCAGGAGC CTATTTTGGA CATTACAAA CTTGTTCAAA GTGGAATAA GGGAGGAGAT 840

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GAAAGAGGAC TGCTAAGCCT CGCATTCCAT CCCAATTACA AGAAAAATGG AAAGTTGTAT 900
GTGTCTTATA CCACCAACCA AGAACGGTGG GCTATCGGGC CTCATGACCA CATTCTTAGG 960
GTGTGGGAAT ACACAGTATC CAGAAAAAAT CCACACCAAG TTGATTGAG AACAGCCAGA 1020
GTCTTTCTTG AAGTTGCAGA ACTCCACAGA AAGCATCTGG GAGGACAAC TCTCTTTGGC 1080
CCTGAOCCGT TTTTGATCAT CATTCTTGGT GATGGGATGA TTACACTGGA TGATATGGAA 1140
GAAATGGATG GGTAAAGTGA TTTCACAGGC TCAGTGCTAC GGCTGGATGT GGACACAGAC 1200
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CCCCCCGAAG TGTTTGCTCA TGGGCTCCAC GATCCAGGCA GATGTGCTGT GGATAGACAT 1320
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CCAGCATGTC GTCATGAGG TGCTGTGTGT AGACOGAACA AGTGCCCTCTG TAAAAAGGA 1980
TATCTTGTGC CTCAATGTGA ACAAGTGAC AGAAACATCC GCAGAGTGAC CAGGGCAGAC 2040
ATCACTAG

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25 Seq ID NO: 18 Protein sequence
Protein Accession #: XP_039209

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1 11 21 31 41 51
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MLKMLSPKLL LLAAVALGFPE GDAKFGERNE GSGARRRRCL NGNPPKRLKR RDRRMSQLE 60
LLSGGEMLCG GFYPRLSCLL RSDSPGLGRL ENKIFSVTNN TECGKLLLEE KCALCSPHSQ 120
SLFHFSPEREV LERDLVPLLL CKDYCKEPPY TCRGHIIPGL QTTADEFCFY YARKDGGLCF 180
PDPFRKQVRG PASNYLDQME EYDKVEEISR KHKHNCFCIQ EVVSQLRQPV GALHSGDQSG 240
RLFILEKEGY VKILTPEGEI FKEPYLDINH LVQSGIKGGD ERGLLSLAFH PNYKNGKLY 300
VSYTNQERW AIGPHDHLIR VVEYTVSRKN PHQVDLRTAR VFLEVAELHR KHLGGQLLFG 360
PDGFYLIILG DGMITLDDME EMDGLSDFTG SVLRDLVDTD MCNVPSYIPR SNPHFNTNQ 420
PPEVFAHLGH DPGRCVDRH PTDININLTI LCSDSNGKNR SSARILQIIK GKDYSEPSL 480
LEFKPFSNPG LVGGFVYRGC QSERLYGSYV FGDRNGNFLT LQSPVTKQW QEKPLCLGTS 540
GSCRGYPSGH ILGFGDEDELG EYILSSSKS MTQTHNGKLY KIVDPKRPLM PEECRATVQP 600
AQTLTSECSR LCRNGYCTPT GKCCSPGWE GDFCRTAKCE PACRHGGVCV RPNKCLCKKG 660
YLGPPQCEQVD RNIRRVTRAD IT

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45 Seq ID NO: 19 DNA sequence
Nucleic Acid Accession #: NM_014331.2
Coding sequence: 1..1506

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AAGAGGAAGT TCACCTTACT GAGGGGAGTC TCCATTATCA TTGGCACCAT CATTGGAGCA 180
GGAATCTTCA TCTCTCTCTA GGGCGTGCTC CAGAACACGG GCAGCGTGGG CATGCTCTG 240
ACCATCTGGA CGGTGTGTGG GGTCTGTGCA CTATTGGGAG CTTTGTCTTA TGCTGAATTG 300
GGAACAACTA TAAAGAAATC TGGAGGTCAT TACACATATA TTTTGGAAAT CTTTGGTCCA 360
TTACCACTCT TTGTACAGAT CTGGGTGGAA CTCTCATATA TACGCCCTGC AGCTACTGCT 420
GTGATATCCC TGGCACTTGG ACGCTACATT CTGGAACCAT TTTTATTACA ATGTGAAATC 480
CCTGAACCTG CGATCAAGCT CATTACAGCT GTGGGCATAA CTGTAGTATG GGTCTTAAAT 540
AGCATGAGTG TCAGCTGGAG CGCCCGGATC CAGATTTTCT TAACTTTTGT CAAGCTCACA 600
GCAATCTGTA TAATTATAGT CCCTGGAGTT ATGCAGCTAA TTAAGGTCAT AACCGAGAAC 660
TTTAAAGACG CGTTTTTCAGG AAGAGATTCA AGTATTACGC GGTGGCACT GGCTTTTAT 720
TATGGAATGT ATGCATATGC TGGCTGTTT TACCTCAACT TTGTACTGTA AGAAGTAGAA 780
AACCTGAAAA AAACCATTC CTTGCAATA TGTATATCCA TGGCCATGT CACCATTTGC 840
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TTAAAGAAAG GTTCTTAGGG GCTACTGTTT ATGAGACACA TCCAGGAGTT ATGTTTAAGT 2160
AAAAATCCTT GAGAACTTAT TATGTCAGAT GTTTTTTCAT TCATTATCAG GAAGTTTATG 2220

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5 TTATCTGTCA TTTTTTTTTT TCACATCAGT TTGATCAGGA AAGTGTATAA CACATCTTAG 2280
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 CAACATGGAG AAACCCCATC TCTACTAAAA ATACAAAATT AGCTGGGCAT GGTGGCAGAT 3000
 GCTGGTAATC TCAGCTATTG AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGGAGGCG 3060
 15 GAGGTGCGAG TGAGCCAAAG TTGCACCACT GTACTCCAGC CTGGGTGACA AAGTCAGACT 3120
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Seq ID NO: 20 Protein sequence
 Protein Accession #: NP_055146.1

20 1 11 21 31 41 51
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 25 GIFISPKGVL QNTGVSVMGL TIWTVCGVLS LFGALSYAEL GTTIKKSQGH YTYILEVFGP 120
 LPAPVVRWVE LLIIIRPAATA VISLAFGRYI LEPPFIQCEI PELAIKLITA VGITVVMVLN 180
 SMSVSWRSRI QIFLTFCKLT AILIIIVPGV MQLIKGTQON FKDAFSGRDS SITRLPLAFY 240
 YGMAYAGWF YLNFVTEVEE NPEKTIPLAI CISMATIGV YVLTNVAYPT TINAEELLS 300
 NAVAVTFSEI LGNFVSLAVP IFVALSCFSG MNGGVFAVR LFPVASREGH LPEILSMIHV 360
 30 RKHTLPAVI VLHPLTMIML FSGDLDSLNL FLSPARWLF I GLAVAGLIYL RYKCPDMHRP 420
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Seq ID NO: 21 DNA sequence
 Nucleic Acid Accession #: NM_002422.2
 Coding sequence: 64..1497

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 AACTACTACG ACCTCAAAAA AGATGTGAAA CAGTTTGTTA GGAGAAAGGA CAGTGGTCTC 240
 45 GTGTGTAAAA AAATCCGAGA AATGCAGAAG TTCCTTGGAT TGGAGGTGAC GGGGAAGCTG 300
 GACTCCGACA CTCTGGAGGT GATGCGCAAG CCCAGGTGTG GAGTTCCTGA TGTGTGTCAC 360
 TTCAGAACTT TTCTTGGCAT CCGAAGTGG AGGAAAACCC ACCTTACATA CAGGATTGTG 420
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 GTTTTGGCCG ATGCCTATGC CCTTGGGCCA GGGATTAATG GAGATGCCCA CTTTGATGAT 660
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Seq ID NO: 22 Protein sequence
 Protein Accession #: NP_002413

75 1 11 21 31 41 51
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 VKIIREMQKF LGLEVTGRKL SDTLEVMRKP ROGVPDVGHF RTPFGIPKWR KTHLTYYRIVN 120
 80 YTPDLPIKAV DSAVEKALKV WEEVTPLTFS RLYEGEADIM ISFAVREHGD FYFPDGPNGV 180
 LAHAYAPGPG INGDAHFDDE EQWTKDTTGT NLPLVAHEHI GHSLGLFHS A NTEALMYPLY 240
 TSLTDLTRFR LSQDDINGIQ SLVGPPFDSP ETPLVPTFEP PPEPGTPANC DPALSFDAYS 300
 HLRGEILIFK DRHPWRKSLR KLEPELHLIS SFWPSLPSPV DAAYEVTSKD LVPIFKGNQF 360
 WAIRGNEVRA GYPRGIHTLG FPPTVRKIDA AISDKKKNKT YFPVEDKYWR FDEKRNSEMP 420
 GFPKQIAEDF PGIDSKIDAV FFEFGFFYFP TGSSQLEFDP NAKKVTHTLK SNWLNLC

Seq ID NO: 23 DNA sequence
Nucleic Acid Accession #: NM_006528
Coding sequence: 57..764

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GCGATGCTCG	TCAGGAGCCA	ACAGGAAATA	ACGCGGAGAT	CTGTCTCCCTG	CCCTAGACT	180
ACGGACCCCTG	CCGGGCCCTA	CTTCTCCGTT	ACTACTACGA	CAGGTACACG	CAGAGCTGCC	240
GCCAGTTCTT	GTACGGGGGG	TGCGAGGGCA	ACGCCAACAA	TTTCTACACC	TGGGAGGCTT	300
GCGACGATGC	TGTCTGGAGG	ATAGAAAAAG	TTCCCAAAGT	TTGCGGCTG	CAAGTGAGTG	360
TGGACGACCA	GTGTGAGGGG	TCCACAGAAA	AGTATTCTTT	TAATCTAAGT	TCATGACAT	420
GTGAAAAATT	CTTTCCCGGT	GGGTGTCAAC	GGAAACCGAT	TGAGAACAGG	TTTCCAGATG	480
AAGCTACTTG	TATGGGCTTC	TGCGCACCAG	AGAAAAATCC	ATCATTTTGC	TACAGTCCAA	540
AAGATGAGGG	ACTGTGCTCT	GCCAAATGTA	CTCGCTATTA	TTTAAATCCA	AGATACAGAA	600
CCTGTGATGC	TTTCACCTAT	ACTGGCTGTG	GAGGGAATGA	CAATAACTTT	GTTAGCAGGG	660
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GCTTTGCCAG	TAGAATCCGG	AAAAATCGGA	AGAAGCAATT	TTAAACATTC	TTAATATGTC	780
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GCATGAGGAA	ACAAATCATT	GGTGATTAT	TCACCAAGTT	TTATTAATAC	AAGTCACTTT	900
TTCAAAAAAT	TGGATTTTTT	TATATATAAC	TAGCTGCTAT	TCAATGTGA	GTCTACCAT	960
TTTAATTTAT	GGTCAACTG	TTTGTGAGAC	GAATTCTTGC	AATGCATAAG	ATATAAAAGC	1020
AAATATGACT	CACCTCATTC	TTGGGGTGGT	ATTCCTGATT	TCAGAAGAGG	ATCATAACTG	1080
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Seq ID NO: 24 Protein sequence
Protein Accession #: NP_006519

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TCEKFFSGGC	HRNRRIENRPP	DEATCMGFCA	PKKIPSPFCS	PKDEGLCSAN	VTRYFENPRY	180
RTCDAFITYG	CGGNDNNFVS	REDCKRACAK	ALKKKKKMPK	LRFASRIKI	RKKQF	

Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: NM_005458.1
Coding sequence: 1..2825

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GGCTGGGCGC	GGGGCGCCCC	CGGGCGCGCG	CCCAGCAGCC	CGCCGCTCTC	CATCATGGGC	180
CTCATGCCGC	TCACCAAGGA	GGTGGCCAAG	GGCAGCATCG	GGGCGGTTGT	GCTCCCCGCC	240
GTGGAACCTG	CCATCGAGCA	GATCGGCAAC	GAGTCACTCC	TGCGCCCTTA	CTTCTCTGAC	300
CTGCGGCTCT	ATGCAACGGA	GTGCGACAAC	GCAAAAGGGT	TGAAAGCCTT	CTACGATGCA	360
ATAAAATAAG	GGCCGAACCA	CTTGATGGTG	TTTGGAGGGG	CTGTCTCCATC	CGTCACATCC	420
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GGCATCTGGG	TCACTGCCAA	GACACTGCAG	AGGGCCATGG	AGACACTGCA	TGCCAGCAGC	1140
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ATCCGCGCTC	TCTTGGAGCA	CTGTGAGAAC	ACCATATGAT	CCATCTGGCT	TGGCATOGTC	1980
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CAGTTCACTC	AGAATCAGAA	GAAAGAAGAT	TCTAAAAAGT	CCACTCGGT	CACCAAGTGT	2340
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5 AAGATCACAG AGCTGGATAA AGACTTGGAA GAGGTACCA TGCAGCTGCA GGACACACCA 2460
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10 Seq ID NO: 26 Protein sequence
 Protein Accession #: NP_005449.1

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 AVNPAILKLL KHYQWKRVTG LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SPSNDPCTSV 240
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 BRMGTIKPTQ PQDSREVKVG EYNAVADTLE IINDTIRFQG SEPPKDKTII LBQLRKISLP 480
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 GSPVSEKTFE TLCTVTRTIL TVGYTTAFGA MFAKTWRVHA IFKNVVKMKK IIKDQKLLVI 600
 VGMMLLIDL ILICWQAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLIV 660
 YAYKGLMLLE GCLFANETRN VSIPALNSDK YIGMSVYNVG IMCIIGAAVS FLTRDQPNVQ 720
 FCIVALVIIF CSTITLCLVF VPKLITLRTN PDAATQNRFP QFTQNKKKED SKTSTSVTSV 780
 NQASTSRLEG LQSENHRLRM KITELDKOLE EVTMQLQDTP EKTYYIKQNH YQELNDILNL 840
 GNFTSTDDG KAILKNHLDQ NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLPLIH 900
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Seq ID NO: 27 DNA sequence
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 Coding sequence: 117..1949

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 GGTCTTACAA CAGCTCCACG GAAGCTATGA CTTATGATGA GGCCAGTGCT TATTGTCAGC 240
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AGAATAAAGT TCTGAGTGT TTTACTACAG TTGTTTTTTG AAAACATGGT AGAATTGGAG 2880
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CCACGATGAA AAACCTTCCAT GAGGCCAAAC GTTTTGAAGT AATAAAAGCA TAAATGCAAA 3000
CACACAAAGG TATAATTTTA TGAATGTCTT TGTGTGAAAA GAATACAGAA AGATGGATGT 3060
GCTTTGCATT CCTACAAAGA TGTTTGTCTAG ATGTGATATG TAAACATAAT TCTTGTATAT 3120
TATGGAGAT TTTAAATTCA CAATAGAAAC TCACCATGTA AAAGAGTCAT CTGGTAGATT 3180
TTTAACGAAT GAAGATGTCT AATAGTTATT CCTATTGT TTTCTTCTGT ATGTTAGGGT 3240
GCTCTGGAAG AGAGGAATGC CTGTGTGAGC AAGCATTTAT GTTTATTTAT AAGCAGATT 3300
AACAAATCCA AAGGAATCTC CAGTTTTCAG TTGATCAGTG GCAATGAAAA ATTCTCAGTC 3360
AGTAATTGCC AAAGCTGCTC TAGCCTTGAG GAGTGTGAGA ATCAAACTC TCCTACACTT 3420
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GCATTAGCAT TTAGTATTTT GAAATACCAG TGTGGTTTGT GTTTGAGTTT TATTGAGAT 3720
TTTAAATTTT AACTTAAAT ATTTTATAAT TTTTAAAGTA TATATTATT TAAGCTTATG 3780
TCAGACCTAT TTGACATAAC ACTATAAAGG TTGACAATAA ATGTGCTTAT GTTT

Seq ID NO: 28 Protein sequence
Protein Accession #: NP_000441.1

1 11 21 31 41 51
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QORYTHLVAI QNKKEIEYLN 60
SILSYSPSYW WIGIRKVMNV WVVVGTKPL TEEKNWAPG EPNNRQKDED CVEIYIKREK 120
DVGMWNDERC SKKKLALCYT AACTNTSCSG HGECEVETINN YTCKCDPGFS GLKCEQIVNC 180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIACNVV 240
ECDAVTNPAN GFVECFQNPQ SPFWNTTCTF DCEEGFELMG AQLSLQCTSSG NWDNEKPTCK 300
AVTCRAVRQP QNGSVRCGSHS PAGEFTFKSS CNFTCEEGFM LQGPQVVECT TQGWQWQIIP 360
VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEFSCEQ GFVLKGSKRL QCQPTGEWON 420
EKPTCEAVRC DAVHOPPKGL VRCASPIGE FTYKSCAFS CEEGFELYGS TQLETSQGG 480
WTEEVPSQCV VKCSLAVPG KINMSCSGEP VFGTVCKPAC PEGWTLNGSA ARTCGATGHW 540
SGLLETCEAP TESNIPVLVAG LSAAGLSLIT LAPFLWLRLK CLRKAKKFVP ASSCQSLESD 600
GSYQPSYIL

Seq ID NO: 29 DNA sequence
Nucleic Acid Accession #: NM_007036
Coding sequence: 56..610

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1 11 21 31 41 51
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TAAATATGCG GTGGACTGCC CTCAACACTG TGACAGCAGT GAGTGCAAAA GCAGCCCGCG 180
CTGCAAGAGG ACAGTGCTCG ACAGCTGTGG CTGCTGCCGA GTGTGCGCTG CAGGGCGGGG 240
AGAACTGTGC TACCGCAGAG TCTCAGGCAT GGATGGCATG AAGTGTGGCC CGGGGCTGAG 300
GTGTGAGCCT TCTAATGGGG AGGATCCTTT TGGTGAAGAG TTTGGTATCT GCAAGACTG 360
TCCCTACGGC ACCTTCGGGA TGGATTGCGA AGAGACCTGC AACTGCCAGT CAGGCATCTG 420
TGACAGGGGG ACGGGAATAA GCCTGAAATT CCCCTTCTTC CAATATTGAG TAACCAAGTC 480
TTCCACAGCA TTTGTTTCTC TCACGGAGCA TGACATGGCA TCTGGAGATG GCAATATTGT 540
GAGAGAGAA GCTGTGAAGG AGAATGCTGC CGGGTCTCCC GTAATGAGGA AATGGTTAAA 600
TCCAGCTGTA TCCCGGCTGT GATTTCGTAG AGAAGGCTCT ATTTTCGTGA TTGTTCAACA 660
CACAGCCAA ACCTTAGGAA CTCTCTAGAT ATAGCATAAG TACATGTAAT TTTTGAAGAT 720
CCAAATTGTG ATGCATGGTG GATCCAGAAA ACAAAGTA GGTACTTAC AATCCATAAC 780
ATCCATATGA CTGAACACTT GTATGTGTTT GTTAAATATT CGAATGCATG TAGATTGTGT 840
AAATGTGTGT GTATAGTAAC ACTGAAGAAC TAAAAATGCA ATTTAGGTAA TCTTACATGG 900
AGACAGGTCA ACCAAGAGG GAGCTAGGCA AAGCTGAAGA CCGCAGTGAG TCAAAATAGT 960
TCTTTGACTT TGATGTACAT TAATGTTGGG ATATGGAATG AAGACTTAAG AGCAGGAGAA 1020
GATGGGGAGG GGGTGGGAGT GGGAAATAAA ATATTAGACC CTTCCTTGGT AGGTAGCTTC 1080
TCTAGAAATT AATTGTGCTT TTTTTTTTTT TTTGGCTTTG GGAAGAGTCA AAATAAAACA 1140
ACCAGAAAC CCTGAAGGA AGTAAGATGT TTGAAGCTTA TGGAAATTG AGTAACAAAC 1200
AGCTTTGAAC TGAGAGCAAT TTCAAAAGGC TGCTGATGTA GTTCCCGGGT TACCTGTATC 1260
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GTAAATATTT ATATATTTTT ATAAATAAAT GTGTAGTGC AAGTCATCTT CCTACCCAT 1440
ATTTATCATC CTCTTGAGGA AAGAAATCTA GTATTATTGT TTGAAATGG TTGAATAAAA 1500
AACCTATGAC TCTATAAGGT TTTCAACAT CTGAGGCATG ATAAATTTAT TATCCATAAT 1560
TATAGGAGTC ACTCTGGAT TCAAAAAATG TCAAAAAATG AGCAACAGAG GGACCTTATT 1620
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GGAGGTTTGT AAAAGAAGAA TCAATTTTCA GCAGAAAACA TGTCAACTTT AAAATATAGG 1740
TGGAAATTAG AGTATATTG AAAGAATCTT AGCACAACA GGACTGTGTG ACTAGATGTT 1800
CTTAGGAAT ATCTCAGAAG TATTTTATT TAGAGTGAAGA ACTTATTTAA GAATTATTTT 1860
AGTATTTACC TGTATTTTAT TCTTGAAGTT GGCCAAACAGA GTTGTGAATG TGTGTGGAAG 1920
GCCTTTGAAT GTAAGCTGC ATAAGCTGTT AGGTTTGTGT TTAAGAGGAC ATGTTTATTA 1980
TTGTTCAATA AAAAGAACA AGATAC

Seq ID NO: 30 Protein sequence
Protein Accession #: NP_008967.1

1 11 21 31 41 51
MKSLLLLTLL LVPAPHLVAAN SNRYAVDCPQ HCDSECKSS PRCKRTVLDD CGCCRVCAAG 60
RGETCYRTVS GMDGMKCGPG LRCQPSNGED PFGEEFGICK DCFYGTFGMD CRETCNCQSG 120
ICDRGTGKCL KPPFPQYSVT KSSNRFVSLT EHDMAAGDGN IVREEVVKEN AAGSPVMRKW 180

LNPR

Seq ID NO: 31 DNA sequence

Nucleic Acid Accession #: NM_000963

Coding sequence: 135..1949

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CTCCTTCAGC TCCACAGCCA GACGCCCTCA GACAGCAAAG CCTACCCCGG CGCCGCGCCC 120
TGCCCGCGCCG TCGGATGCTC GCCCGCGCCC TGCTGCTGTG CGCGGTCTTG GCGCTCAGCC 180
ATACAGCAAA TCCTTGCTGT TCCACCCCAT GTCAAAACCG AGGTGTATGT ATGAGTGTGG 240
GATTTGACCA GTATAAGTGC GATTGTACCC GGACAGGATT CTATGGAGAA AACTGCTCAA 300
CACCGGAATT TTGACAAGA ATAAATTAT TTCTGAAACC CACTCCAAC ACAGTCACT 360
ACATACTTAC CCACCTCAAG GGATTTTGA ACGTTGTGAA TAACATTCCC TTCCTTCGAA 420
ATGCAATTAT GAGTTATGTC TTGACATCCA GATCACATT GATTGACAGT CCACCAACTT 480
ACAAATGCTGA CTATGGCTAC AAAAGCTGGG AAGCCTTCTC TAACCTCTCC TATTATACTA 540
GAGCCCTTCC TCCTGTGCCG GATGATTGCC CGACTCCCTT GGGTGTCAA GGTAAAAAGC 600
AGCTTCCTGA TTCAATGAG ATTGTGAAA AATTGCTTCT AAGAAGAAAG TTCATCCCTG 660
ATCCCCAGGG CTCAAACATG ATGTTTGATC TCTTTGCCCA GCACCTCACG CATCAGTTTT 720
TCAAGACAGA TCATAAGCGA GGGCCAGCTT TCACCAACGG GCTGGGCCAT GGGGTGGACT 780
TAAATCATAT TTACGGTGAA ACTCTGGCTA GACAGGTAA ACTGCGCCTT TTCAGGATG 840
GAAAAATGAA GTATCAGATA ATTGATGGAG AGATGTATCC TCCCAAGTC AAAGATACTC 900
AGGCAGAGAT GATCTACCTT CCTCAAGTCC CTGAGCATCT ACGGTTTGTCT GTGGGCGAGG 960
AGGTCTTTGG TCTGTGGCCT GGTCTGATGA TGTATGCCAC AATCTGGCTG CGGGAAACACA 1020
ACAGAGTATG CGATTGTGCT AAACAGGAGC ATCCTGAATG GGGTGAATGA CAGTTGTTC 1080
AGACAGCAGG GCTAATACTG ATAGGAGAGA CTATTAAGAT TGTGATTGAA GATTATGTGC 1140
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AATTCCAGTA CCAAAATCGT ATTGCTGCTG AATTAAACAC CCTCTATCAC TGGCATCCCC 1260
TTCTGCCCTGA CACCTTTCAA ATTCATGACC AGAAATACAA CTATCAACAG TTTATCTACA 1320
ACAACTATCT ATTGCTGGAA CATGGAATTA CCCAGTTTGT TGAATCATTC ACCAGGCAAA 1380
TTGCTGGCAG GGTGTGCTGT GGTAGGAATG TTCCACCCGC AGTACAGAAA GTATCACAGG 1440
CTTCCATTGA CCAGAGCAGG CAGATGAAT ACCAGTCTTT TAATGAGTAC CGCAAACGCT 1500
TTATGCTGAA GCCCTATGAA TCATTGTAAG AACTTACAGG AGAAAAGGAA ATGCTCGCAG 1560
AGTTGGAAGC ACTCTATGCT GACATCGATG CTGTGGAGCT GTATCCTGCC CTTCTGGTAG 1620
AAAAAGCCTG GCCAGATGCC ATCTTTGGTG AAACCATGGT AGAAGTGTGC GCACCATCT 1680
CCTTGAAAGG ACTTATGGGT AATGTTATAT GTTCTCCTGC CTACTGGAAG CCAAGCACTT 1740
TTGGTGAGGA AGTGGGTTTT CAAATCATCA ACATGCCCCT AATTCAGTCT CTCATCTGCA 1800
ATAACGTGAA GGGCTGTCCC TTTACTTCAT TCAGTGTCC AGATCCAGAG CTCATTAAAA 1860
CAGTCACCAT CAATGCAAGT TCTTCCCGCT CCGGACTAGA TGATATCAAT CCCACAGTAC 1920
TACTAAAGA ACCTTCGACT GAACCTGAGA AGTCTAATGA TCATATTAT TTATTATAT 1980
GAACCATGTC TATTAATTTA ATTATTTAAT AATATTTATA TTAACCTCCT TATGTTACTT 2040
AACATCTTCT GTACAGAGAG TCAGTACTCC TGTGCGGAG AAAGGAGTCA TACTTGTGAA 2100
GACTTTTATG TCACTATGCT AAAGAATTTG CTGTGTCTGT TAAGTTTGA AAACAGTTTT 2160
TATTCTGTTT TATAAACCA AGAGAAATGA GTTTTACGT CTTTTTACTT GAATTTCAAC 2220
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AAATGCTGAA AGTTTTTACA CTGTGATGTT TTCCAATGCA TCTTCCATGA TGCATTAGAA 2340
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AGGTATATTG TCAAAATTTA ATGAATATTT AAATTAGACA TTACCAGTAA TTTCTATGCT 2460
ACTTTTAAAA ATCAGCAATG AAACAATAAT TTGAAATTTT TAAATTCATA GGGTAGAATC 2520
ACCTGTAAAA GCTTGTTTGA TTTCTTAAAG TTATTAACCT TGTACATATA CCAAAAAGAA 2580
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TCTCAAAATA AGAATATTTT GTTGAGATAT TCCAGAAATTT GTTTATATGG CTGTAACAT 2820
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CAAAATATTG TTCAAATTTA GGTTTAAACT TTTGAAGCAA ACTTTTTTTT ATCCTTGTGC 2940
ACTGCAGGCC TGGTACTCAG ATTTTGTCTT GAGGTTAATG AAGTACCAAG CTGTGCTTGA 3000
ATAACGATAT GTTTTCTCAG ATTTTCTGTT GTACAGTTTA ATTTAGCAGT CCATATCACA 3060
TTGCAAAAGT AGCAATGACC TCATAAAATA CCTCTTCAAA ATGCTTAAAT TCATTTTACA 3120
CATTAATTTT ATCTCAGTCT TGAAGCCAAT TCAGTAGGTG CATTTGGAATC AAGCCTGGCT 3180
ACCTGCATGC TGTTCCTTTT CTTTCTCTCT TTTAGCCATT TTGCTAAGAG ACACAGTCTT 3240
CTCATCACTT GGTTCCTCCT ATTTTGTTTT ACTAGTTTAA AGATCAGAGT TCACCTTCTT 3300
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AGGACTGCTA TTTAGCTCCT CTTAAGAAGA TTAAGAGAGA AAAAAAAGG CCCTTTTAAA 3420
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ATCTGTAAAC AAGATGGATG CAAAGAGGCT AGTGCCCTCAG AGAGAACTGT ACGGGGTTTG 3540
TGACTGGAAA AAGTTACGTT CCATTCTAA TTAATGCCCT TTCTTATTTA AAAACAAAAC 3600
CAATGATAT CTAGTAGTT CTACGCAATA ATAATAATGA CGATAATACT TCTTTTCCAC 3660
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AACAAATCAA AGAAATGATT GTATTAAGAT TTGTGAATAA ATTTTAGAA ATCTGATTGG 3900
CATATTGAGA TATTTAAGGT TGAATGTTTG TCCTTAGGAT AGGCCATGCT GCTAGCCAC 3960
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GGGATCTGTG GATGCTTCGT TAATTTGTTT AGCCCAATT TATTAGAAA ATATTCTGTG 4080
TCRAGCACTG TGGGTTTTAA TATTTTAAA TCAAACGCTG ATTAAGATA ATAGTATTTA 4140
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AAAGATAACT CAGGAGAAAT TTTCTTACAA TTTTACGTTT AGAATGTTTA AGGTAAAGAA 4260
AGAAATAGCT ATATGCTTGA TATAAAACAC TGTCTACTGT TTTTAAAAA AAAAAAACTT 4320
GATTTGTTAT TAACATTGAT CTGCTGACAA AACCTGGGAA TTTGGGTGT GTATGCGAAT 4380
GTTTCACTGC CTCAGACAAA TGTGATTTTA ACTTATGTAA AAGATAAGTC TGGAAATAAA 4440
TGTCTGTTTA TTTTGTACT ATTTA

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Seq ID NO: 32 Protein sequence
Protein Accession #: NP_000954

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TRIKLFLKPT PNTVHYILTH PKGFWNVVNN IPFLRNAIMS YVLTSRSLHI DSPPTYNADY 120
GYKSWFAFSN LSYVYTRALPP VPDDCPTPLG VKGKKQLPDS NEIVEKLLLR RKFPIDPQGS 180
NMFFAFAQH FTHQFFKTDH KRGPAFTNGL GHGVDLNIHY GETLARQRIK RLKFDGKMKY 240
10 QIIDGEMYP TVKDQAEML YPPQVPEHLR FAVGQEVFGL VPGLMMYATI WLRHNRVCD 300
VLKQEHPEWG DEQLFQTSRL ILIGETIKIV IEDYVQHLGS YHFKLKFDPE LLFNKQFQYQ 360
NRIAAEFNTL YHWHPLLFDI FQIHDQKYN YQFIYNNISL LEHGITQFVE SPTRQIAGRV 420
AGGRNVPPAV QKVSQASIDQ SRQMKYQSFN EYRKRFMLKP YSFERLTGE KEMSAEAL 480
15 YGDIDAVELY PALLVEKPRP DAIPGETWVE VGAPPSLKGL MGNVICSPAY WKPSTFGGEV 540
GFQIINTASI QSLICNNVKG CPFTSFSVPD PELIKTVTIN ASSRSGLDD INPTVLLKER 600
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Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: NM_001508.1
Coding sequence: 1..1361

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AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC 240
TTGGTGTTC TCATGGGCAT GCCATGGAG TTCTACAGCA TCATCTGGAA TCCCCTGACC 300
AGCTCCAGCT ACACCTCTGC CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC 360
30 GCTACGCTGC TGCACTGTCT GACGCTCAGC TTTGAGOGCT ACATCGCCAT CTGTACCCCC 420
TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTGCTCTGG 480
GTCACCTCCG CCTGTGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTTG 540
GTGAAGTGGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCAAGAG 600
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35 CAGTCCAGCA TCTTCGGCGC CTTGCTGGTC TACCTGCTGG TCCTGCTCTC CGTAGCCTTC 720
ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTGCTG GGCCTGGGGC 780
AOGCGGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
ACCATCATCT TCCTGAGGCT GATTGTGTG ACATTGGCCG TATGCTGGAT GCCCAACCAG 900
40 ATTGCGAGGA TCATGGCTGC GGCCAAACCC AAGCAGCACT GGACGAGGTC CTACTTCCGS 960
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CGCTCTCTGT ACACGGTGTG CTCGAGCAG TTTGCGCGGG TGTGCTGTGA GGTGCTGTGC 1080
TGCCGCTCTG CGCTGAGCA CGCCAAACCAG GAGAAGCGCC TGCGGTGACA TGCGCACTCC 1140
ACCAACGACA GCGCCGCTTT TGTGAGCGC CGGTGCTCT TCGCGTCCCG GCGCCAGTCC 1200
45 TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGACGAGGC CGAGCCCCAG 1260
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Seq ID NO: 34 Protein sequence
Protein Accession #: NP_001499.1

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50      1      11      21      31      41      51
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KGYLQKEVTD HMYSLACSDI LVFLIGMPME FYSLIWNPLT TSSYTLSCKL HTFLFEACSY 120
55 ATLLHVLTL FERYIAICHP FRYKAVSGPC QVKLLIGFVH VTSALVALPL LFAMGTEYPL 180
VNVPSRHLGT NCRSSRHHB QPETSNNMSIC TNLSSRWTFV QSSIFGAFVV YLVVLLSVAF 240
MCWNMQVLM KSQKGLAGG TRFPQLRKSE SEESRTARRQ TIIPLRLIIV TLAVCMFENQ 300
IRRIINAAPK KHDWTRSYFR AYMLLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFQVLK 360
60 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPO 420
SKSQSLSLSS LEPNSGAKPA NSAAENGFEV HEV

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Seq ID NO: 35 DNA sequence
Nucleic Acid Accession #: NM_006475.1
Coding sequence: 28..2538

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70 AGTCGTATCA GGGGTGCGGA CCAAGGCCCA AATGTCTGTG CCTTCAACA GATTTTGGGC 180
ACCAAAAAGA AATACTTFCG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG 240
AAAACGACTG TTTTATATGA ATGTTGCCCT GGTATATGA GAATGGAAGG AATGAAAGGC 300
TGCCAGCAG TTTTGCCCAT TGACCATGTT TATGGCACTC TGGCATGCT GGGAGCCACC 360
75 ACAACGCAGC GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATGAGGG AAAGGGATCC 420
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AAGAGATGT TGACCAAGGA CTTAAAAAAT GGCATGATTA TTCTTCAAT GTATAACAAT 600
TTGGGGCTTT TCAATTAACA TTATCCTAAT GGGGTGTGCA CTGTTAATTG TGCTCGAATC 660
80 ATCCATGGGA ACCAGATTGC AACAAATGGT GTTGCCATG TCATTGACOG TGTGCTTACA 720
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GCAGCTGCCA TCACATGGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTCACTC 840
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GGAGACAAG TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
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GGATGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGGTGAACAA AAAGGATATT 1080
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 GACACACCTG TTGGAATAGA TCAACTGCTG GAAATACCTA ATAAATTAAT CAAATACATC 1980
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 ACAGAAAGAA ATCTGAAGAA ATTGTTACAA GAAGAGGTCA CCAAGGTGAC CAAATTCATT 2400
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 CACCTCTGAC CCTTTTTCAT CTGACATTA AAGTTCTGG CTAATCTTGG AATCCATTAG 2820
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 CCATTGAAAA GACGAGACCT TGTATGTATG TTATGGATAC ATAAATGCA CGCAAGCCAT 2940
 TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA 3000
 TCAAAAGGCT TTGCACATTT CTATATGAGT GGGTTTACTG GTAAATATATG TTATTTTTTA 3060
 CAACTAATTT TGTACTCTCA GAATGTTTGT CATATGCTTC TTGCAATGCA TATTTTTTAA 3120
 TCTCAACGTT TTCAATAAAA CCATTTTCCA GATATAAAGA GAATTACTTC AAATTGAGTA 3180
 ATTCAGAAAA ACTCAAGATT TAAGTTAAAA AGTGGTTTGG ACTTGGGAA

Seq ID NO: 36 Protein sequence
 Protein Accession #: NP_006466.1

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 50
 55

1 11 21 31 41 51
 MIPFLPMFSL LLLLLIVNPIN ANNHYDKILA HSRIRGRDQG FNVCALQOIL GTKKCYFSTC 60
 KNWYKKSICG QKTTVLVECC PGYMRMEGKM GCPAVLPIDH VYGTGLGIVGA TTTQRYSDAS 120
 KLREEIEGKG SFTYFAPSNE AWDNLDSDIR RGLSENVNVE LNLALHSHMI NKRMLTKDLK 180
 NGMIIPSMYN NLGLFINHYF NGVVTVNCAR IIHGNQIATN GVHVHIDRVL TQIGTSIQDF 240
 IEAEDLSSF RAAAITSDIL EALGRDGHFT LFAPTNEAPE KLRPGVLERF MGDKVASEAL 300
 MKVHILNLTQ CSESIMGAV FETLEGNTIE IGCDDGSITV NGIKMVNKKD IVTNNGVIHL 360
 IDQVLIPDSA KQVIELAGKQ QTTFTDLVAQ LGLASALRPD GEYTLAPFVN NAFSDTLMS 420
 VQRLKLLIQ NHLLKRVGL NELYNGQILE TIGGKQLEVP VYRTAVCIEN SCMEKGSKQG 480
 RNGAIIHIFR IIKLPAEKSLH EKLKQDKRFS TFLSLLBAAD LKELLTQPGD WTLFVPTNDA 540
 FKGMTSEEEK ILIRDKNALQ NIILYHLTPG VFIRGFEPEP VTINILKFTQG SKIFLKEVND 600
 TLLVNELKSK ESDIMTNGV IHVVDKLLYP ADTPVGNQDL LEILNKLKLY IQIKFVRGST 660
 FKEIPVTYVT TKIITKVVEP KIKVIEGSLQ PIKTEGPTL TKVKIEGPEE PRLIKEGETI 720
 TEVHIEGPII KVIYKIDGV PVEITEKETR BERIITGPEI KYTRISTGGG ETEBTLKELL 780
 QREVTKVTFK IEGGDHLPB DBEIKRLQGG DTPVRKLQAN KKVQGSRRRL REGRSQ

60
 Seq ID NO: 37 DNA sequence
 Nucleic Acid Accession #: NM_002416
 Coding sequence: 40..417

65
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 75
 80

1 11 21 31 41 51
 ATCCAATACA GGAGTGACTT GGAACCTCCAT TCTATCACTA TGAAGAAAAG TGGTGTCTCT 60
 TTCCTCTTGG GCATCATCTT GCTGGTTCTG ATTGGAGTGC AAGGAACCCC AGTAGTGAGA 120
 AAGGGTGGCT GTTCTGTCAT CAGCACCAAC CAAGGAGCTA TCCACCTACA ATCCTTGAAA 180
 GACCTTAAAC AATTTGCCCC AAGCCCTTCC TGGAGAAAAA TTGAAATCAT TGTCTACTG 240
 AAGAATGGAG TTCAAAACATG TCTAAACCCA GATTGAGCAG ATGTGAAGGA ACTGATTAAA 300
 AAGTGGGAGA AACAGGTCAG CCAAAAGAAA AAGCAAAAGA ATGGGAAAAA ACATCAAAAA 360
 AAGAAGGTTT TGAAGTTTCG AAAATCTCAA CGTTCTGCTG AAAAGAAAGC TACATAAGAG 420
 ACCACTTCAC CAATAAGTAT TCTGTGTTAA AAATGTTCTA TTTTAATTAT ACCGCTATCA 480
 TTCCAAGGGA GGATGGCATA TAATACAAAG GCTTATTAAAT TTGACTAGAA AATTTAARAC 540
 ATTACTCTGA AATTGTAACT AAAGTTAGAA AGTTGATTTT AAGAATCCAA ACGTTAAGAA 600
 TTGTTAAAGG CTAATGATTGT CTTGTGTTCT CTACCAACCA CCAGTTGAAT TTCAATCATG 660
 TTAAGGCCAT GATTTTAGCA ATACCCATGT CTACACAGAT GTTCAACCAA CCACATCCCA 720
 CTCACAACAG CTGCTCGGAA GAGCAGCCCT AGGCTTCCAC GTACTGCAGC CTCAGAGAG 780
 TATCTGAGGC ACATGTGAGC AAGTCTTAAG CCGTTGAGCA TGCTGTGTAG CCAAGCAGTT 840
 TGAATGGAG CTGAAGCTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC 900
 CTACAGGCT CACACACAA GTGTCTGAGA GATTCTGCT GATTGTTATT GGGTATCACC 960
 ACTGGAGATC ACCAGTGTGT GGCTTTTCAA GCCTCTTTTC TGGCTTTGGA AGCCATGTGA 1020
 TTCCATCTTG CCGGCTCAGG CTGACCACTT TATTCTTTT TGTTCCTCTT TGCTTCAATC 1080
 AAGTCAGCTC TTCTCCATCC TACCACAATG CAGTGCTTTT CTCTCTTCCA GTGCACCTGT 1140
 CATATGCTCT GATTTATCTG AGTCAACTCC TTTCTCATCT TGTCCCCAAC ACCCCACAGA 1200

5 AGTGCTTTCT TCTCCCAATT CATCCTCACT CAGTCCAGCT TAGTTCAAGT CCTGCCTCTT 1260
 AAAATAAACCT TTTTGGACAC ACAAAATTATC TTAATACTOC TGTTCACCTT GGTTCAGTAC 1320
 CACATGGGTG AACACTCAAT GGTAACTAA TTCTTGGGTG TTTATCCTAT CTCTCCAACC 1380
 AGATTGTGAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCTGTGTTCT TCCACAGTGC 1440
 CTAATAATAC TGTGGAACCT GGTTTTAATA ATTTTAAAT TGATGTTGTT ATGGGCAGGA 1500
 TGGCAACCCG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG 1560
 CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCACTACAGG GACCAAGGAT 1620
 GATGCAACAT CCTGTCTTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680
 GCACGTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740
 10 AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800
 CCAACCATAC AAAAATTCCT TTTCCCGAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT 1860
 TCTAAGATCT AACAGATAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAAAATATG 1920
 AGTTTATTG TCCGTTTACT TGTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA 1980
 TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040
 15 TAGTGAAGC ATGATTGGTG CCCAGTTAGC CTCGACAGGA TGTGGAAACC TCCTTCCAGG 2100
 GGAGGTCAG TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTAAAA CCTATACTCA 2160
 CTTTCCCAA TTGAATCACT GCTCACACTG CTGATGATTT AGAGTGCTGT CCGGTGGAGA 2220
 TCCCACCCGA ACGTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280
 AAAAATCTAA GTGTTTCATA AATTTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340
 20 GTAGACAGTA TATAACTAAC AACCAAAGAC TACATATTGT CACTGACACA CAGTTATAAA 2400
 TCAATTATCA TATATATACA TACATGCATA CACTCTCAAA GCAAAATATT TTTCACTTCA 2460
 AAACAGTATT GACTTGTATA CCTGTAAAT TGAAATATTT TCTTTGTTAA AATAGAATGG 2520
 TATCAATAAA TAGACCATTA ATCAG

25 Seq ID NO: 38 Protein sequence
 Protein Accession #: NP_002407

30 1 11 21 31 41 51
 MKKSGVLFLL GIILLVLIGV QGTFVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK 60
 IEIIATLXNG VQTCLNPDAS DVKELIKKWE KQVSQKKQK NGKHKQKKV LKVRKSQRSR 120
 QKKTT

35 Seq ID NO: 39 DNA sequence
 Nucleic Acid Accession #: NM_006670
 Coding sequence: 85..1347

40 1 11 21 31 41 51
 CGSGCTCGCG CCTCCGGGCG CAGCCTTCCC GAGCCTTCGG AGCGGGGCGC GTCCAGAGCC 60
 AGCTCCGGGG AAACCGGAGC CGCGATGCCT GGGGGGTGCT CCCGGGGGCC CGCGCCGGGG 120
 GACGGGCGCT TCGGGCTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCTCGTCT 180
 TCTCCCACTT CCTCGGCATC CTCTTCTCC TCCTCGGCGC CGTTCCTGGC TTCCGCGGTG 240
 TCGGCCAGCG CCGCGCTGCC GGAACAGTGC CCGCGCTGT GCGAGTGCTC CGAGGCAGCG 300
 45 CGCACAGTCA AGTGGGTTAA CGCAATCTG ACGAGGTGC CCAACGACCT GCCCGCTAC 360
 GTGCGCAACC TCTTCTTAC CGGCAACCAG CTGGCCGTGC TCCCTGCGCG CGCCTTGGCC 420
 CGCCGCGCGC CGCTGGCGGA GCTGGCCGCG CTCAACCTCA GCGGCAGCGC CTGGGAGGAG 480
 GTGCGGCGCG GCGCCTTCCA GCATCTGCCC AGCCTGCGCC AGCTCGACCT CAGCCACAAC 540
 CCACTGGCGG ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGGCT CTGCGCCCCC 600
 50 AGTCCCTTTC TGAACCTGAT CCTGAACCAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC 660
 CGGAGCTTCG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCGGTGCACT GCAGGGGCTC 720
 CGCGCTTCGG AGCTGGCCAG CAACCACTTC CTTTAACCTG CCGCGGATGT GCTGGCCCCA 780
 TCGCCCTGGG TCAGGGCACCT GGACTTAAGT AATAATTGCG TGGTGAGCCT GACCTACGTG 840
 TCCTTCGCGA ACCTGACACA TCTAGAAAGC CTCCAACCTG AGGACATGCT CCTCAAGGTC 900
 55 CTTCACAATG GCACCTTGGC TGAATTGCAA GGTCTACCCC ACATTAGGCT TTTCTGGAC 960
 AACAAATCCCT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAACA 1020
 GAGGTAGTGC AGGCGAAGA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080
 GTCTCTTGG AACCTAACAG TGCTGACCTG GACTGTGACC AGATTCTTCC CCACTCCCTG 1140
 CAAACCTCTT ATGCTTCTCT GGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCTCTG 1200
 60 GTTTTGATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCTGC 1260
 AGGATCACCA TGGAAAGGTA TCATTACAGA TATGAAATCA ATGCGGACCC CAGATTAACA 1320
 AACCTCAGTT CTAACCTCGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG 1380
 CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
 65 TAGATACAC GGACTTTGAC TAAAAGCAGT GAAGGGGATT TGCTTCTTGT TTAGTAAAG 1500
 TTTCTCGGTG TGTCTGTGTA ATGTAAGAGC ATGAACAGTT GTGTATAGTG TTTTACCTCT 1560
 TTCTTTTCT TGGAACTCCT CAACAAGTAT GGAGGGATTT TTCAGGTTTC AGCATGAACA 1620
 TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
 ACAGATAGCA TTCAACAAAA GCTGCCTCAA CTTTTCGAG AAAAAACTT TATTATATAA 1740
 70 TATCAGTTTT ATTCTCATGT ACCTAAGTGG TGGAGAAAAA AATTGCATCC TATAAACTGC 1800
 CTGCAGACGT TAGCAGGCTC TTCAAAATAA CTCCATGGTG CACAGGAGCA CCTGCATCCA 1860
 AGAGCATGCT TACATTTTAC TGTCTGTCAT ATTACAAAAA ATAACCTTGA ACTTCATAAC 1920
 TTTCTTGACA AAGTAAATTA CTTTITTGAT TGCACTTTAT ATGAAATGT ACTGATTTT 1980
 75 TTTTAATAAA CTCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040
 ATCTTAAAA GAA

80 Seq ID NO: 40 Protein sequence
 Protein Accession #: NP_006661

1 11 21 31 41 51
 MPGGCSRGP AGDGRLELR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPLPLD 60
 QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLAVLPAGA FARRPPLAEL 120
 AALNLSGSR LDEVRAQFEH LPSLRQLDLS HNLADLSPP APGSGNASVS APSPLVELIL 180
 NHIVPPEDER QNRSPEGMVV AALLAGRALQ GLRRLASLN HFLYLPDVL AQLPSLRHLD 240

LSNNSLVSLT YVSPRNLTSL ESHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWCDC 300
 HMADMVTLWK ETEVVQKDR LTCAYPERMR NRVLLELNSA DLDGDPILPP SLQTSYVPLG 360
 IVLALIGATF LLVLYLNRKG IKKMMENIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

5

Seq ID NO: 41 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..927

10 1 11 21 31 41 51
 | | | | | |
 ATGCTGCGGG GGTGCTCCCG GGGCCCCGCC GCGGGGACG GGGGTCTGCG GCTGGGCGGA 60
 CTAGCGCTGG TACTCCTGGG CTGGGTCTCC TCGTCTTCTC CCACCTCCTC GGCACTCCTC 120
 TTCTCCTCCT CGGCGCCGTT CTGGGCTTCC GCGGTGTCCG CCCAGCCCCC GCTGCCGGAC 180
 CAGTGCCCGG CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC 240
 15 AATCTGACCG AGGTGCCCCA GGACCTGCCC GCCTACGTGC GCAACCTCTT CCTTACCGGC 300
 AACCAGCTGG CCAGCAACCA CTTCCTTTAC CTGCCGCGGG ATGTGCTGGC CCAACTGCCC 360
 AGCCTCAGCG ACCTGGACTA AAGTAATAAT TCGCTGGTGA GCCTGACCTA GGTGTCCTTC 420
 CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCTCTCAC 480
 AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCACATTA GGGTTTTCCT GGACAACAAT 540
 20 CCCTGGGTCT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA 600
 GTGCAGGGCA AAGACCGGCT CACCTGTGCA TATCCGGAAG AAATGAGGAA TCGGGTCTCT 660
 TTGGAATCA ACAGTGACTG CCTGGAATGT GACCCGATTC TTCCCTCATC CTGCAAAACC 720
 TCTTATGTCT TCCTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTTCCT CCTGGTTTGT 780
 TATTTGAACC GCAAGGGGAT AAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT 840
 25 CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900
 AGTTCTAACT CGGATGTCTT CGAGTGA

30

Seq ID NO: 42 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | | |
 MPGGCSRGPFA AGDGRRLRLAR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD 60
 35 QCPALCEBCE AARTVKCVNR NLTEVPTDLP AYVRNLFLTG NQLASNHFLY LPRDVLALPL 120
 SLRHLDSLNN SLVSLTYVSF RNLTHLESLH LEDNALKVLH NGTLAELOGL PHIRVPLDNN 180
 PMVCDCHMAD MVTWLKETEV VQKDRILTCA YPEKMRNRVL LELNSADLDC DPILPPSLQT 240
 SYVFLGIVLA LIGAIPLVLV YLNRKGIKKW MENIRDACRD HMEGYHYRYE INADPRLTNL 300
 SSNSDVLBE

40

Seq ID NO: 43 DNA sequence
 Nucleic Acid Accession #: NM_058173
 Coding sequence: 68..340

45 1 11 21 31 41 51
 | | | | | |
 AGCGCCTTGC CTTCCTTAGT GCTTTGAAGC ATTTTGTGCT GTGCTCCCTG ATCTTCAGGT 60
 CACCACCATG AAGTTCTTAG CAGTCTCTGT ACTCTTGGGA GTTTCCATCT TTCTGGTCTC 120
 TGCCCAAGAT CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCTGCTGTA 180
 50 TGATGAAGCC CCGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC 240
 TACCACCTGA ACCACCGCTG CTCTTACCAC TGCTGTGAAA GACATTCCAG TTTTACCCAA 300
 ATGGGTGGGG GATCTCCCGA ATGGTAGAGT GTGTCCCTGA GATGGAATCA GCTTGAGTCT 360
 TCTGCAATTG GGTCACAACT ATTCACTGCT CCGTGATATT CATCCAATA CTTACCTTGC 420
 CTAGATATAC CCCTTTATCT CTAATCAGTT TATTTTCTTT CAAATAAAAA ATAACATGA 480
 55 GCGAGCTAAC AT

55

Seq ID NO: 44 Protein sequence
 Protein Accession #: NP_477521

60 1 11 21 31 41 51
 | | | | | |
 MKFLAVLVLL GVSIFLVSAQ NPPTAAPADT YPATGPADDE APDAETTAAA TTATTAAPT 60
 ATTAASTIAR KDIFVLPKWV GDLPNGRVCP

65

Seq ID NO: 45 DNA sequence
 Nucleic Acid Accession #: NM_000095.1
 Coding sequence: 26..2299

70 1 11 21 31 41 51
 | | | | | |
 CAGCACCCAG CTCCCGGCCA CGGCATGGT CCCGACACC GCCTGCGTTC TTCTGCTCAC 60
 CTGCGCTGCC CTGGGGCGGT CGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCCC 120
 GCAGATGCTT CGGGAACGTC AGGAAACCAA CGCGCGCGTG CAGGACGTGC GGGACTGGCT 180
 GCGGCAGCAG GTCCAGGAGA TCACGTTCTT GAAAAACAG GTGATGGAGT GTGACGCGTG 240
 75 CGGGATGAGC CAGTCACTAC GCACCGGCTT ACCCAGCGTG CGGCGCTGTC TCCACTGGCG 300
 GCGCGGCTTC TGCTCCCGCG GCGTGGCGTG CATCCAGACG GAGAGCGGCG GCGCTGCGG 360
 CCCTGCCCC CGGGGCTTCA CGGGCAACGG CTCGCACTGC ACGACGTCA ACGAGTGCAA 420
 CGCCACCCC TGCTCCCGCG GAGTCCGCTG TATCAACACC AGCCCGGGGT TCGCTGCGA 480
 GGCTTGCCCG CGGGGTGACA GCGGCCCCAC CCACAGGGC GTGGGGCTGG CTTTGGCCAA 540
 80 GGCCACACAG CAGGTTTGCA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAACCTGGT 600
 CCCCACTCC GTGTGATCA ACACCGGGG CTCCCTCCAG TGGGCGCGT GCCAGCCGG 660
 CTTGCTGGCG GACCAAGCGT CGGGTGCCA GCGGGGCGCA CAGCGCTTCT GCCCGACGG 720
 CTGCCCCAGC GAGTGCCACG AGCATGCAGA CTGCGTCTTA GAGCGCATG GCTGCGGCTC 780
 GTGCGTGTGT CGCGTTGGCT GGGCGGCAA CGGGATCCTC TGTGTCGCG ACACCTGACCT 840
 AGACGGCTTC CGGACGAGA AGCTGCGCTG CCGGAGCGG CAGTGCCGTA AGGACAACTG 900

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CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACGGC GATGGCATCG GAGACGGCTG 960
CGATCCGGAT GCCGACGGGG ACGGGGTCCC CAATGAAAAG GACAACTGCC CGCTGGTGGC 1020
GAACCCAGAC CAGCGCAACA CGGACGAGGA CAAGTGGGGC GATGGGTGGC ACAACTGGCG 1080
GTCCCAAGAG AACGACGACC AAAAGGACAC AGACCAGGAC GGCCGGGGCG ATGCGTGCGA 1140
CGACGACATC GACGGCGACC GGATCCGCAA CCAGGCGGAC AACTGCCCTA GGGTACCCAA 1200
CTCAGACCAAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCCA 1260
GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG 1320
CGATCAAGAC CAGGATGGAG ACGGACATCA GGAATCTCGG GACAACTGTC CACGGTGCC 1380
TAACAGTGCC CAGGAGGACT CAGACCAAGA TGGCCAGGGT GATGCCTGGC ACGACGAAGA 1440
CGACAATGAC GAGTCCCTG ACAGTCCGGA CAATGCGCGC CTGGTGCTTA ACCCGGCCA 1500
GGAGGACGGG GACAGGGAAG GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
GGTGTAGAC AAGATCGAGC TGTGTCCGGA GAACTGTGAA GTCACTGCTA CCGACTTCAG 1620
GGCCTTCCAG ACAGTCCGTC TGGACCCGGA GGGTGAACCG CAGATTGACC CCACTGGGT 1680
GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAAATGAA AGCGACCCAG GCCTGGCTGT 1740
GGGTTCATC GCGTCCACTT CGAGGGCAAG TTCCATGTGA ACACGGTCA 1800
GGATGACGAC TATCGGGCTT TCATCTTTGG CTACCCAGGAC AGCTCCAGCT TCTACGTGGT 1860
CATGTGGAAG CAGATGGAGC AAAAGTATTG GCAGGCGAAC CCCTTCCGTG CTGTGGCCGA 1920
GCCTGGGATC CAATCAAGG CTGTGAAGTC TTCCACAGGC CCGGGGGAAC AGCTGGGAA 1980
CGCTCTGTGG CATAACAGG ACACAGAGTC CCAGGTGGGG CTGCTGTGGA AGGACCCGG 2040
AAACGTGGGT TGGGAAGACA AGAAGTCTTA TCGTTGGTTC CTGCAGACCC GGCCCAAGT 2100
GGGCTACATC AGGCTGCGAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT 2160
CTTGGACACA ACCATGGGGG GTGGCCGCGT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT 2220
CATCTGGGCC AACCTGGCTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
TCAGCTGGGG CAAGCCTAGG GACCAAGGGT AGGACCCGCC GGATGACAGC CACCTCACC 2340
GCGCTGGAT GGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCTGAGG GGGAAGTGAG 2400
AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGGG
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Seq ID NO: 46 Protein sequence
Protein Accession #: NP_000086.1

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1 11 21 31 41 51
| | | | |
MVPDTCALL LTLAALGASG QGQSPILGSDL GPQMLRELQE TNAALQDVVD WLRQVREIT 60
PLKNTVMEDC ACGMQQSVRT GLPSVRPLLH CAPGFCPPGV ACIQTESGGR CGPCPAGFTG 120
NGSHCTDVNE CNAHPCFFRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
INECTVQHVN CVPNSVCINT RGSFQCGPQ PGFVGDAQSG CQRGAQRFCP DGSFSSCHEH 240
ADCVLERDGS RSCVCRVWGA GNGILCGRDT DLGPPDEKL RCPEPQCRKD NCVTVPNSGQ 300
EDVDRDGIID ACDPDDADGG VPNEKDNCPV VRNPDQRNTD EDKWDACDN CRSQKNDQK 360
DTDQDGRGDA CDDIDIGDRI RNQADNCPRV PMSDQKSDSG DGIQDADNDC FQKSNPDQAD 420
VDHDFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDMDGVFDS 480
RDNCRLLVFN QGEDADRDGV GDVCQDDPDA DKVVDKIDVC PENAEVLTLD FRAFTVVLID 540
PEGDAQIDPN WVVLNQGREI VQTMNSDPLG AVGYTAFNGV DFEGTFHVNT VTDDYAGFI 600
FGYQSSSFY VVMWQMEQY YWQANPPRAV AEPGIQLKAV KSSTGPEQL RNALWHTGDT 660
ESQVRLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRPY EGPELVADSN VVLDTTMRGG 720
RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA
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Seq ID NO: 47 DNA sequence
Nucleic Acid Accession #: NM_001565.1
Coding sequence: 67..363

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1 11 21 31 41 51
| | | | |
GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCAGTCTC 60
AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCCTA TCTTCTGAC TCTAAGTGGC 120
ATCAAGAGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
CTGTGTAATC CAAGGTCTTT AGAAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
CGTGTGTAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
TCGAAGGCCA TCAAGAAATT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360
TAAACCAGGA GGGGAGCAAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTC TTAGTTTGCA 480
GTCACTATAA AAGGTGACCA ATGATGGTCA CCAATCAGC TGCTACTACT CCTGTAGGAA 540
GGTTAATGTT CATCATCTTA AGCTATTCTG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
GCTCTACTGA GGTGCTATGT TCTTAGTGGG TGTCTGACC CTGCTTCAAA TATTTCCTC 660
ACCTTCCCA TCTTCCAAGG GTACTAAGGA ATCTTCTGCG TTTGGGGTTT ATCAGAATTC 720
TCAGAATCTC AAATAACTAA AAGGTATGCA ATCAAACTCG CTTTATAAAG AATGCTCTT 780
ACTTCAATGA CTTCCTATGC CATCTCCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA 840
CATACAATTC CAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT 900
CTTATTATAT GAAAGACTGT ACAGAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT 960
TTTCAGTGTA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
TTTTCAATAA AAAATGAGGT ACTCTCCTGG AAATATTAAG
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Seq ID NO: 48 Protein sequence
Protein Accession #: NP_001556.1

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80

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1 11 21 31 41 51
| | | | |
MNQTAILICC LIFLTLGSIQ GVPLSRTVRC TCISISNPV NPSLEKLEI IPASQFCPRV 60
EIIATMKKKG EKRLNPKESK AIKNNLLKAVS KEMSKRSP
```

Seq ID NO: 49 DNA sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..874

	1	11	21	31	41	51	
	GGGAGGGAGA	GAGGCGGCGG	GGTGAAGGCC	GCATTGATGC	AGCCTGCGGC	GGCCTCGGAG	60
	CGCGGCGGAG	CCAGACGCTG	ACCAAGTTCC	TCTCTCGGT	CTCCTCGGC	TCCAGCTCGG	120
5	CGCTGCCCGG	CAGCCGGGAG	CCATGCGACC	CCAGGGCCCC	CGCGCTCCC	CGCAGCGGCT	180
	CGCGGGCCTC	CTGCTGCTCC	TGCTGCTGCA	GCTGCCCGCG	CGCTCGAGCG	CCTCTGAGAT	240
	CCCCAAGGGG	AAGCAAAAGG	CGCAGCTCCG	GCAGAGGGAG	GTGGTGGACC	TGTATAATGG	300
	AATGTGCTTA	CAAGGGCCAG	CAGGAGTGCC	TGGTCGAGAC	GGGAGCCCTG	GGGCCAATGG	360
	CATTCCGGGT	ACACCTGGGA	TCCCAGGTCG	GGATGGATTC	AAAGGAGAAA	AGGGGGAATG	420
10	TCTGAGGGAA	AGCTTTGAGG	AGTCCTGGAC	ACCCAACTAC	AAGCAGTGTT	CATGGAGTTC	480
	ATTGAATTAT	GGCATAGATC	TTGGGAAAAT	TGCGGAGTGT	ACATTTACAA	AGATGCGTTC	540
	AAATAGTGCT	CTAAGAGTTT	TGTTCACTGG	CTCACTTCGG	CTAAAATGCA	GAAATGCATG	600
	CTGTACGCGT	TGTTATTTC	CATTCAATGG	AGCTGAATGT	TCAGGACCTC	TCCCATTGA	660
	AGCTATRAAT	TATTTGGACC	AAGGAAGCCC	TGAAATGAAT	TCAACAATTA	ATATTTCATG	720
15	CACCTCTTCT	TGGGAAGGAC	TTTGTGAAGG	AATTGGTGCT	GGATTAGTGG	ATGTTGCTAT	780
	CTGGGTGGGC	ACTTGTTCAG	ATTACCCAAA	AGGAGATGCT	TCTACTGGAT	GGAAATCAGT	840
	TTCTCGCATC	ATTATTGAAG	AACCTACCAA	ATAAATGCTT	TAATTTTCAT	TTGCTACCTC	900
	TTTTTTTATT	ATGCCTTGGG	ATGGTTCAC	TAAATGACAT	TTTAAATAAG	TTTATGTATA	960
	CATCTGAATG	AAAAGCAAAG	CTAAATATGT	TTACAGACCA	AAGTGTGATT	TCACACTGTT	1020
20	TTTAAATCTA	GCATTATTCA	TTTGTCTTCA	ATCAAAAGTG	GTTCATATAT	TTTTTTTATG	1080
	TGGTTAGAAT	ACTTCTCTCA	TAGTCACATT	CTCTCAACCT	ATAATTTGGA	ATATTGTTGT	1140
	GGTCTTTTGT	TTTTCCTCTT	AGTATAGCAT	TTTTAAAAAA	ATATAAAGC	TACCAATCTT	1200
	TGTACAATTT	GTAATGTGTA	AGAATTTTTT	TTATATCTGT	TAAATAAAAA	TTATTTCCAA	1260
25	CAACCTTAAA	AAAAAAAAAA	AAAA				

Seq ID NO: 50 Protein sequence
Protein Accession #: XP_057014

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	MRPQGAASP	QRLRGLLLLL	LLQLPAPSSA	SEIPKKGKKA	QLRQREVVDL	YNGMCLQGPA	60
	GVPRGRDSPG	ANGIPGTPI	PGRDGFKEK	GECLRESFEE	SWTPNYKQCS	WSSLNYGIDL	120
	GKIAECTFTK	MRSNSALRVL	FSGSLRLKCR	NACQQRWYFT	FNGAECSGPL	PIEALIIYLDQ	180
35	GSPEMNSTIN	IHRTSSVEGL	CEGIGAGLVD	VAIWVGTCS	YPKGDASTGW	NSVSRIIIIE	240
	LPK						

Seq ID NO: 51 DNA sequence
Nucleic Acid Accession #: NM_020974
Coding sequence: 81..3080

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45	CGGTGCTGCT	GCTGCTGCTG	CTGCTGCCCG	CACCTGCTGCT	GCTGGCGGGG	GCGTCCCGGC	180
	CGGGTCCGGG	CGGTGCGCGG	GGGCGCGAGG	AGGATGTAGA	TGAGTGTGCC	CAAGGGCTAG	240
	ATGACTGCCA	TGCCGACGCC	CTGTGTGAGA	ACACACCCAC	CTCTTACAAG	TGCTCTGCA	300
	AGCCTGGCTA	CCAAGGGGAA	GGCAGGCAGT	GTGAGGACAT	CGATGAATGT	GGAAATGARG	360
	TCAATGAGAG	CTGTGTCCAT	GACTGTITGA	ATATTCCAGG	CAATTATCGT	TGCACTTGTT	420
50	TTGATGGCTT	CATGTGGGCT	CATGACGCTC	ATAATTGTCT	TGATGTGGAC	GAGTGCTGCT	480
	AGAACCAATG	CGCGTCCGAG	CATACCTGTG	TCAACGTCAT	GGGGAGCTAT	GAGTGTGCT	540
	GCAAGAGAGG	GTTTTCCTCT	AGTGACAATC	AGCACACCTG	CATTACCCGC	TGGAAGAGGG	600
	GCCTGAGCTG	CCAGAAATAG	GATCAACGCT	GTAGTCACAT	CTGCAAGGAG	GCCCCAAGGG	660
	GCAGCGTCCG	CTGTGAGTGC	AGGCCTGGTT	TTGAGCTGGC	CAAGAAACCG	AGAGACTGCA	720
55	TCTTGACCTG	TAACCATGGG	AACGGTGGGT	GCCAGCACTC	CTGTGACGAT	ACAGCCGATG	780
	GCCCAGAGTG	CAGCTGCCAT	CCACAGTACA	AGATGCACAC	AGATGGGAGG	AGCTGCCTTG	840
	AGGAGAGGGA	CAGTGTCTCT	GAGGTGACAG	AGAGCAACAC	CACATCAGTG	GTGGATGGGG	900
	ATAAAGCTGT	GAAACGGCGG	CTGCTCATGG	AAACGTGTGC	TGTCAACAAT	GAGGAGCTGT	960
	ACCGCACCTG	TAAGGATACT	TGACAGGTG	TCCACTGCAG	TTGTCTGTTT	GGATTCACTC	1020
60	TCCAGTTGGA	TGGGAAGACA	TGTAAAGATA	TTGATGAGTG	CCAGACCCGC	AATGGAGGTT	1080
	GTGATCATTT	CTGCAAAAAC	ATCGTGGGCA	GTTTGTACTG	CGGCTGCCAG	AAAGGATTTA	1140
	AATTTATTAAC	AGATGAGAAG	TCTTGCCAAG	ATGTGGATGA	GTGCTCTTTG	GATAGGACCT	1200
	GTGACCAACG	CTGCATCAAC	CACCTGGSCA	CATTGCTTGG	TGCTTGCAAC	CGAGGGTACA	1260
65	CCCTGTATGG	CTTCACCCAC	TGTGGAGACA	CCAATGAGTG	CAGCATCAAC	AACGGAGGCT	1320
	GTGAGCAGGT	CTGTGTGAAC	ACAGTGGGCA	GCTATGAATG	CCAGTGCCAC	CCTGGGTACA	1380
	AGCTCCACTG	GAATAAAAAA	GACTGTGTGG	AAGTGAAGGG	GCTCTGCCCC	ACAAGTGTGT	1440
	CACCCGCTGT	GTCCCTGCAC	TGCGGTAAAG	GTGGTGGAGG	AGACGGGTGC	TTCTCTCAGT	1500
	GTCACTCTGG	CATTACCTCT	TCTTCAGATG	TCACCAACAT	CAGGACAAGT	GTAACCTTTA	1560
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	GCAGCTCTGG	CAAGCAAGTG	CCAGGAGCCC	CTGGCCGACC	AAGCAACCCCT	AAGGAAATGT	1740
	TTATCAGTGT	TGAGTTTGGG	CTTGAAACTA	ACCAAAAGGA	GGTGACAGCT	TCTTGTGACC	1800
	TGAGCTGCAT	CGTAAAGCGA	ACCGAGAAGC	GGCTCCGTAA	AGCCATCCGC	ACGCTCAGAA	1860
75	AGGCGGTCCA	CAGGAGGCAG	TTTCACCTCC	AGCTCTCAGG	CATGAACCTC	GAGTGGGCTA	1920
	AAAAGCCTCC	CAGAACATCT	GAAACGCCAG	CAGAGTCCCTG	TGAGTGGGCG	CAGGGTCAATG	1980
	CAGAAAACCA	ATGTGTGAGT	TGCAGGGCTG	GGACCTATTA	TGATGGAGCA	CGAGAACGCT	2040
	GCATTTTATG	TCCAAATGGA	ACCTTCCAAA	ATGAGGAAGG	ACAAATGACT	TGTGAACCAT	2100
	GCCCAAGACC	AGGAAATCTT	GGGGCCCTGA	AGACCCAGAA	AGCTTGGAAAT	ATGTCTGAAT	2160
80	GTGGAGGTCT	GTGCAACCTT	GGTGAATATT	CTGCAGATGG	CTTTGCACCT	TGCCAGCTCT	2220
	GTGCCCTGGG	CAGGTTCCAG	CCTGAAGCTG	GTCGAACCTC	CTGCTTCCCC	TGTGGAGGAG	2280
	GCCTTGGCCAC	CAAAACATCAG	GGAGCTACTT	CCCTTCAGGA	CTGTGAAACC	AGAGTTCAAT	2340
	GTTCACTCTG	ACATTTCTAC	AACACCAACA	CTCACCGATG	TATTCGTTGC	CCAGTGGGAA	2400
	CATACAGGCC	TGAATTTGGA	AAAAATAATT	GTGTTTCTTG	CCCAGGAAAT	ACTACGACTG	2460
	ACTTTGATGG	CTCCACAAAC	ATAACCCAGT	GTAAAAACAG	AAGATGTGGA	GGGAGCTGG	2520

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 CAAGAGGGGA GGAAGAGAGA CCCCTGCAGG CTCCCTCCAC CCACTCTGAG ACCTGGGAGG 3600
 ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACCTG 3660
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 AGCACCTCTG GAGACAT

Seq ID NO: 52 Protein sequence
 Protein Accession #: NP_066025

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1 11 21 31 41 51
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 HDGHNCLDLD ECLENNNGGQ HTCVNVMSY ECCKEGFFL SDNQHTCIHR SEEGLSMNMK 180
 DHGCSHICKE APRGSVACEC RPFELAKNQ RDCILTCNHG NGGQHSODD TADGPECSC 240
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 PEAGRTSCFP CGGLATKHQ GATSPQDCET RVQCSPGHFY NTTTHRCIRC PVGTQYQBEF 780
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 PPPKRRILIV VPEIFLPIED DQGDYLVMRK TSSSNSVTYI ETCQTYERPI AFTSRSKLW 900
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Seq ID NO: 53 DNA sequence
 Nucleic Acid Accession #: NM_014211
 Coding sequence: 157..1479

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65
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75
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1 11 21 31 41 51
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 TTCTGTGTCT TGAGTCTCTT CACTGAGAGG ATGTGCTATC AGGGGAGTCA GTTCAACGTC 240
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 ATTGCAAGTA TCTCTAGCAT TTCAGAGAGT AACATGGACT ACACAGCCAC CATATACTCT 420
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25 Seq ID NO: 54 Protein sequence
 Protein Accession #: NP_055026

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40 Seq ID NO: 55 DNA sequence
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 Coding sequence: 138..2405

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20 Seq ID NO: 56 Protein sequence
 Protein Accession #: XP_084007

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 SVSASEVTST VINTVSEBTH FLETIETPRP GLFPKDVSS STPPSVTSKS RVSRLAGRKT 240
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 Protein Accession #: NP_056234.1

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Seq ID NO: 66 Protein sequence
Protein Accession #: AAH10423

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Nucleic Acid Accession #: NM_001203
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Seq ID NO: 68 Protein sequence

Protein Accession #: NP_001194

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TNEVDIPNT RVGTKRYMPP EVLDBSLNRM HFQSYIMADM YSPGLILWEV ARRCVSGGIV 420
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Seq ID NO: 69 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 166..1737

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Seq ID NO: 70 Protein sequence
 Protein Accession #: Eos sequence

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Seq ID NO: 71 DNA sequence
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Seq ID NO: 72 Protein sequence
 Protein Accession #: NP_004685

70 1 11 21 31 41 51
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Seq ID NO: 74 Protein sequence
Protein Accession #: NP_002175.1

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SHIAQWSPPT PPRNPNFSKD QMYSNGFTD VSVVEIAND KKPFPEDLKS LDLFKKEKIN 720
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80 ESTQPLDSE ERPEDQLVD HVDGGDGLP RQQYFKQNC QHESPDPIS FERSKQVSSV 840
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MPKSYLQTV RQGGYMPQ

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Seq ID NO: 75 DNA sequence
Nucleic Acid Accession #: NM_022131
Coding sequence: 11..2878

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Seq ID NO: 76 Protein sequence
 Protein Accession #: NP_071414

1 11 21 31 41 51
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 NEFNLEVSIL HEDQVSDKEH VNHLIVQPPF LQSVHHPESR SSIQHSSVVP SIATVVIIS 840
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Seq ID NO: 77 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 482...3007

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Seq ID NO: 78 Protein sequence

Protein Accession #: Eos sequence

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5 PPQNPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNRRIE VLEEGSFNNL TRLQKLYLNG 420
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Seq ID NO: 79 DNA sequence

Nucleic Acid Accession #: NM_016640.2

Coding sequence: 39..1358

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Seq ID NO: 80 Protein sequence

Protein Accession #: NP_057724.1

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Seq ID NO: 81 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..2070

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15 Seq ID NO: 82 Protein sequence
 Protein Accession #: PGENESH predicted

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 30 EKAEMASNAGA ACMNSQHQG RQMAGAHFP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600
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35 Seq ID NO: 83 DNA sequence
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 Coding sequence: 557..1954

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Seq ID NO: 84 Protein sequence
 Protein Accession #: NM_005264.1

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Seq ID NO: 85 DNA sequence

Nucleic Acid Accession #: XM_027172.1

Coding sequence: 143..1405

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	TGATGCTAAG	CGAGGACTGT	GACTTTCCCA	CCCACATGGC	TGTTGGTGAC	AGACACCGGA	3360
	TTTGAGGACA	GTCTGTGTGC	ACTCAGAGGC	CTCTGCTTCT	CTCTTGTCTC	TAGAGTCTCT	3420
	CTGAGGAGTC	GGGGCTGTC	CTGAGCCAC	CCTGCTGTTG	AAGGTGCTTC	CTCAGGCCCA	3480
35	GCTCCCATG	CCCCCACAAC	CCCTCCTCAT	CACCTCCTAC	TCCCAAAAG	GACAAAGCCT	3540
	CAGGGAACCT	TTTTCTTTT	TTTAGAGACG	GGGTCTTGCT	ATGTTGGTCA	GGCTGGTCTT	3600
	GAACCTCTGG	GGCCAGGCAA	TCTTCCCGCC	TCGTCTCTCT	AAAGTGCTGG	GATTCTGGGC	3660
	CTTAGGGAAC	CTTTTGAAC	TGAAAGTGAC	GCTCGAAGCC	TTCTGTAGA	GTGAGGTGGG	3720
	TGGCTGGGCG	TAAACCATG	GGGAAGGAGA	GAOCTGGTGG	GGGCACACAG	CTGCTATATA	3780
40	GAGGAACAGA	AGGTGGGCCA	GGCTCCACAG	CTGTGAGGAA	ATCTGGCTCA	GTCCCCAGAC	3840
	CGCTGTGTGG	CTTTGGGGTG	GCCAGTCCCT	CTCTCTCTGC	AACACTCTCC	TCATGAGGAC	3900
	TTCTGTGAAA	AATGGGGGTT	GTAAACCTCT	GAGTCTGGGG	GGCCCAACCA	TTTCTAATCT	3960
	CCAGAACTTG	GGCACCACAG	ACTCCACCAA	CTTCTAGTCC	TGGGGCTGG	GCCTCTGGCC	4020
	ATTGCCATAG	GCAACCACTG	CTCTGTGACG	GCAGCGCCCC	CCTCTGCCAG	GATCCTCCGA	4080
45	GGTCAGCTGC	TGGGTCTGAC	CGCAGACCC	TGGCTGAGCG	ACGGATGAAC	GGAGTATGCA	4140
	GACACAGGCT	TGCTTGTGAG	CAGATGGGGG	ACCOCTGCCA	GAGTCAGCAG	CGGCCCCCAT	4200
	AAGCCTGCCA	CGCTTGCATT	TATTTAGTAC	AGATGTAATG	ACAAAGGCCT	AAAGCAAAC	4260
	CCATTGTGGG	GTAAATTAACA	TTGTGCGCCC	CCAGAAAGGA	GCAGTCTCTC	GCATGATGAT	4320
	TAAAGGCCAG	GTTCGAGGCG	CTAAGTAAAC	CAACTTATCT	AGATCAATTC	CCTTACTTCT	4380
50	TGTTATCTAC	TCTGAGAGAA	TTGAGCTGCC	TTGAGCAAA	TCCTTTCCCG	AAGCTTTTGC	4440
	AAAACTCCCG	AGCCTTCCAA	GGTTTGCTTC	TTTCTGTAAT	TTTTCTCACC	ACCTTGACCT	4500
	ATCTCCTGCA	AGCCTTCCAG	TGGAGGCTTC	TGTGTTTCCC	CCAGTGTCTG	CAGCCTAGAG	4560
	GCTGAGATGG	CCAGAAACAA	GGTGGTGACA	GTGGCGTGCT	CAGGGCTTGG	GAACCCCAAG	4620
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55	GAGGTGGGTC	TTGGAGAGGA	AGGACTTAGG	GAGGCAGAGT	GGAGGAAGTG	AGAGGACACC	4740
	CCAAGCCAAAG	AGGGGCGCAG	GACCAAGGC	TCAGAAAGCA	GGGCGCTGCA	GAGGGGCTGT	4800
	GTGCGACAGG	GTGAAGAGTT	TGTGTGGCAG	AAGGGCAGGG	GGCTTGCATC	AGGGGTGACA	4860
	GCTGTCTTTT	TGTCCAGCA	TAGCCCTGT	ACATCCCTGG	AGAGCTGGGG	CGTCCACAAC	4920
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60	AGGAGGGAAG	ACTCTTGGAG	ATGAGCCTGG	TGAAGGGATA	ATGGCATCCC	GGGCCGAGGA	5040
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	TGAGCCAGAA	AAAGAAAGGT	TAGGGCAGGT	CCTGGAGGAG	ATGAGTGGCT	GTTTGGGCTT	5160
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65	ATGAGCAGGA	AAAGACCCCC	TCAAGGCTCA	CGTCTTAGTG	GGGAGACAAG	AAACACAGAT	5340
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70	GGCCGTCTGT	TGGCTGGAGT	GCTGCAGGTG	TCAAGGAAAT	TGTAGGAGAT	GTCTCTTGAG	5640
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	GCAGTCCGAT	AATGAGAGCC	GTAGGGCAAG	GCCAGCAGGA	TCCTAGAGTG	AGACGGGAGG	5880
75	TAAAGTCAGG	GGGACTTGTG	GTCTCCACGT	CAGGGGCAAG	GGAAAGGAG	AGGACAAGGG	5940
	TGACCCGGGA	GGTTAAAGAT	GGGACCGGGG	CCAGACGAG	TGGCTCATGC	CTGTAATCCT	6000
	AGCACCTTGG	GAGGCTGAGG	CGGGCGGATG	GCTTGAGGTC	AGGAGTTTGA	AACCGGCTGG	6060
	GCCAAACATG	TGAACCCCG	TCTCTACTAA	AATATACAAA	AATTAGCCTG	GCGTGGTGGT	6120
	GCATGCCCTC	AGTCCAGCT	ATTACAGGAG	CTGAGGCGAC	AAGAACTGCT	TGAACCTGGG	6180
80	AGGCGGAGGT	TGCAGTGAGC	CGAGATCGCG	CCATAGCACT	CCAGCCTTAG	CTGGGCGGAC	6240
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Seq ID NO: 88 Protein sequence
Protein Accession #: BAA32297.1

1 11 21 31 41 51
 5 VETPPQGSVH SGHLGSVVG D PHTGTGNAGE RGPRGKGARV LALDSGGMDS SPSLPLIRTP 60
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 ILLAGNMKE AQMLCQRHRR KSSVTDSPSS LVNRPTLQGP TEEIHAIEVC YAECLLQRAA 180
 LTFPLQSSHG GAVRPRALHD PSHACSCPPG PGRQHLFLQ DENMVSFIMG GIKVRNSYQT 240
 YKELDSLVSQ SQYCKGENHP HFEGGVKLG VAFNLTL SML PTRILRLLEF VGPSGNKYD 300
 10 LLQLEBSAGS HSFRSVCVM LLLCYHTFLT FVLGTGNVNI EEAELKLPY LNRYPKGAIF 360
 LFFAGRIEVI KGNIDAVSDG GPGRGWGSLG VSQTSRKSQT CDILDRIDW GRGGGPRENQ 420
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Seq ID NO: 89 DNA sequence

Nucleic Acid Accession #: AF007170

Coding sequence: 73..1725

1 11 21 31 41 51
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 25 TTCAGCAGCC TGGTGAACCG CCCACGCTG GGCCAATTCA CTGAAGAAGA AATCCACGCT 360
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 GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCCTACT 600
 AGGATCTCTGA GGCTGTTGGA GTTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660
 30 CAGCTGTGAG AGGGGAGCTG AGGGCACAGC TTCGCTCTG TGCTCTGTGT CATGCTCCTG 720
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 35 GAGTCTGTGT AGGCCGAGCA GCATCTGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG 960
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 50 CCCCCTGCCC TGCCCTGCTC TTGGGGTCCA CCGGCACTCC AGTTGGATGG CACAACATAG 1860
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 55 TATCATCTGG AGGTAAATCT CTTTATATGA TGATGCCAAA GGGCAAAATG CTTTCAAAAT 2160
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Seq ID NO: 90 Protein sequence

Protein Accession #: AAC39582.1

1 11 21 31 41 51
 70 KEAASGKSDR RTPESSLHEA LDQCMALDL FLTNQFSEAL SYLKPRTKES MYHSLTYATI 60
 LEMQAMTFD PQDILLAGNM MKEAQMLQQR HRRKSSVTD SSVLVNRPTL GQFTTEIHA 120
 EVCYAECLLQ RAALTFLQDE NMVSFIRGGI KVRNSYQTYK ELDSLVSQSSQ YCKGENHPHF 180
 EGGVKLGVA FNLTLMLPT RILRLLEFVG FSGNKDYGLL QLEEGASGHS FRSLVLCVML 240
 75 LCYHTFLTIV LGTGNVNIEE AEKLLKPYLN RYPKGAIFLF FAGRIEVIK NIDAAIRRFE 300
 ECCEAQHMK QFHEMCYWEI MWCFTYKQW KMSYFYADLL SKENCWSKAT YIYMKAAYLS 360
 MFGKEBHKPF QHEVELFRA VPGLKLIAG KSLPTEKFAL RKSRRYFSSN PISLPVPALE 420
 MMVYWNQYAV IKGQPKLTDG ILEIITKAE MLEKGFENBY SVDDECLVKL LKGLCLKYLK 480
 RVQEAENFR SISANEKKIK YDHYLIPNAL LELALLMEQ DRNEBAIKLL BSAKQNYKRY 540
 80 SMESRTHFRI QAATLQAKSS LENSRSNVS SVSL

Seq ID NO: 91 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 31..906

1 11 21 31 41 51
 5 CGGGTCGACC CAAGCGTCCG GGGAGAAAGG ATGGCCGGCC TGGCGGGCGG GTTGGTCCTG 60
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 GACTGGGTAC TGCAGTGCAG AGAGCAGAAC TGCTCTGGGG GCGCTCTGAA TCACTTCGCG 180
 TCCCGCCAGC CAATCTACAT GAGTCTAGCA GGCTGGACCT GTGCGGACGA CTGTAAGTAT 240
 GAGTGTATGT GGGTCACCGT TGGGCTCTAC CTCCAGGAAG GTCACAAAGT GCCTCAGTTC 300
 CATGGCAAGT GGCCTTCTC CCGGTTCTGT TTCTTCAAG AGCCGGCATC GGCGGTGGCC 360
 10 TCGTTTCTCA ATGGCCTGGC CAGCCTGGTG ATGCTCTGCC GCTACCGCAC CTCTGTGCCA 420
 GCCTCTCCCC CCATGTACCA CACCTGTGTG GCCTTCGCTT GGGTGTCCCT CAATGCATGG 480
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 15 CTGGCCTGGT GCCTGTGGAA CCAAGGCGCG CTGCTCAAG TGGCAAGTG CGTGGTGGTG 720
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 20 CCCTTCTCCC CTCACCCCTT GAGATGATT TCTCTTTTCA ACTTCTTGA CTGTGACATG 1020
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 25 GCGCTCTGTC TACCTGGGAG ACCAGGGACC ACAGGCCCTA GGGATACAGG GGTCCCCCTT 1320
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 30 GTTGAGAGCC TGCCACCGTG TGTGCGGAGT GTGGGCCAGG CTGAGTGCAT AGGTGACAGC 1620
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 35 TAATCACTTG TGGAGCGCCA CTGGGCCCAA GAGGCCACCT GGGCGGACAG CAGGAGCTCT 1920
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 40 TTTGGGAGG AGGAAGGGGC GATTTGAGGG AGAAGGGGAG AAGCTTATG GCTGGGTCTG 2220
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 45 TCCGTGGTGT AAGCAGACTG GATTTTGTCT CTGCCCCGTA CCCCTTGTCC CTCTTGGAG 2460
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 AAGCCTCAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

Seq ID NO: 92 Protein sequence
 Protein Accession #: Eos sequence

50 1 11 21 31 41 51
 MAGLAARLVL LAGAAALASG SQGDREPVYR DCVLQCEQN CSGGALNHFR SRQPIYMSLA 60
 55 GWTCDRDKY ECMWVTVGLY LQEGHKVPQF HGKWPFSRFL PFQEPASAVA SPLNGLASLV 120
 MLCRVTETVP ASSPMYHTCV AFAMVSLNAW FWSVTFBTRD TDLTEKMDYF CASTVILHSI 180
 YLCCVRTVGL QHFAVVSAGR ALLLLMLTVH VSYLSLIRPD YGYMLVANVA IGLVNVVWML 240
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 FLEDDSLYLL KESEDKFKLD

Seq ID NO: 93 DNA sequence
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 Coding sequence: 18..980

65 1 11 21 31 41 51
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 70 TCTACATGAG TCTAGCAGCG TGAACCTGTC GGGACGACTG TAAGTATGAG TGTATGTGGG 240
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 75 TGTAACACAC CTGTGTGGCC TTGCTCTGGG TGTCTCTCAA TGCAATGTTT TGTGTCCAG 480
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Seq ID NO: 94 Protein sequence
Protein Accession #: NP_219487.1

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1 11 21 31 41 51
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LWPAKVHGDG PHGILRDQAA GIGKEPHFDH CPSQVPRRP HTPFQGGSS KPRARILCCC 180
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Seq ID NO: 95 DNA sequence
Nucleic Acid Accession #: XM_090469
Coding sequence:

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CTCAGCCGCA GCCCGGCCCT GTCCCAAGT ACACCAATGG CGCCCTTCCC GACCTCTGAC 660
CGCAGCTAG AGCGCCAGG CCGCCGCCCT GGGCTGCGGA GCTGCGCAGC AGCCCTCAC 720
TGCCTGCCCG CGGCTCCAGA AGCCAGAAA CTCTTCTTCC TGCTGCCCCT TTATCCAGAT 780
GGCAGCCCAAC CACTAAGGA CATCTTGAG ACCTCCAGC ACAAGGCACC TGGGAAGAGA 840
CTGCATCAAG AATCACCAGG TTCAITTTCA ATAGGTTTAT GTAACAGAAC AGCTGAACCA 900
TGTATCAAG GGGCTCTGGG TGTGGCTGCT GAAGCAGCAT TTCATTACA GTTTTCCAGT 960
GAATGA

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Seq ID NO: 96 Protein sequence
Protein Accession #: XP_090469

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PPEVKMFAS QGLLTMETNQ SLAQGTGCSV CWFVNGPGL MSLPGVLSAD AGQVEHRRQM 120
NSADTDWGTG EPGSLDFAV AAHQEDTFPL KDIKHTSTFR QSVQQNCIY SPREKPCGNV 180
RAPCAPPRRE APLALSRPWR LSRSPAPSPR TFMAPPFTSD RELDAPGPPP GLRSSAAAPH 240
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Seq ID NO: 97 DNA sequence
Nucleic Acid Accession #: NM_003474.2
Coding sequence: 37..3036

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CTTTTAAAAA AATGAAGAGC TAGAAGAGCT CAGCGCGCGC GCGGGCCGTG CGCGAGGGCT 180
CCGAGCTGTA CTCGCGAGG CAGGAATCC CTCGCTCGC GACGCGCGC CCGCTCGGC 240
GCCCGGTGG GATGGTGCAG CGCTCGCGC CCGGCCGAG AGCTGCTGCA CTGAAGGCCG 300

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	GCGACGATGG	CAGCGCGCCC	GCTGCCCGTG	TCCCCCGCCC	GCGCCCTCCT	GCTCGCCCTG	360
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	GCTGATGAAG	TGTGAGTGC	CTCTGTTCGG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
5	TTGAGCTCCA	AGAATCATCC	AGAAGTGCTG	AATATTGAC	TACAAACGGG	AAGCAAAGAA	540
	CTGATCATAA	ATCTGGAAAG	AAATGAAGGT	CTCATTGCCA	GCAGTTTCAC	GGAAACCCAC	600
	TATCTGCAAG	ACGGTACTGA	TGCTCCCTC	GCTCGAAATT	ACACGGTAAT	TCTGGGTGAC	660
	TGTTACTACC	ATGGACATGT	ACGGGGATAT	TCTGATTGAG	CAGTCAGTCT	CAGCACTGCT	720
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	TCCCATGACA	ATGGCGAGCT	TGTCAGTGGG	GTTTATTTC	AAGGGACCAC	CATCGGCATG	1260
	GCCCCAATCA	TGAGCATGTG	CACGGCAGAC	CAGTCTGGGG	GAATTGTCT	GGACCAATTCA	1320
	GACAATCCCC	TTGGTGCAGC	CGTGACCTCG	GCACATGAGC	TGGGCCACAA	TTTCGGGATG	1380
20	AATCATGACA	CACTGGGACG	GGGCTGTAGC	TGTCAAATGG	CGGTTGAGAA	AGGAGGCTGC	1440
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25	AAGCCGAGCG	CTGTGTGCGC	ACATGGGCTG	TGCTGTGAAG	ACTGCCAGCT	GAAGCCTGCA	1740
	GGAAACAGCT	CGACGAGCTC	CAGCAACTCC	TGTGAOCTCC	CAGAGTTCTG	CACAGGGGCC	1800
	AGCCCTCACT	GCCACGCCAA	CGTGTACCTG	CAOGATGGGC	ACTCATGTCA	GGATGTGGAC	1860
	GGCTACTGCT	ACAATGGCAT	CTGCCAGACT	CACGAGCAGC	AGTGTGTCT	ACTCTGGGGA	1920
	CCAGGTGCTA	AACCTGCCCC	TGGGATCTGC	TTTGAGAGAG	TCAATTCTGC	AGGTGATCCT	1980
30	TATGGCAACT	GTGGCAAGT	CTCGAAGAGT	TCCTTTGCCA	AATGCGAGAT	GAGAGATGCT	2040
	AAATGTGGAA	TGAAGAGGTT	TCAAGGAGGT	GCCAGCGGCG	CAGTCATTGG	TACCAATGCC	2100
	GTTCCTACT	AAAACAACAT	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160
	CACGTGTACT	TGGGCGATGA	CATGCCGAGC	CCAGGGCTTG	TGCTTGCAGG	CACAAAGTGT	2220
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35	GAGTGTGCAA	TGCAGTGCCA	CGGCAGAGGG	GTGTGCAACA	ACAGGAAGAA	CTGCCACTGC	2340
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	TGTCCTCTTG	CTGCCGATT	TGTGGTTTAT	CTCAAAGGA	AGACCTTGAT	ACGACTGCTG	2520
	TTTACAATA	AGAAGACCA	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGGCCACCC	2580
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	CGCGCAGCT	CCTACCCACC	GAAGGACAA	CCCAGGAGAT	TGCTGCACTG	TCAGAAATGT	2700
	GACATCAGCA	GACCCCTCAA	CGCCCTGAAT	GTCCCTCAGC	CCCAGTCAAC	TCAGCGAGTG	2760
	CTTCTCTCCC	TCCACGGGGC	CCCACTGTCA	CCTAGCTGCC	CTGCCAGACC	CCTGCCAGCC	2820
	AAGCCCTGAC	TTAGGCAAGC	CCAGGGGACC	TGTAAGCCAA	ACCCCTCTCA	GAAGCCTCTG	2880
45	CCTGCAGATC	CTCTGGGACG	AACAACCTCG	CTCACTCATG	CCTTGGCCAG	GACCCCAAGG	2940
	CAATGGGAGA	CTGGGCTCCG	CCTGGCACCC	CTCAGACCTG	CTCCACAATA	TCCACACCAA	3000
	GTGCCCAGAT	CCACCCACAC	CGCCTATATT	AAGTGAGAAG	CCGACACCTT	TTTTCAACAG	3060
	TGAAGACAGA	AGTTTGCAT	ATCTTTGAGC	TCCAGTTGGA	GTTTTTTGTA	CCAACTTTTA	3120
	GGATTTTTTT	TAAATGTTAA	AACATCATT	CTATAAGAAC	TTTGAGCTAC	TGCCGTGAGT	3180
50	GCTGTGCTGT	GCTATGGTGC	TCTGTCTACT	TGCACAGGTA	CTTGTAATTT	ATTAATTTAT	3240
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	CCATGGCAGG	AAGGCTTGT	GTGCTTTTAG	TATTTTAGTG	AACCTGAAAT	ATCCTGCTTG	3360
	ATGGGATCT	GGACAGGATG	TGTTTGTCTT	CTGATCAAGG	CCTTATTGGA	AAGCAGTCCC	3420
	CCAAGCTGAC	CCAGCTGTGC	TTATGGTACC	AGATGCACTG	CAAGAGATCC	CAAGTAGAAT	3480
	CTCAGTTGAT	TTTCTGGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGC	3540
55	TGRTTGTGCG	TTTCAAGGAG	GCCCTGTGCC	CCTTGACAAC	TGGCAGGCAG	GCTCCCGGGG	3600
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	TGACCTGAGC	CTGACAGGCC	GTGAGCATGT	TTGGAAGGGG	TCTGTAGTGT	CACTCAAGGC	3780
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65	AATTAGGCAG	ACTCTTTATG	CTTGCAAAAA	CTACAACCAA	TGGAATGTGA	TGTTTATGGG	4140
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70	CTCTTCACTC	TTCAAAATGCC	TGACTAGGGA	GCCATGTTTC	ACRAGGTCTT	TAAAGTGACT	4440
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75	TCCCCACTGT	ATCTAGGCAA	CATAGTATTC	ATGACTATGG	ATAAACTAAA	CAGGTGACAC	4740
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Seq ID NO: 98 Protein sequence
Protein Accession #: NP_003465

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YHGHVRGYS SSVLSSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLPPAK KLKSVRSGCG 180
SHRNTPNLAA KNVFPPPSQT WARRHKRETL KATKYVELVI VADNREFORQ GKDLSEVKQR 240
LIEIANHVDK FYRPLNIRIV LVGVEVWNDM DKCSVSQDFF TSLHEFLDWR KMKLLPRKSH 300
DNAQLVSGVY FQGTITIGMAP IMSMCTADQS GGIWMDHSDN PLGAAVTLAH ELGHNFGMNH 360
DTLDRGCSQ MAVKGGGIM NASTGYPFPM VFSKSRKDL ETSLEKMGV CLFNLPEVRE 420
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ACRDSNSDC LPEFCTGASP HCPANVYLHD GHSCQDVG Y CYNGICQTHE QQCVTLWPG 540
AKPAPGICPE RVNSAGDPY NGKVSXSSP AKCEMRDAKC GKIQCGGAS RPVIQTNVAVS 600
IETNIPLOQG GRILCRGTHV YLGDDMPDFG LVLAGTKCAD GKICLNRCQ NISVFGVHEC 660
AMQCHGRGVC NNRKNCHCEA HWAPPCDKF GFGGSTDGFP IRQADNQLT IGLVLTILCL 720
LAAGFVVYLK RKTILRLFT NKKTITIEKLR CVRPSRPPRG FQPCQAHLG LGKGLMRKPP 780
DSYPPKNDR RLLQCNVDI SRPLNGLNVP QPQSTQVLP FLHRAPRAPS VPAPPLPAKP 840
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Protein Accession #: NP_003705

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ISRKCPAIRE MVSQQLRECY LKHDLCAAAQ ENTRVIVEMI HFQDLLLHEP YVDLVNLLLT 180
CGEVKBAIT HSVQVQCEQN WSLSCILSP CTSAIQKPPT APPERQPVQD RTKLRSRAHNG 240
EAGHHLPEPS SRETGRGAKG BRGSKSHFNA HARGRVGGLG AQGPSGSSSW EDEQSEYSDI 300
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80 Seq ID NO: 101 DNA sequence
Nucleic Acid Accession #: NM_005940
Coding sequence: 23..1489

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Seq ID NO: 102 Protein sequence

Protein Accession #: NP_005931

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VSTIRGELEF FKAGFVWRLR GGQLQPGYPA LASHWQGLP SPVDAAFEDA QGHVFFQGA 360
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Seq ID NO: 103 DNA sequence

Nucleic Acid Accession #: NM_033151.2

Coding sequence: 351..4499

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ACTAAGTGAT TTGGGCTGTA GGCCCTGAGAA GATGTTTAAA AAGAGGGATC AAGCACAGGC 180
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GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCCACCG TGGGGGAAGT 540
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AGCCCTGGA CAATGCTGGC CTGTTCTCCT ACCTCACGCT GTCATGGCTC ACCCGCTCA 660
TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCTCCACTG TCAGTCCATG 720
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 Protein Accession #: NP_149163.2

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Seq ID NO: 105 DNA sequence
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Seq ID NO: 106 Protein sequence
 Protein Accession #: Eos sequence

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Seq ID NO: 108 Protein sequence

Protein Accession #: NP_076927

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 CCAGGAACCTC CCAGCACGCA GAATCCATCT GAGAATATGC TGCCACAAAT ACCCTTTTGT 120
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 15 ACAGGCATAA AAGGCCCACT ACCCAACACC AAGACACAGT TCTTCATTCC CTACACCATTA 240
 AAGAGTAAAG GTATAGCAGT AAGAGGAGAG CAAGGTACTC CTGGTCCACC AGGCCCTGCT 300
 GGACCTCGAG GGCACCCAGG TCCTTCTGGA CCACAGGAA AACCCAGGCTA CGGAAGTCCT 360
 GGACTCCAAAG GAGAGCCAGG GTTGCACGGA CCACCGGGAC CATCAGCTGT AGGGAAACCA 420
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 20 GTTGACCACG CTGGCCTACC AGGACCCCGG GGGCCACCAG GACCACTCGG AATCCCTGGA 540
 CGGGCTGGAA TTTCTGTGCC AGGAAACCTT GGACCAACAG GACCCACAGG AGCCCCAGGA 600
 CCCAGGGGCT TTCTTGAGGA AAAGGGTGCA CCAGGAGTCC CTGGTATGAA TGGACAGAAA 660
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 GGTCACACAG GACCATCTGG CCTCTCTGGA GTGGGAAAAA GAGGTGAAAA TGGGTTTCCA 780
 25 GGACAGCCAG GCATCAAAGG TGATAGAGGT TTTCCGGGAG AAATGGGACC AATTTGGCCA 840
 CCAGGTCCCC AAGGCCCTCC TGGGGAAACG GGGCCAGAA GCAATGGAAA GCCAGGAGCT 900
 GCTGGAGGCC CAGGCCAGCC AGGGAATCCA GGAACAAAG GTCTCCCTGG GGCTCCAGGA 960
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 GAAAGAGGAC CTGCTGGCCT TCCTGGGGGT CCAGGTGCCA AAGGGGAACA AGGGCCAGCA 1080
 30 GGTCTTCCTG GGAAGCCAGG TCTGACTGGA CCCCTTGGGA ATATGGGACC CCAAGGACCA 1140
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 AAAGGTGATC CTGGAGTGGG AGGACCTCCT GGTCTCCCGG GCCCTGTGGG CCCAGCAGGA 1380
 35 GCAAGGGGAA TGCCCGGACA CAATGGAGAG GCTGGCCCAA GAGGTGCCCC TGGAAATACA 1440
 GGTAAGTACG GCGCTATTGG GCCACACAGC ATTCCAGGAT TCCTGGGTGC TAAAGGGGAT 1500
 CCAGGAAGTC CCGGTCTCTC TGGCCAGCTT GGCATAGCAA CTAAGGGCTT CAATGGACCC 1560
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 ATACCATTTG ATAAAAATTT GTATAACAGG CAACAGCATT ATGACCCAAG GACTGGAATC 1860
 TTTACTTGTG AGATACCAGG AATATACTAT TTTTCATACC ACGTGCATGT GAAAGGGACT 1920
 45 CATGTTTGGG TAGGCCTGTA TAAGAAATGG ACCCTGTAA TGTACACCTA TGATGAATAC 1980
 ACCAAAGGCT ACCTGGATCA GGCTTCAGGG AGTGCCATCA TCGATCTCAC AGAAATAGAC 2040
 CAGGTGTGGC TCCAGCTTCC CAATGCCGAG TCAATGGCC TACTCTCTC TGAATATGTC 2100
 CACTCTCTCT TCTCAGGATT CCTAGTGGCT CCAATGTGAG TACACCCAC AGAGCTAATC 2160
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 AACAAACCTT CCCCCTGAAA AGTGAGCAGC AACGTAAAAA CGTATGTGAA GCCTCTCTTG 2340
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 CAAAGAAATC CTGCTATGTT AAAAACAAAC AACAAAAAAC AAAGCAACAA AAAAAAAT 2460
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 55 ATTTCTTTTT TAAAAAGGCC TGTTTCTAAC TATGAATATG AGAACTCTTA GGAACATACC 2580
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 60 CCCAAATATG TGAAGTTTCT CTGAAATGCA AGGTGCTTTC ATCAATGAAC CTTTTCAAAA 2820
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 GACCTATCTT TATTTAGTTA ACACAAGTGT GATTAATTTG ATTTCTTTAA TTCCTTATG 2940
 AATCTTATGT GATATGATTT TCTGGATTTA CAGAACATTA GCACATGTAC CTTGTGCTC 3000
 CCATCAAGT GAAGTTATAA TTTACACTGA GGGTTTCAAA ATTCGACTAG AAGTGGAGAT 3060
 65 ATATTATTTA TTTATGCACT GTACTGTATT TTTATATTGC TGTTTAAAC TTTTAAGCTG 3120
 TGCCTCACTT ATTAAGCAC AAAATGTTT ACCTACTCCT TATTACGAC ACAATAAAT 3180
 AACATCAATA GATTTTATAG CTGAATTAAT TTGAAAGCAG CAATTTGCTG TTCTCAACCA 3240
 TTCTTTCAAG GCTTTTCTAT CGACACAATA AATAACATC AATAG

Seq ID NO: 110 Protein sequence
 Protein Accession #: NP_000484.2

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1 11 21 31 41 51
 MLQPPIFLLL VSLNLVHGVF YAERYQMPTG IKGPLNTRKT QFFIPYTIKS KGIIVRGEQG 60
 TPQPPGPAGP RGHPPGSGPP GKPGYGSPLG QGEPGLPGPP GPSAVGKPGV PGLPGKPGER 120
 75 GPYVPRKDVG PAGLPGRPRP PGPPGIPGPA GISVPGKPGQ QGPTGAPGPR GFPGEKGAPG 180
 VPGMNGQKGE MGYGAPGRPG ERGLPGPQGP TGPSGPPGVG KRGENGVPGQ PGIKDGRGFP 240
 GEMGPPIPPG PQGPPGERGP EGIGKPGAAG APGQPGIPGT KGLPGAPGIA GPPPGPGFGK 300
 PGLPLGLKER GPAGLPQSGP AKGEQGPAGL PGKPLGTGPP GNMGPQGPFG IPGSHGLPGP 360
 80 KGETGPAGPA GYPGAKGERG SPGSDGKPGY PGKPLDGPK GNPGLPGPKG DRPGVGGPGL 420
 PGVPGPAGAK GMPGNGEAG PRGAPGIPGT RGPIGPPGIP GFPPGSKDGP SPGPPGPAGI 480
 ATKGLNGPTG PPGPPGPRGH SGEPGLPGPP GPPGPPGQAV MPEGFIKAGQ RPSLSGTPLV 540
 SANQGVGTMP VSAFTVLSK AYPAGTPIP FDKILYNRQ HYDPTGTIFT CQIPGIYYFS 600
 YHVHVKGTHV WFLGKNGTIP VMTYDEYTK GYLDQASGSA IDLTENDQV WLQLPNAESN 660
 GLYSSEYVHS SFGSPLVAPM

Seq ID NO: 111 DNA sequence
Nucleic Acid Accession #: NM_000949
Coding sequence: 285..2153

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CTCCCTCTTT	CTGGATTTTA	CGGACCGTTC	GCGAAACAGC	TTTCCACACA	ATGGAGCTTC	120
ATGTCTCTGT	GCAGGAAGTA	CTCATCGACT	GATGTGGCAG	ACTTTGCTCC	CTGACAAAAC	180
TAAAGAACTC	TCCTATTTCAT	GGAGGCGAAC	ACTGAGGATG	CTTTCCACAT	GAACCCCTGAA	240
GTGAACCTTC	GATACATTTTC	CTGCAGCAAG	AGAAGGCAGC	CAACATGAAG	GAAAATGTGG	300
CATCTGCAAC	CGTTTTCAC	CTGCTACTTT	TTCTCAACAC	CTGCCTTCTG	AATGGACAGT	360
TACCTCTGCG	AAAACCTGAG	ATCTTTAAAT	GTGCTTCTCC	CAATAAGGAA	ACATTACACT	420
GCTGGTGGAG	GCCTGGGACA	GATGGAGGAC	TTCTTACCAA	TTATTCACTG	ACTTACCACA	480
GGGAAGGAGA	GACACTCATG	CATGAATGTC	CAGACTACAT	AACCGGTGGC	CCCAACTCCT	540
GCCACTTTGG	CAAGCAGTAC	ACCTCCATGT	GGAGGACATA	CATCATGATG	GTCAATGCCA	600
CTAACAGAT	GGGAAGCAGT	TTCTCGGATG	AACCTTATGT	GGACGTGACT	TACATAGTTC	660
AGCCAGACCC	TCCTTTGGAG	CTGGCTGTGG	AAGTAAACCA	GCCAGAAGAC	AGAAAAACCT	720
ACCTGTGGAT	TAAATGGTCT	CCACCTACCC	TGATTGACTT	AAAAACTGGT	TGGTTCACGC	780
TCCTGTATGA	AATTCGATTA	AAACCCGAGA	AAGCAGCTGA	GTGGGAGATC	CATTTTGCTG	840
GGCAGCAAA	AGAGTTTAA	ATTCTCAGCC	TACATCCAGG	ACAGAAATAC	CTTGTCCAGG	900
TTGCTGCAAA	ACCAAGCCAT	GGATACTGGA	GTGCATGGAG	TCCAGCGACC	TTCAATTCAGA	960
TACCTAGTGA	CTTCACCATG	AATGATACAA	CCGTGTGGAT	CTCTGTGGCT	GTCTTTCTG	1020
CTGTCTCTGT	TTTGATTATT	GTCTGGGCAG	TGGCTTTGAA	GGGCTATAGC	ATGGTGACCT	1080
GCATCTTTCC	GCCAGTTCC	GGGCCAAAA	TAAAAGGATT	TGATGCTCAT	CTGTGGGAGA	1140
AGGGCAAGTC	TGAAGAACTA	CTGAGTGCCT	TGGGATGCCA	AGACTTTTCT	CCCACTTCTG	1200
ACTATGAGGA	CTTGCTGGTG	GAGTATTTAG	AAGTAGATGA	TAGTGAGGAC	CAGCATCTAA	1260
TGTCAGTCCA	TTCAAAAGAA	CACCCAAAGT	AAGGTATGAA	ACCCACATAC	CTGGATCCTG	1320
ACACTGACTC	AGGCGGGGG	AGCTGTGACA	GCCCTTCCCT	TTTGTCTGAA	AAGTGTGAGG	1380
AACCCAGGCG	CAATCCCTCC	ACATTCTATG	ATCCTGAGGT	CATTGAGAAG	CCAGAGAATC	1440
CTGAACAAC	CCACAACCTG	GACCCCACTG	GCATAAGCAT	GGAAGGCAAA	ATCCCTATT	1500
TTTATGCTGG	TGGATCCAAA	TGTTCAACAT	GGCCCTTACC	ACAGCCAGC	CAGCACAAAC	1560
CCAGATCCTC	TTACCACAAT	ATTACTGATG	TGTGTGAGCT	GGCTGTGGGC	CCTGCAGGTG	1620
CACCGGCCAC	CTCTGTGAAT	GAAGCAGGTA	AAGATGCTTT	AAAATCCTCT	CAAAACATTA	1680
AGTCTAGAGA	AGAGGGAAAG	GCAACCCAGC	AGAGGGAGGT	AGAAAGCTTC	CATTCTGAGA	1740
CTGACCAGGA	TACGCCCTGG	CTGCTGCCCC	AGGAGAAAAC	CCCTTTTGGC	TCCGCTAAAC	1800
CCTTGGATTA	TGTGGAGATT	CACAAGGTCA	ACAAAGATGG	TGCATTATCA	TTGCTACCAA	1860
AACAGAGAGA	GAACAGCGGC	AAGCCCAAGA	AGCCCGGGAC	TCCTGAGAAC	AATAAGGAGT	1920
ATGCCAAGGT	TCTGTGGGTC	ATGATAAACA	ACATCCTGGT	GTTGGTGCCA	GATCCACATG	1980
CTAAAAACGT	GGCTTGCTTT	GAAGAATCAG	CCAAAGAGGC	CCCAACCATCA	CTTGAACAGA	2040
ATCAAGCTGA	GAAGGCCCTG	GCCAACTTCA	CTGCAACATC	AAGCAAGTGC	AGGCTCCAGC	2100
TGGGTGGTTT	GGATTACCTG	GATCCCGCAT	GTTTACACAT	CTCCTTTCAC	TGATAGCTTG	2160
ACTAATGGAA	TGATTGGTTA	AAATGTGATT	TTTCTTCAGG	TAACACTACA	GAGTACGTGA	2220
AATGCTCAAG	AATGTAGTCA	GACTGACACT	ACTAAAGCTC	CCAGCTCCTT	TCATGCTCCA	2280
TTTTTAACCA	CTTGCCCTCT	TCTCCAGCAG	CTGATTCCAG	AACAAATCAT	TATGTTTCTT	2340
AACGTGATT	TGTAGATTTA	CTTTTGTCTG	TTAGTTATAA	AACATATGTT	TCAATGAAAT	2400
AAAAGCACAC	TGCTTAGTAT	TCTTGAGGGA	CAATGCCAAT	AGGTATATCC	TCTGGAAAAA	2460
GCTTTCTATG	TTTGGCATGG	GACAGACGGA	AATGAAATTG	TCAAAATTGT	TTAOCATAGA	2520
AAGATGACAA	AAGAAAATT	TCCACATAGG	AAATGCCAT	GAAAAATTGCT	TTTGA AAAAC	2580
AACTGCATAA	CCTTTACACT	CCTCGTCCAT	TTTATTAGGA	TTACCCAAAT	ATAACCAATT	2640
AAAGAAAGAA	TGCATTCCAG	AACAAATTGT	TTACATAAGT	TCCTATACCT	TACTGACACA	2700
TTGCTGATAT	GCAAGTAAGA	AAT				

Seq ID NO: 112 Protein sequence
Protein Accession #: NP_000940

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1	11	21	31	41	51	
MKENVASATV	FTLLFLNTC	LLNQQLPPGK	PEIFKCRSPN	KETFTCWNR	GTGGGLPTNY	60
SLTYHREGTE	LMHECPDYIT	GGPNSCHFGK	QYTSWRTYI	MMVNATNQMG	SSPSDELYVD	120
VTYIVQPPDP	LELAVEVKQP	EDRKPYLWIK	WSPTLIDLK	TGWPTLLYEI	RLKPEKAAEW	180
EIHFAQQQTE	FKILSLHPGQ	KYLQVVRCKP	DHGYNSAWSP	ATFIQIPSD	TMNDTTVNIS	240
VAVLAVICL	IIWVAVALKG	YSMVTCTIPP	VPKPKIRGPD	AHLLEKKGSE	ELLSALGOOD	300
FPPTSDYEDL	LVEYLEVDD	EDQHLMSVHS	KEHPSQGMKP	TYLDPDIDSG	RSGCDSPSLL	360
SEKCEPQAN	PSTFYDPEVI	EKPENPETTH	TWDPQCISME	GKIPYFHAGG	SKCSTWPLPQ	420
PSQHNPSSRY	HNITDVCELA	VGPAGAPATL	LNEAGKDALK	SSQTIKSREE	GRATQOREVE	480
PSHSETDQDT	PWLLPQEKTP	FGSAKPLDYV	EIHKVNDGGA	LSLLPKQREN	SGKPKKPGTP	540
ENNKEYAKVS	GVMDNNILVL	VPDPKAKNVA	CFESSAKEAP	PSLEQNQAEK	ALANFTATSS	600
KCRLQLGGILD	YLDPACTH	PH				

Seq ID NO: 113 DNA sequence
Nucleic Acid Accession #: XM_062811
Coding sequence: 1..888

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TGGCTGGAGC	CGCAGGGCGT	CTGGCGCATC	GGCTTCCAGT	GTCCCGAGCG	CTTGAACGGC	180
GGCGAGGCCA	CATCTGCTG	CGGCGAGCTG	CGCTTGCGCT	ACTGCTGCTC	CAGCGCGAGG	240
GCGGCGCTGG	ACCAGGGCGG	CTGCGACAAT	GACCGCCAGC	AGGGCGCTGG	CGAGCCTGGC	300
CGGGCGGACA	AAGACGGCCC	CGACGGCTCG	GCAATGCCCA	TCTACGTGCC	GTTCTCAATT	360
GTTGGCTCCG	TGTTTGTCGC	CTTTATCATC	TTGGGGTCCC	TGGTGGCAGC	CTGTTGCTGC	420

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AGATGTCCTCC GGCTTAAGCA GGATCCCCAG CAGAGCCGAG CCCCAGGGGG TAACCGCTTG 480
ATGGAGAGCA TCCCCATGAT CCCCAGTGCC AGCACTCCCC GGGGGTGCTC CTCACGCCAG 540
TCCAGCACAG CTGCCAGTTC CAGCTCCAGC GCCAAGTCAG GGGCCCGGGC GCCCCAACA 600
AGGTACACAG CCAACTGTTG CTTGCCGGAA GGGACCATGA ACAACGTGTA TGTCAACATG 660
CCCAAGCAAT TCTCTGTGCT GAACTGTGAG CAGGCCATCC AGATTGTGCC ACATCAAGGG 720
CAGTATCTGC ATCCCCATA CGTGGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA 780
GCTGTGCCAC CTTTCATGGA CGGCCTGCAQ CCTGGCTACA GGCAGATTCA GTCCCCCTTC 840
CCTCACACCA ACAGTGAACA GAAGATGTAC CCAGCGGTGA CTGTATAA
  
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Seq ID NO: 114 Protein sequence
 Protein Accession #: XP_062811

1 11 21 31 41 51
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MVGARRSSVS SSWNAASLLQ LLLAALLAAG ARASGEYCHG WLDAQGVWRI GFQCPERFDG 60
GDATICCGSC ALRYCCSSAE ARLDQGGCDN DRQQGAGEPG RADKDPDGS AVPIYVPLI 120
VGSVFVAPII LGSLLVAACCC RCLRPKQDPQ QSRAPGGNRL METIPIPIPSA STSRGSSSRQ 180
SSTAASSSSS ANSGARAPPT RSQTNCLPE GTMNNVYVNM PTNFSVLWCQ QATQIVPHQG 240
QYLLPPYVGY TVQHDSPVMT AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV
  
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Seq ID NO: 115 DNA sequence
 Nucleic Acid Accession #: NM_013257
 Coding sequence: 223..1512

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TATAAAGTTC TGGTTTCAGT GGAAGAAGT GAATGGTTTG TCTTCAGGAG ATATGCAGAG 180
TTTGATAAAC TTTATAACAC TTTAAAAAAA CAGTTTCCTG CTATGGCCCT GAAGATTCTT 240
GCCAAGAGAA TATTGTGTA TAATTTTGAT CCAGATTITA TTAACAAGAG ACGAGCAGGA 300
CTAAAGCAAT TCATTAGAA CCTAGTTAGG TATCCAGAAC TTTATAACCA TCCAGATGTC 360
AGAGCATTC TCAATGGA CAGTCCAAA CACCAGTCAG ATCCATCTGA AGATGAGGAT 420
GAAAGAAGTT CTCAGAAGCT ACACCTTACC TCACAGAACA TCAACCTGGG ACCGCTGGA 480
AATCCTCATG CCAAACCAAC TGACTTTGAT TTCTTAAAG TTATTGGAAA AGGCAGCTTT 540
GGCAAGGTT TTTCTGAAA ACGGAAACTG GATGGAAAAT TTTATGCTGT CAAAGTGTTA 600
CAGAAAAAAA TAGTTCTCAA CAGAAAAGAG CAAAAACATA TTATGGCTGA ACCTAATGTG 660
CTCTGAAAA ATGTGAAACA TCCGTTTTTG GTTGATTGCT ATTATCTCTT CCAACAACCT 720
GAAAAGCTTT ATTTTGTCTT GGAATTTGTT AATGGAGGGG AGCTTTTTTT CCCTTACAA 780
AGAGAAGCGT CCTTTCCTGA GCACAGAGCT AGGTTTACG CTGCTGAAT TGCTAGTGCA 840
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CAGAATCATC CTTTTTTTGA ATCACTCAGC TGGGCTGACC TTGTACAAA GAAGATTCCA 1320
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ACAGAAGAAA CAGTTTCTGA TTCTGTGTGT GIATCTCTG ACTATCTAT AGTGAATGCC 1440
AGTGATTGG AGGCAGATGA TGCAATCGTT GGTTCCTCT ATGCACCTCC TTCAGAGAC 1500
TTATTTTGT GAGCAGTTG CCATTCAGAA ACCATTGAGC AAAATAAGTC TATAGATGG 1560
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ATTTAAAGC TATTATCTT AGCATTAACC TATTTTAA GAAACCTTT TTGCTATTGA 1800
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CAATTTCAGT TCAGTCAACA TATATTAATA CCTTTGTAAC TCTTTGCTAT GGCTTTTGT 1920
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ACTAAAATA CAAAATTGGC AGGGTGTGGT GGCACATGCC TATAATCCA GCTACTTGG 2280
AGGCTAAGGC AGGAGAATCG CTTGAACCGG GGAGGCGGAG GTTGCAGTGA GCCAGATCG 2340
CACCATGCA CTCCTGCTG GCAACAAGA GTGAAACTCC ATCTCCAAAA A
  
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Seq ID NO: 116 Protein sequence
 Protein Accession #: NP_037389

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MALKIPAKRI FGDNDPDPFI KQRRAGLNEF IQNLVRYPEL YNHPDVRAFL QMDSFKHQSD 60
PSEDEDERSS QKLEHSTQNI NLGPSGNPHA KPTDFDLKV IGKGSFGKVL LAKRKLDGKF 120
YAVKVLQKKI VLNRKQKHI MAERNVLLIK VKHPFLVGLH YSFQTEKLY FVLDPVNGGE 180
LPFHQRERS FPEHRARFYA AEIASALGYL HSIKIVYRDL KPENILLDSV GHVVLDTDFGL 240
CKEGIAISDT TTTFCGTPEY LAPEVIREQP YDNTVDWNCI GAVLYEMLYG LPPFYCRDVA 300
EMVDNLIHKP LSLRPGVSLT AWSILEELLE KDRQNRIGAK EDFLEIQNHP PFESLSWADL 360
VQKIPPPFN FNVAGPDDIR NFDTAFTET VPYSVCVSSD YSIVNASVLE ADDAPVGPVS 420
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Seq ID NO: 117 DNA sequence
 Nucleic Acid Accession #: NM_004004.1

Coding sequence: 1..681

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AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCCCTGCA GCCAGGCTGC 180
AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCACCA TCCGGCTATG GGGCCTGCAG 240
CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT 300
10 GAGAAGAAGA GGAAGTTCAT CAAGGGGGAG ATAAGAGTG AATTTAAGGA CATCGAGGAG 360
ATCAAAACCC AGAAGGTCCG CATCGAAGGC TCCTGTGGT GGACCTACAC AAGCAGCATC 420
TTCTTCCGGG TCATCTTCGA AGCGCCTTC ATGTACGTCT TCTATGTCAT GTACGACGGC 480
TTCTCCATGC AGCGGTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540
15 TTTGTGTCCC GGCCCAAGGA GAAGACTGTC TTCACAGTGT TCATGATTGC AGTGTCTGGA 600
ATTGTCATCC TGCTGAATGT CACTGAATTG TGTATTATGC TAATTAGATA TTGTTCTGGG 660
AAGTCAAAAA AGCCAGTTTA A

Seq ID NO: 118 Protein sequence

Protein Accession #: NP_003995.1

20 1 11 21 31 41 51
MDWGTQLTIL GGVNKHSTSI GKIWLTVLFI FRIMILVVAA KEVWGDEQAD FVCNTLQPGC 60
KNVCYDHYFP ISHRLNALQ LIPVSSPALL VAMHVAYRRH EKRRKFIKGE IKSEPKDIEE 120
25 IKTKQVRIEG SLWWTYTSI PFRVIFEAAP MYVIFYMYDG FSMQRLVKCN ANPCPNTVDC 180
FVSRPTEKTV FTFVMIASVG ICILNVTEL CYLLIRYCSG KSKKPV

Seq ID NO: 119 DNA sequence

Nucleic Acid Accession #: XM_061091.1

Coding sequence: 1..2481

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CCCGGGTACC CGCCAGTGCC GGCTGCCGAT GACCGATTCA CGCTCCCGAT GATGGAGGT 180
CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTAA 240
40 GTTGGGAAGC CTCCTTTTGA GGCAAAACGAA GTCCATGTAA GCAAGAAAC CATCGGGAAG 300
ATTTAGCTTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTTCTGTGA 360
GATGGGTCTA ACAGCGTCCG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA 420
GTCTGTGACG GTCTGGACAT CAGCCCGAG AGGGTCAGAG TGGGAGCATT CCAGTTCAGT 480
TCCACTCCTC ATCTGGAATT CCCCTTGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA 540
AGAATCAAGA GGATGGTTT CAAAGGAGGG CGCACCGAGA CGGAACCTGC TCTGAATATC 600
45 CTCTGACACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
GTCACTCATG GGAAGTCCCA GGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG 720
GGTGTACATG TGTGTCTGT GGGGGTCAGG TTTCCAGGT GGGAGGAGCT GCATGCACTG 780
GCCAGGAGC CTAGAGGGCA GCACTGTCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840
GGCCTCTTCA GCACCTCAG CAGCTCGGCC ATCTGTCTCA GCGCCACGCC AGCTGGGAGC 900
50 CCGAGCTTG TCTTCAATGA GCGGTAAATG GGCATCTCTC TGATAGGCCC CTGTGACTCG 960
CAGCCCTGCC AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCCTC 1020
TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
GTGACCTTCC TCTTCTCTGT GGACAGCTCT GCGGGCACCA CTCTGGACGG CTTCCTCGGG 1140
GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG GCGCTGTCTG GCGAGGACTC TCGGGCCCGA 1200
55 GTGGGTGTGG CCACATACAG CAGGAGCTG CTGGTGGCGG TGCCCTGTGG GGAGTACCAG 1260
GATGTGCTCG ACCTGTCTG GAGCCTCGAT GGCATTCCCT TCCGTGTGGG CCCCACCTG 1320
ACGGGCACTG CCTTGGCGCA GCGGCGCAGG CGTGGCTTCC GGAGCGCCAC CAGGACAGGC 1380
CAGGACCGGC CAGTAGAGGT GGTGGTTTTC CTCACTGAGT CACACTCCGA GGATGAGGTT 1440
GCGGGCCAGC CGCGTACGCG AAGGGCGCGA GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG 1500
60 GCGGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG 1560
GATCTCTCAG ATCTGTTCAA CCAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCGGCGAG 1620
CGGCCAGGGT GCGGACACA AGCCCTGGAC CTCGTCTTCA TGTGGACAC CTCTGCCCTCA 1680
GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT 1740
GAGGTGAACC CTGACGTGAC ACAGGTCCGC CTGGTGTGT ATGGCAGCCA GGTCCAGACT 1800
65 GCCTTCGGGC TGGACACCAA ACCCAACCGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC 1860
CCCTACCTAG GTGGGGTGGG CTCAGCCGCG ACCGCCCTGC TGACATCTA TGACAAAGTG 1920
ATGACCGTCC AGAGGGGTGC CCGGCTGGT GTCCCCAAG CTGTGGTGGT GCTCACAGGC 1980
GGGAGAGGGC CAGAGGATGC AGCCGTTCTT GCCCAGAAGC TGAGGAACAA TGGCATCTCT 2040
70 GTCTTGGTGG TGGGGTGGG GCCTGTCTTA AGTGAGGCTC TGCGGAGGCT TGCAGGTCCC 2100
CGGATTTCCC TGATCCAGGT GGCAGCTTAC GCGAGCTGCG GGTACCACCA GGAAGTGTCT 2160
ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG CCAGTCAACC TCTGCAAAAC CAGCCCGTGC 2220
ATGAATGAGG GCAGCTGCGT CCTGCAGAAAT GGGAGCTACC GCTGCAAGTG TCGGGATGGC 2280
TGGAGGGGCC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340
75 GGATGATATC TTGAGACGCC CCTGAGGCAC ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT 2400
ACCCCTCCCA GCAACTACAG AGAAGGCGCT GGCAGTGAAA TGGTGCCTAC CTCTGGAAT 2460
GTCGTGCCCC CAGGTCCTTA G

Seq ID NO: 120 Protein sequence

Protein Accession #: XP_061091.1

80 1 11 21 31 41 51
MPNTSGITRI EINLLQEPFG HRALVAALLP VSPSPALALA PGYPVPAAD DRFTLPMWGG 60
QMGHEKVDLW SLGVLCYEFL VGKPPFEANE VHVSKETIGK ISAASROMWC SAAVDIMFLL 120

5 DGSNSVKGKS FERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEFPLD SFSTQOEVKA 180
 RIKRMVFKGG RTETELALKY LLHRGLPOGR NASVPQILII VTDGKSQGDV ALPSKQLKER 240
 GVTTFVAVGVR FPRWELHAL ASEPRQHVH LABQVEDATN GLFSTLSSSA ICSSATPAGS 300
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR 360
 VDLLFLDLSS AGTTLDGFLR AKVFVKRFVR AVLSEDSRAR VGVATYSREL LVAVFVGEYQ 420
 DVDPDLVWLD GIPFRGGPTL TGSALRQAAE RGFSGATRTG QDRPRRVVVL LTESHSEDEV 480
 AGPARHARAR ELLLLGVGSE AVRAELEET GSFRHVMVYS DPQDLFNQIP ELQGLKLSRQ 540
 10 RPGCRTQALD LVFMLDTSAS VGPENFAQMQ SFVRSALQF EVNPDVTQVG LVVYGSQVQT 600
 AFGLDTKPTR AAMLRALISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG 660
 GRGAEDAVP AQKLNNNGIS VLVVGVGPVL SEGLRLLAGP RDSLTHVAAY ADLRYHQDVL 720
 IENLCEAKQ PVNLCKPSPC MNEGSCVLQV GSYRCKCRDG WEGPHCENRE WSSCSVCVSQ 780
 GWILETPLRH MAPVQEGSSR TPPSNYREGL GTEMVPTFWN VCAPGP

Seq ID NO: 121 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..2424

20 1 11 21 31 41 51
 ATGCCCCCTT TCCTGTTGCT GGAGGCGCTG TGTGTTTTCC TGTTTTCCAG AGTGCCCCCA 60
 TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120
 AGCAAAATGA TGTGGTGCCT GGCTGCAGTG GACATCATGT TTCTGTTAGA TGGGTCTAAC 180
 AGCGTCGGGA AAGGGAGCTT TGAAGAGTCC AAGCATTGT CCATCACAGT CTGTGACGGT 240
 25 CTGGACATCA GCCCGAGAG GGTGAGAGTG GGAGCATTCC AGTTGAGTTC CACTCCTCAT 300
 CTGGAATTCC CTTGGATTTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
 ATGGTTTTCA AAGGAGGGCG CACGAGAGAG GAACTTGCTC TGAATACCTT TCTGCACAGA 420
 GGGTTCCTCG GAGGAGAGAA TGCTTCTGTG CCCAGATCC TCATCATCGT CACTGATGGG 480
 AAGTCCACAG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTACTGTG 540
 30 TTTGCTGTGG GGGTCAGGTT TCCCAAGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600
 AGAGGGCAGC ACGTGTCTGT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660
 ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
 CCTGTGAGC CACGAGCGCT GGAGATGGTC CGGAGTTGCG CTGGCAATGC CCCATGCTGG 780
 AGAGGATCGC GGCGGACCTT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
 35 AGAGTGTTC TAAACCAACC TGCCACCTGC TACAGGACCA CCGTCCAGG CCCCTGTGAC 900
 TCGCAGCCCT GCCAGAAATG AGGCACATGT GTTCCAGAA GACTGGAAGG CTACCACTGC 960
 CTCTGCCCGC TGGCCTTTGG AGGGAGGAGT AACTGTGCCC TGAAGCTGAG CTTGGAATGC 1020
 AGGTCGACC TCCTCTCTCT GCTGGACAGC TCTGCGGCA CCACTCTGGA CGGCTTCCTG 1080
 CGGGCCAAAG TCTTCGTGAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
 40 CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGTGCTGCTG GGGGAGTAC 1200
 CAGGATGTGC TAGGTGGGGT CTGGAGCCTC GATGGCATT CCTTCCGTGG TGGCCCCACC 1260
 CTGACGGGCA GTGCCTTGGG CGAGCGGGCA GAGCGTGGCT TCGGAGCGGC CACGAGGACA 1320
 GGCCAGGACC GGCCACGTAG AGTGGTGGTT TTGCTCACTG AGTCACACT CGAGGATGAG 1380
 GTTGGGGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440
 45 GAGGCGGTGC GGGCAGAGCT GGAGGAGATC ACAGGAGGCC CAAAGCATGT GATGGTCTAC 1500
 TCGGATCTCT AGGATCTGTT CAACCAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCTGG 1560
 CAGCGGCCAG GTGCGCGGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC 1620
 TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTC TGAGAAGCTG TGCCCTCCAG 1680
 TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCTGCTGGG TGTATGGCAG CCAGGTGCAG 1740
 50 ACTGCCCTTC GGCTGGACAC CAAACCCACC GGGGCTGCGA TGCTGCGGGC CATTAGCCAG 1800
 GCCCCTTACC TAGGTGGGGT GGGCTCAGCC GGCAACGCCC TGCTGCACAT CTATGACAAA 1860
 GTGATGACCG TCCAGAGGGG TGCCCGGCTT GGTGTCCCA AGCTGTGGT GGTGCTCACA 1920
 GCGGGGAGAG GCGCAGAGGA TGCAGCGGTT CCTGCCGAGA AGCTGAGGAA CAATGGCATC 1980
 TCTGTCTTGG TGTGGGGGCT GGGGCTGTG CTAAGTGAGG GTCTGCGGAG GCTTGAGGT 2040
 55 CCGCGGGATT CCTGATCCA CGTGGCAGCT TACGCGGACC TGCGGTACCA CCAGGACGTG 2100
 CTCATTGAGT GGCTGTGTGG AGAAGCCAA CAGCCAGTCA ACCTCTGCAA ACCGAGCCG 2160
 TGCATGAATG AGGCGAGCTG CGTCTGTCAG AATGGGAGCT ACCGCTGCAA GTGTGGGAT 2220
 GGCTGGGAGG GCGCCACTG CGAGAACCGT GAGTGGAGCT CTGTCTCTGT ATGTGTGAGC 2280
 CAGGGATGGA TTCTTGAGAG GCCCCTGAGG CACATGGCTC CGGTGCAGGA GGGCAGCAGC 2340
 60 CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG 2400
 AATGTCTGTG CCCCAGGTCC TTAG

Seq ID NO: 122 Protein sequence

Protein Accession #: Eos sequence

65 1 11 21 31 41 51
 MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SRMMWCSAAV DIMFLLDGSN 60
 SVGKGSFERS KHFAITVCDG LDISPFRVVR GAFQFSSTPH LEFPLDSFST QQEVKARIK 120
 70 MVFKGGRTET ELALKYLLER GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKRGVTV 180
 FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLPS TLSSSAICSS ATPDCRVEAH 240
 PCERTLEMV REFAGNAPCW RGSERTLAVL AAHCFFYSWK RVFLTHPATC YRTTCRPGCD 300
 SQPCQNGGTC VPBGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
 RAKVFKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWLD DGIPFRGGPT 420
 75 LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTESHSEDE VAGPARHARA RELLLGVGS 480
 EAVRAELEET GSFRHVMVYS SDPQDLFNQI PELQGLKLSR QRPGRCTQAL DLVFMLDTSA 540
 SVGPENFAQM SFVRSALQF FEVNPDTQV GLVYGSQVQ TAFGLDTPKT RAAMLRALISQ 600
 APYLGGVGSAG TALLHIYDK VMTVQRGARP GVPKAVVVL GGRGAEDAAV PAQKLNNNGI 660
 SVLVGVGFV LSEGLRLLAG PRDSLTHVAA YADLRYHODV LIENLCEAK QPVNLCKPSP 720
 80 CMNEGSCVLQ NGSYRCKCRD WEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
 RTPPSNYREG LGTEMVPTFW NVCAPGP

Seq ID NO: 123 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 89..2356

	1	11	21	31	41	51	
5	GCCCCCTGGC	COGAGCCGCG	CCCGGGTCTG	TGAGTAGAGC	CGCCCGGGCA	COGAGCGCTG	60
	GTGCGCGCTC	TCCTTCGGTT	ATATCAACAT	GCCCCCTTTC	CTGTTGCTGG	AAGCCGCTG	120
	TGTTTTCTCT	TITTTCCAGAG	TGCCCCCATC	TCTCCCTCTC	CAGGAAGTCC	ATGTAAGCAA	180
	AGAAACCATC	GGGAAGATT	CAGCTGCCAG	CAAAATGATG	TGGTGCTCGG	CTGCAGTGGA	240
	CATCATGTTT	CTGTAGATG	GGTCTAACAG	CGTCGGGAAA	GGGAGCTTTG	AAAGGTCCTA	300
10	GCACCTTGCC	ATCACAGTCT	GTGACGGTCT	GGACATCAGC	CCCGAGAGGG	TCAGAGTGGG	360
	AGCATTCCAG	TTCAATTCCA	CTCCTCATCT	GGAATTCCCC	TTGGATTTCAT	TTTCAACCCA	420
	ACAGGAAGTG	AAGGCAAGAA	TCAAGAGGAT	GGTTTTCAAA	GGAGGGCCCA	CGGAGACCGA	480
	ACTTGCTCTG	AAATACCTTC	TGCACAGAGG	GTTGCCTGGA	GGCAGAAATG	CTTCTGTGCC	540
	CCAGATCTCT	ATCATCGTCA	CTGATGGGAA	GTCGCCAGGG	GATGTGGCAC	TGCCATCCAA	600
15	GCAGCTGAAG	GAAAGGGGTG	TCACTGTGTT	TGCTGTGGGG	GTCAAGTTTC	CCAGGTGGGA	660
	GGAGCTGCAT	GCACTGGCCA	GCGAGCCTAG	AGGGCAGCAC	GTGCTGTGGG	CTGAGCAGGT	720
	GGAGGATGCC	ACCAACGGCC	TCTTCAGCAC	CCTCAGCAGC	TGGCCATCT	GCTCCAGCGC	780
	CACGCCAGCT	TGCAGGTCG	AGGCTCACCC	CTGTGAGCAC	AGGACGCTGG	AGATGGTCCG	840
	GGAGTTCGCT	GGCAATGCC	CATGCTGGAG	AGGATCGCGG	CGGACCCCTG	CGGTGCTGGC	900
20	TGCACACTGT	CCCTTCTACA	GCTGGAAGAG	AGTGTTCCTA	ACCCACCCTG	CCACCTGCTA	960
	CAGGACCACC	TGCCCAGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAATGGAG	GCACATGTGT	1020
	TCCAGAAGGA	CTGGACGGCT	ACCAGTGCCT	CTGCCCGCTG	GCCTTTGGAG	GGGAGGCTAA	1080
	CTGTGCTCTG	AAGCTGAGCC	TGGAAATGCAG	GGTCGACCTC	CTCTTCTCTG	TGGACAGCTC	1140
	TGCGGGCACC	ACTCTGGAGC	GCTTCTCTCG	GGCCAAAGTC	TTCGTGAAGC	GTTTGTGGGG	1200
25	GGCCGTGCTG	AGCCGAGACT	CTCGGGCCCG	AGTGGGTGTG	GCCACATACA	GCAGGGAGCT	1260
	GCTGGTGGCG	GTGCTGTGGG	GCGAGTACCA	GGATGTGCTT	GACCTGGTCT	GGAGCCTCGA	1320
	TGGCATTCCC	TTCCGTGGTG	GCCCCACCTT	GACGGGCAGT	GCCTTGGCGC	AGGCGGCAGA	1380
	GGGTGGCTTC	GGGAGCGCCA	CCAGGACAGG	CCAGGACCGG	CCACGTAGAG	TGGTGGTTTT	1440
	GCTCACTGAG	TCACTCTCCG	AGGATGAGGT	TGCGGGCCCA	GCGCGTCACG	CAAGGGCGCG	1500
30	AGAGCTGCTC	CTGCTGGGTG	TAGGCAGTGA	GGCCGTGCGG	GCAGAGCTGG	AGGAGATCAC	1560
	AGGCAGCCCA	AGCATGTGTA	TGGTCTACTC	GGATCCTCAG	GATCTGTTC	ACCAAATCCC	1620
	TGAGCTGAGC	GGGAAGCTGT	GCAGCCCGCA	GCGGCCAGGG	TGCCGGACAC	AAGCCCTGGA	1680
	CCTCGTCTTC	ATGTTGGACA	CCTCTGCTCT	AGTAGGGCCC	GAGAAATTTG	CTCAGATGCA	1740
	GAGCTTTGTG	AGAAGCTGTG	CCCTCCAGTT	TGAGGTGAAC	CCTGACGTGA	CACAGGTCCG	1800
35	CTGCTGGTGT	TATGGCAGCC	AGGTGCAGAC	TGCCTTCCGG	CTGGACACCA	AACCCACCCG	1860
	GGCTGCGATG	CTGCGGGCCA	TAGCCAGGCG	CCCCACCTTA	GGTGGGGTGG	GCTCAGCCGG	1920
	CACCCCGCTC	CTGCACATCT	ATGACAAAGT	GATGACCGTC	CAGAGGGGTG	CCCGGCTTGG	1980
	TGTCGCCCAA	GCTGTGGTGT	TGCTCACAGG	CGGGAGAGGC	GCAGAGGATG	CACCGGTTC	2040
	TGCCCAGAAG	CTGAGGAACA	ATGGCATCTC	TGCTTTGGTC	GTGGGCGTGG	GGCCTGTCTT	2100
40	AAGTGAGGGT	CTGCGGAGGC	TTGCAGGTCC	CCGGGATTCC	CTGATCCACG	TGGCAGCTTA	2160
	CGCCGACCTG	CGGTACACCC	AGGACGTGCT	CATTGAGTGG	CTGTGTGGAG	AAGCCAAGCA	2220
	GCCAGTCAAC	CTCTGCAAA	CCAGCCCGTG	CATGAATGAG	GGCAGCTGCG	TCTCTCAGAA	2280
	TGGGAGCTAC	CGCTGCAAGT	GTCGGGATGG	CTGGGAGGGC	CCCCACTGCG	AGAACCGATT	2340
	CTTGAGAGCG	CCCTGAGGCA	CATGGCTCCC	GTGCAGGAGG	GCAGCAGCCG	TACCCCTCCC	2400
45	AGCACTACA	GAGAGGGCCT	GGGCACTGAA	ATGTGTGCTA	CCTTCTGGAA	TGTCTGTGCC	2460
	CCAGGTCTCT	AGAAATGTCT	CTTCCGCGCG	TGGCCAGGAG	CACATTTCTC	ACTGAGGGAG	2520
	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTCAACCCAC	2580
	AAACGATGTT	GTGAAAGT	TTTGATGTGT	AAGTAAATAC	CCACTTTCTG	TACCTGTCTG	2640
	GCCTTGTGTA	GGCTATGTGA	TCTGCCACCT	TTCCTTGAG	GATAAACAA	GGGTCTTGAA	2700
50	GACTTAAATT	TAGCGGCTCT	ACGTTCTCTT	GCACACAATC	AATGCTCGCC	AGAATGTTGT	2760
	TGACACAGTA	ATGCCACGA	GAGGCTTTTA	CTAGAGCATC	CTTTGGACGG		

Seq ID NO: 124 Protein sequence
Protein Accession #: Eos sequence

55	1	11	21	31	41	51	
	MPPFLLEAV	CVFLPSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
	SVKGSGSFERS	KHPAITVCDG	LDISPERVRV	GAFQFSSTPH	LEFPLDSPT	QDEVKARIKR	120
60	MVFKGGRTE	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKRGVTV	180
	FAVGVRFPRT	EELHALASEP	RQHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCEVEAH	240
	PCEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCPGPCD	300
	SQPCQNGGTC	VPEGLDGYQC	LCPLAFGSEA	NCALKLSLEC	RVDLLFLDLS	SAGTTLDGFL	360
	RAKVFVKRFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVPDLVNSL	DGIPFRGGPT	420
65	LTGSALRQAA	ERGFGSATRT	GQDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLVGVS	480
	EAVRAELEBI	TGSPKHMVY	SDPQDLFNQI	PELQGLKCSR	QRPGCRTQAL	DLVFMIDTSA	540
	SVGFENFAQM	QSFVRSCALQ	FEVNPDTVQV	GLVVYGSQVQ	TAFGLDTKPT	RAAMLRAISQ	600
	APYLGGVGSA	GTAALLHIYDK	VMTVQRGARP	GVPKAVVVL	GGRGAEDAAV	PAQKLNNNGI	660
	SVLVVGVGVF	LSEGLRRLAG	PRDSLIIHVA	YADLRYHQDV	LIEWLCGEAK	QPVNLCKPSP	720
70	CWNEGSCVLQ	NGSVYRCKRD	GWE3PHECNR	FLRRP			

Seq ID NO: 125 DNA sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

75	1	11	21	31	41	51	
	CCCGAGCCCC	GCCCCCTCGG	GCCCGGGTGG	GCGCGCCGAC	CCTGCCAGCC	GCGCTGCTGC	60
	TGCTCTCTCT	GCTGTGGGAC	CGCTGACCGC	GCGGCTGCTC	CGCTCTCCCC	GCTCCAAGCG	120
80	COGATCTGGG	CACCGGCCAC	CAGCATGGAC	GCTCGCCGCG	TGCCCGAGAA	AGATCTCAGA	180
	GTAAGAAGAA	ACTTAAAGAA	ATTGAGATAT	GTGAAGTTGA	TTTCCATGGA	AACCTCGTCA	240
	TCCTCTGATG	ACAGTTGTGA	CAGCTTTGCT	TCTGATAATT	TTGCAAAACAC	GAGGCTGCAG	300
	TCAGTTGGGG	AAGGCTGTAG	GACCCGACGC	CAGTGCAGGC	ACTCTGGACC	TCTCAGGGTG	360
	GCGATGAAGT	TTCCAGCGCG	GAGTACCAGG	GGAGCAACCA	ACAAAAGAGC	AGAGTCCCCG	420
	CAGCCCTCAG	AGAATTCTGT	GACTGATTCC	AACTCOGATT	CAGAAGATGA	AAGTGAAGT	480

5 AATTTTITGG AGAAAAGGCG TTTAAATATA AAGCAAAACA AAGCAATGCT TGCAAAACTC 540
 ATGCTCTGAAT TAGAAAGCTT CCCTGGCTCG TTCGTTGGAA GACATCCOCT CCCAGGCTCC 600
 GACTCACAAAT CAAGGAGACC GCGAAGGCGT ACATTCCCGG GTGTTGCTTC CAGGAGAAAC 660
 CCTGAACCGA GAGCTCGTCC TCTTACCAGG TCAAGGTCCC GGATCCTCGG GTCCCTTGAC 720
 GCTCTACCCA TGGAGGAGGA GGAGGAAGAG GATAAGTACA TGTGTTGAG AAAGAGGAAG 780
 ACCGTGGATG GCTACATGAA TGAAGATGAC CTGCCAGAA GCCGTGCTC CAGATCATCC 840
 GTGACCTTTC CGCATATAAT TCGCCAGTGA GAAGAAATTA CAGAGGAGGA GTTGAGAAC 900
 GTCTGCAGCA ATTCTGAGA GAAGATATAT AACGTTTAC TGGGCTCTAC TTGTCATCA 960
 10 TGCCTGAGA AGACTATTGA TACCAAAACA AACTGCAGAA ACCCAGACTG CTGGGGCTT 1020
 CGAGGCCAGT TCTGTGGCCC CTGCCTTCGA AACGTTATG GTGAAGAGGT CAGGGATGCT 1080
 CTGCTGGATC CGAACTGGCA TTGCCCGCCT TGTGAGGAA TCTGCACTG CAGTTTCTGC 1140
 CGGCAGCGAG ATGGAAGGTG TGGACTGGG GTCCTTGTG ATTTAGCCAA ATATCATGGC 1200
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 15 TATCTGGAAT ATTTGCTGCC TGCCCTCTAC TTCTCAATC TTTCTGTAA AAGTTTCCAA 1320
 TTTTCTACT GAAACCTGAG TTAATAATCT TGATGATCAG CCTGTTTCAT AAGAACTCC 1380
 AATCAAGTTA ATCTTAGCAG ACATGTGTTT CTGGAGCATC ACAGAAGTTA TATTGCTAGT 1440
 TACACTTTGC CCTCTGAG TTTCTTCTCT GCTCCCAACC CCCATCTCAT AGCATCCCC 1500
 TCTATTTCCA ATGCTCCTCT CCAACCGCTT AGTTTCTGAA TTTCTTTTAA ATTACAGTTT 1560
 20 TATGAAAGCA TATTTTATTT ACTTGTGTTT GAAATAGCCC TCATAAAAC TAAGCACTTG 1620
 GAAACACAAAT AATAGTATTA ACTAATAGA TCTATTGAAT TTCAGAGAAG AGCCTCTAA 1680
 CTGTGTTTCA CAAAACGAG TATGATTTAG CACTCATACT AGTTGAAAT TTTAATAGAA 1740
 TCAAGGCACA AAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT 1800
 CTCTCAATCC CATGATTGCG GCTTATGTTA CAAGTTGTTG TCACAGTTGA GACTTAATTT 1860
 25 CTCTTAATTT CTCTGCCCCG AAGGTAAGT GGTGCGTCCA GCTTACCGA TCATAATTCA 1920
 AAGGTTGTGG GGCATGTAA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGAGATT 1980
 ATGAGTAAGC TGATTTGAAT TTTCAGTATA AAACCTTAGT ATAATTGTAG TTTGCAAGT 2040
 TTATTTCAGT TCACATGTAA GGTATTGCAA ATAAATTCIT GGCAAAATTT GTATGGAAC 2100
 TTGATATTAA AACTAGTCT GTGGTTCTTT GCAGTTTCTT GTAAATTTAT AAACCAAGCA 2160
 30 CAAGGTTCAA GTTTAGATT TAAGCACTTT TATAACAATG ATAAGTGCCT TTTTGAGAT 2220
 GTAACTTTTA GCAGTTTGT AACTGACAT CTCTGCCAGT CTAGTTTCTG GGCAGGTTTC 2280
 CTGTGTCACT ATTCGCCCTC CTCTTTCAT TAATCAAGGT ATTTGGTAGA GGTGGAATCT 2340
 AAGTGTGTTT ATGTCCAATT TACTTGATA TGTAAACCAT TGCTGTGCGA TTCATGTTT 2400
 GATGCATAAT TGGACCTTGA ATCGATAAGT GTAAATACAG CTTTGTATCT GTAATGCTT 2460
 35 TATACAAAG TTTATTTTAA TAATAAAATG TTTGTCTTAA AAAAAAATA

Seq ID NO: 126 Protein sequence
 Protein Accession #: NP_114148.1

40 1 11 21 31 41 51
 MDARRVPQKD LRVKKNLKKF RYVKLISMET SSSSDDSCDS FASDNFANTR LQSVREGCRT 60
 RSQCRHSGL RVAMKFPARS TRGATNKKAE SRQPSNSVT DSNSDSEDES GMINFLEKRAL 120
 NTKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRRPR RRTFPGVASR RNPERRARPL 180
 45 TRSRRIILGS LDALPMEESE EEDKMYLVRK RKTVDGYMNE DDLPRSRSR SSVTLPHIIR 240
 FVEEITEEEL ENVCNSNREK IYNRSLGSTC HQCRQKTIIDT KTNCRNPDCW GVRGQFCGPC 300
 LRNRGYEEVR DALLDPNWHC PPCRGICNCS FCRQRDGRCA TGVLVYLAKY HGPNVHAYL 360
 KSLKQEFEMQ A

Seq ID NO: 127 DNA sequence
 Nucleic Acid Accession #: AF305616.1
 Coding sequence: 1..863

55 1 11 21 31 41 51
 ATGCACCGCT TGATGGGGGT CAACAGCACC GCGCGCGCGG CCGCGGGGCA GCCCAATGTC 60
 TCTGCAAGT GCAACTGCAA ACGCTCTTTG TTCCAGAGCA TGGAGATCAC GGAGCTGGAG 120
 TTTGTTTCTA TCAATCATAT CTTGTTGTTG ATGATGTTGA TGGTGGTGGT GATCACTGTC 180
 CTGCTGAGCC ACTACAAGCT GTCTGCACGG TCTTTCATCA GCCGGCACAG CCAGGGGGGG 240
 60 AGGAGAGAAG ATGCCCTGTC CTGAGAAGGA TGCTGTGGC CCTCGGAGAG CACAGTGTCA 300
 GGCAACGGAA TCCAGAGGCC GCAGGTCTAC GCGCGCCTC GGCCCAACCA CCGCTGSCC 360
 GTGCCCGCCT TCGCCAGCGG GAGCGGCTTC CACCGCTTCC AGCCCACTA TCGGTACCTG 420
 CAGCAAGAGA TCGACCTGCC ACCACCATC TCGCTGTGAG ACGGGGAGGA GCCCCACCC 480
 TACCAGGGCC CTGCAACCTT CCAGCTTTCG GACCCGAGC AGCAGCTGGA ACTGAACCGG 540
 GAGTCTGGTC GCGCACCCCC AAACAGAAC ATCTTCGACA GTGACCTGAT GGATAGTGCC 600
 65 AGGCTGGGCG GCCCTTGCCC CCCAGCAGT AACTCGGGCA TCAGCGCCAC GTGCTAAGGC 660
 AGCGCGGGGC GCATGGAGGG GCGCGCGCCC ACCTACAGCG AGGTATCGG CCACTACCCG 720
 GGGTCTCTCT TCCAGCACCA GCAGAGCAGT GGGCGCGCCT CCTGTCTGGA GGGGACCCGG 780
 CTCCACCACA CACATATGCG GCCCTTAGAG AGCGCAGCCA TCTGGAGCAA AGAGAAGGAT 840
 70 AAACAGAAAG GACACCTCT CTAG

Seq ID NO: 128 Protein sequence
 Protein Accession #: AAL09357.1

75 1 11 21 31 41 51
 MHRIMGVNST AAAAAGQPNV SCTCNCKRSL PQSMEITELE FVQIIIVVV MMVMVVVITC 60
 LLSHYKLSAR SPISRHSQGR RREDALSSEG CLWPSSESTVS GNGIPEQVY APPRPTDRLA 120
 VPPFAQRERF HRFQPTYPYL QHEIDLPTT SLSDGSEPPF YQGPCTQLR DPEQQLNLR 180
 80 ESVRAPPNRT IPDSLDMSA RLGGPCFPSS NSGISATCYG SGGRMBGPPP TYSEVIGHYP 240
 GSSFQHQSS GPPSLLEGTR LHTHTIAPLE SAAIWSKEKD RQKQHL

Seq ID NO: 129 DNA sequence
 Nucleic Acid Accession #: NM_004952.1

Coding sequence: 1..718

1 11 21 31 41 51
5 ATGGCGGGG CTCCGCTGCT GCTGCTGCTG CTGCTCGTGC CGTGCCGCT GCTGCGCTG 60
CTGGCCCAAG GGCCCGGAGG GCGCTGGGA AACCGGCATG CGGTGTACTG GAACAGCTCC 120
AACCAGCACC TGCCGCGAGA GGGCTACACC GTGCAGGTGA ACGTGAACGA CTATCTGGAT 180
ATTTACTGCC CGCACTACAA CAGCTCGGGG GTGGGCCCGG GGGCGGGACC GGGGCCCGGA 240
10 GGCGGGCAGG AGCAGTACGT GCTGTACATG GTGAGCCGCA ACGGCTACCG CACCTGCAAC 300
GCCAGCCAGG GCTTCAAGCG CTGGGAGTGC AACCGGCCCG ACGCCCGCA CAGCCCATC 360
AAGTTCTGGG AGAAGTTCCA GCGCTACAGC GCCTTCTCTC TGGGCTACGA GTTCCAAGCC 420
GGCCACGAGT ACTACTACAT CTCCACGCCC ACTCACAACC TGCACCTGAA GTGTCTGAGG 480
ATGAAGGTGT TGTCTGCTG GCGCTCCACA TCGCACTCCG GGGAGAAGCC GGTCCCCACT 540
15 CTCCCCAGT TCACCATGGG CCCCAGTGTG AAGATCAACG TGCTGGAAGA CTTTGAGGGA 600
GAGAACCCTC AGGTGCCCAA GCTTGAGAAG AGCATCAGCG GGACCCAGCC CAAACGGGAA 660
CACCTGCCCC TGCCGCTGGG CATCGCCTTC TTCCTCATGA CGTCTTGCC CTCCAG

Seq ID NO: 130 Protein sequence
Protein Accession #: NP_004943.1

1 11 21 31 41 51
20 MAAAPLLLLL LLVPVPLLLP LAQGGGALG NRHAVYWNSS NQHLRREGYT VQVNVNDYLD 60
IYCPHYNSSG VGPAGGPGPG GGAEQYVLYM VSRNGYRTCN ASQGFKRWEC NRPHAPHSPI 120
25 KPSEKFPQYS AFSLGYEFHA GHEYYIISTP THNLHWKCLR MKVFVCCAST SHSKEKFPVT 180
LPQFTMGPNV KINVLDFEG ENPQVPKLEK SISGTSKREB HPLAVGIAF FLMTFLAS

Seq ID NO: 131 DNA sequence
Nucleic Acid Accession #: NM_012445.1
Coding sequence: 276..1271

1 11 21 31 41 51
35 GCACGAGGGA AGAGGTGAT CCGACCCGGG GAAGGTGCTT GGGCAGGGCG AGTTGGGAAA 60
GGCGCAGCCC CGCCCGCCCC CGCAGCCCCC TCTCTCTCTT TCTCCACGCT CCTATCTGCC 120
TCTGCTGGA GGCCAGGCGG TGCAAGCATG AAGACAGGAG GAAGTGGAGC CTCATTGGCC 180
GGCCCGGGCG GCGCGCTCG GGCCTAAATA GGAGCTCCGG GCTCTGGCTG GGACCGGACC 240
GCTGCGGCGC GCGCTCCGCG TGCTCTCTCC GGGTGTGGA AAACCCGAGC CCGCGCGCGC 300
40 CCTGGGCAA GGCCCTCTGC GCTCTCTCTC TGGCCACTCT CGGCGCGCGC GGCCAGCCTC 360
TTGGGGGAGA GTCCATCTGT TCGCCAGAG CCGCGGCCAA ATACAGCATC ACCTTCACGG 420
GCAAGTGGAG CAGACCGGCC TTCCCCAAGC AGTACCCCTT GTTCCGCCCC CCTGCGCAGT 480
GGTCTTCTGT GCTGGGGGCG GCGCATAGCT CCGACTACAG CATGTGGAGG AAGAACCACT 540
ACGTGAGTAA CCGGCTGCGC GACTTTGCGG AGCGCGGCGA GGCCTGGGCG CTGATGAAGG 600
45 AGATCGAGGC GGCGGGGAGG GCGCTGCAGA GCGTGCAAGC GGTGTTTTCG GCGCCGCGCG 660
TCCCGAGCGG CACCGGGCAG ACGTCCGCGG AGCTGGAGGT GCGCGCAGG CACTCGCTGG 720
TCTGTTTGT GGTGCGCATC GTGCCAGGCC CCGACTGCTT CGTGGCGGTG GACAGCCTGG 780
ACCTGTGCGA CCGGAGACGT TGGCGGGAAC AGCGCGCGCT GGACCTGTAC CCTACGAGC 840
50 CCGGAGCGGA CAGCGGCTTC ACCTTCTCTT CCGCCACTT CGCCACCATC CCGCAGGACA 900
CGGTGACCGA GATAAGCTCC TCTCTCTCCA GCGACCGGCG CACTCTCTTC TACTACCCGC 960
GGCTGAAGGC CTGCGCTCCC ATCGCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCCA 1020
GGGCTTCTAT CCTCCCGGCC CAGTCTCTCG CAGCAGGGA CAATGAGATT GTAGACAGCG 1080
CCTCAGTTCC AGAAACGCGG CTGGAAGTGG AGGTCTCCCT GTGGTCTGTC TGGGGACTGT 1140
GGCGAGGCGA CTGTGGGAGG CTGGGAGCA AGAGCAGGAC TCGCTACGTC GGGTCCAGC 1200
55 CCGCCACCAA CCGGAGCGCC TGCCCGGAGC TCGAAGAAGA GGTGAGTGC GTCCCTGATA 1260
ACTGCGTCTA AGACCAAGGC CCGCAGGCC CTGGGGCCCC CGGAGCCATG GGGTGTGCGG 1320
GGCTCTGTG CAGGCTCATG CTGCGGCGG CCGAGGCACA GGGGTTTCG CGCTGCTCTT 1380
GACCGCGTGT AGGCGCGGCC GACCATCTCT GCACTGAAGG GCGCTCTGTT GGCGCGGACG 1440
GGCATTTGGA AACAGCTTCC TCTTCTCCA ACCTTGCTTC TTAGGGGCGC CCGTGTCCCG 1500
60 TCTGCTCTCA GCTCTCTCT CTTGAGGAT AAAGTCAATC CCAAGGCTCC AGCTACTCTA 1560
AATTATGTC TCCTTATAAG TTATTGCTGC TCCAGGAGAT TGTCTTCTAT GGTCCAGGGG 1620
CTGCTCTCCC AGTGTGTTGC AGATACCTCA GACCTGGTGC TCTAGGCTGT GCTGAGCCCA 1680
CTCTCCGAG GCGGCATCCA AGCGGGGGCC ACTTGAGAAG TGAATAAATG GGGCGGTTTC 1740
65 GGAAGCGTCA GTGTTTCCAT GTTATGGATC TCTCTGCGTT TGAATAAAGA CTATCTCTGT 1800
TGCTCAC

Seq ID NO: 132 Protein sequence
Protein Accession #: NP_036577.1

1 11 21 31 41 51
70 MENPSPAAL GKALCALLL TLGAAGQPLG GESICBARAP AKYSITFTGK WSQTAPFKQY 60
PLFRPPAQWS SLGAAHSSD YSMWRKNQYV SNGLRDPFER GEAWALMKEI EAAGEALQSV 120
HAVPSAPAVP SGTGQTSABL EVQRRHSLVS FVVRIVPSPD WFGVDSLDL CDGDRWREQA 180
75 ALDLYPYDAG TDSGFTFSSP NFATIPQDTV TEITSSSPSH PANSFYYPRL KALPPIARVT 240
LVRLRQSPRA FIPPAFVLPF RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRLGTGS 300
RTRYVRVQPA NNGSPCELE EEAECVPDNC V

Seq ID NO: 133 DNA sequence
Nucleic Acid Accession #: NM_019894
Coding sequence: 1..1314

1 11 21 31 41 51
80 ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60

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AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
CTGAGCCCTGG CGAGTATCAT CATTTGTGGTT GTCTCTCATCA AGGTGATTCT GGATAAATAC 180
TACTTCTCTT GCGGGCAGCC TCTOCACITC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
CTGGAATGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTGCGCCACA 360
GGGAACCTGGT TCTCTGCTCG TTTGACAAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGCATGCG GAACTCAAGT 540
GGGCCCTGTC TCTCAGGCTC CTTGGTCTCC CTGCACGTGC TTGCTGTGGG GAAGAGCCTG 600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
CTCAGGCGAG CCCACTGCTT CAGGAAACAT AOCGATGTGT TCAACTGAGG GGTGGGGSCA 780
GGCTCAGACA AACTGGGCGG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
ACTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
GCCACCCCACT CTGTGATCAT TGGATGGGCG TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
GACATATGTC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
GGGTACCAAG GGGAGGTGAC CGAGAAGATG ATGTGTGACG GCATCCCGGA AGGGGGTGTG 1140
GACACTGCGC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCACAG AGTATACACC 1260
AAGGTCTCAG CCTATCTCAA CTGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
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Seq ID NO: 134 Protein sequence
Protein Accession #: NP_063947.1

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1 11 21 31 41 51
| | | | |
MLQDPDSQPL LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY 60
YFLCQQLPHF IPRKQLCDGE LDCPLGEDEE HCVKSPFEPG AVAVRLSKDR STLQVLSAT 120
GWNFSACFDN FTALALATAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWFWQV SIQYDKQHVC GGSILDPHWV 240
LTAHCPRKH TDVFNWKVRA GSDKLGSPFS LAVAKIIIE FNPMPKMD IALMKLQFPL 300
TFSGTVRPIC LPFFDEELTP ATPLWIIWGW FTQNGGKMS DILLQASVQV IDSTRCNADD 360
AYQGEVTEKM MCAGIFEGGV DTCQDSGGP LMYQSDQMHV VGIWSWGYGC GGPSTPGVYT 420
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Seq ID NO: 135 DNA sequence
Nucleic Acid Accession #: NM_003045
Coding sequence: 148..2037

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1 11 21 31 41 51
| | | | |
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CTGAGACATC TTTGCTGCAA GATCGAGGCT GTCTCTGGT GAGAAGGTGG TGAGGCTTCC 120
CGTCATATTC CAGCTCTGAA CAGCAACATG GGGTGCAAG TCCTGCTCAA CATTGGGCAG 180
CAGATGCTGC GGGCGAAGGT GGTGGACTGT AGCCGGGAGG AGACGCGGCT GTCTCGCTGC 240
CTGAACACTT TTGATCTGGT GGCCTCGGG GTGGGCAGCA CACTGGGTGC TGGGTCTAC 300
GTCCGGCTG GAGCTGTGGC CGGTGAGAAT GCAGGCCCTG CCATTGTCTC CTCTCTCTG 360
ATCGCTGCGC TGGCTTCAGT GCTGGCTGGC CTGTGCTATG GCGAGTTTGG TGCTCGGGTC 420
CCCAAGACGG GCTCAAGCTTA CCTCTACAGC TATGTACCG TTGGAGACTC CTGGCCCTTC 480
ATCACCGGCT GGAACCTAAT CCTCTCTAC ATCATCGGTA CTTCAAGCGT AGCGAGGGCC 540
TGGAGCGCCA CCTTGAAGA GCTGATAGG AGACCCATCG GGGAGTTCTC ACGGACACAC 600
ATGACTCTGA ACGCCCCCGG CGTCTGGCT GAAAACCCCG ACATATTGCG AGTGATCATA 660
ATTCTCATCT TGACAGGACT TTAACTCTT GGTGTGAAAG AGTCGGCCAT GGTCAACAAA 720
ATATTCACTT GTATTAAOCT CCTGGTCTCG GGCTTCATAA TGGTGTGAGG ATTTGTGAAA 780
GGATCGGTTA AAAACTGGCA GCTCACGGAG GAGGATTTTG GGAACACATC AGGCGTCTC 840
TGTTTGAAAC ATGACACAAA AGAAGGGAAG CCGGTGTGTG GTGATTATC GCCCTCGGG 900
TTCTCTGGTG TCTGTGCGG GGCAGCGACT TGCTTCTATG CCTTGGTGGG CTTTGACTGC 960
ATCGCCACCA CAGGTGAAGA GGTGAAGAAC CCACAGAAGG CCATCCCGT GGGGATCGTG 1020
GCGTCCCTCT TGATCTGCTT CATCGCCTAC TTTGGGGTGT CGGCTGCCCT CACGCTCATG 1080
ATGCCCTACT TCTGCTGGA CAATAACAGC CCGCTGCCCG AGCGCTTAA GCACGTGGGC 1140
TGGGAAGGTG CCAAGTACGC AGTGGCCGTG GGTCTCCCTC GCGCTCTTTC CGCCAGTCTT 1200
CTAGGTTCCA TGTTTCCCAT GCCTCGGGTT ATCTATGCCA TGGCTGAGGA TGGACTGCTA 1260
TTTAAATTCT TAGCCAAOCT CAATGATAGG ACCAAAACAC CAATAATGCG CACATTAGCC 1320
TCGGGTGCGG TTGTGCTGTG GATGGCCTTC CTCTTTGACC TGAAGGACTT GGTGGACCTC 1380
ATGTCCATTG GCACTCTCTT GGCTTACTCG TTGTGGCTG CTGTGTGTT GGTCTTACGG 1440
TACCAGCCAG ASCAGCCTAA CCTGGTATAC CAGATGGCCA GTACTTCCGA CGAGTTAGAT 1500
CCAGCAGACC AAAATGAATT GGCAAGCACC AATGATTCCC AGCTGGGGTT TTTACCAGAG 1560
GCAGAGATGT TCTCTTTGAA AACCACTACT TCACCCAAAA ACATGGAGCC TTCCAAAAATC 1620
TCTGGGCTAA TTGTGAACAT TTCAACCAGC CTTATAGCTG TTCTCATCAT CACTTCTGTC 1680
ATTGTGACCG TGCTTGAAG GAGGCTCTC ACCAAGGGG CGCTGTGGGC AGTCTTTCTG 1740
CTGCGAGGCT CTGCCCCCTT CTGTGCGGTG GTCAAGGGG TCATCTGGAG GCAGCCCGAG 1800
AGCAAGACCA AGCTCTCAT TAAGTTCCC TTCTGCCAG TGCTCCCATC CTTGAGCATC 1860
TTGTGAAAG TCTATCTCAT GATGCAGCTG GACCAAGGCA CTGGGTCCG GTTGTCTGTG 1920
TGGATGCTGA TAGGCTTCAT CATCTACTTT GGCTATGGCC TGTGGCACAG CGAGGAGGCG 1980
TCCTTGATG CCGACCAAGC AAGGACTCCT GACGGCAACT TGGACCAAGT CAAGTGAGGC 2040
ACAGCCCCGC CCGCCGAGG TGGCAGCAGC CCGAGGGGAC GCGCCAGAG GACCGGGAGG 2100
CACCCACACC TGCCACAGAA ACCACTGGG TCCACACCTC CACTGCA
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Seq ID NO: 136 Protein sequence
Protein Accession #: NM_003045

1 11 21 31 41 51
| | | | |

5 MGCKVLLNIG QQMLRRKVVD CSREETRLSR CLNTFDLVAL VVGSTLGAGV YVLGAVARE 60
NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELNA FITGWNLLLS 120
YIIGTSSVAR AMSATFDELI GRPIGEFSRT HMTLNAPGVL AENPDIFAVI IILILITGLLT 180
LGVKESAMVN KIFTICINLV LGFIMVSGFV KGSVKWQLT BEDFGNTSGR LCLMNDTKEG 240
KPGVGGMPF GFSGLVSGAA TCFYAFVGF D CIATTGEEVK NPQKAIPVGI VASLLICFIA 300
YFGVSAALTL MPMYFCLDNN SPLPDAPKHV GWEGAKYAVA VGLCALSLAS LLGSMFPMPR 360
VIYAMAEDGL LFKFLANVND RTKTPIIATL ASGAVAAVMA FLFDLKDLDV LMSIGTLLAY 420
SLVAACVLVL RYQPEQPNLV YQMASTDEL DPADQNELAS TNSQLGLFLP EAEMFSLKTI 480
LSPKNMEPSK ISGLIVNIST SLIAVLIITF CTVTVLGRE A LTKGALWAVF LLAGSALLCA 540
10 VVTGVINRQP ESKTKLSFKV PFLPVLPILS IFNVVYLMQ LDQGTWVRFA VMMLIGFIY 600
FGYLWHSEE ASLDADQART PDGNLDQCK

Seq ID NO: 137 DNA sequence

Nucleic Acid Accession #: NM_032044.1

Coding sequence: 182..658

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1 11 21 31 41 51
AAGATATAAA AGCTCCAGAA ACGTTGACTG GGACCACTGG AGACACTGAA GAAGGCAGGG 60
GCCCTTAGAG TCTTGGTTGC CAAACAGATT TGACAGATCAA GGAGAACCCA GGAGTTTCAA 120
AGAAGCGCTA GTAAGGCTCT TGAGATCCTT GCACCTAGCTA CATCTCAGG GTAGGAGGAA 180
GATGGCTTCC AGAAGCATGC GGCTGCTCCT ATTGCTGAGC TGCCCTGGCCA AAACAGGAGT 240
CCCTGGGTGAT ATCATCATGA GACCCAGCTG TGCTCTCTGA TGGTTTATCC ACAAGTCCAA 300
TTGCTATGGT TACTTCAGGA AGCTGAGGAA CTGGTCTGAT GCGAGCTCG AGTGTCACTC 360
TTACGGAAAC GGAGCCCAACC TGGCATCTAT CCTGAGTTTA AAGGAAGCCA GCACCATAGC 420
AGAGTACATA AGTGGCTATC AGAGAAGCCA GCGATATGG ATTGGCTCG ACACCCACA 480
GAAGAGGCAG CAGTGGCAGT GGATTGATGG GGCATATGAT CTGTACAGAT CCTGGTCTGG 540
CAAGTCCATG GGTGGGAACA AGCACTGTGC TGAGATGAGC TCCAATAACA ACTTTTAAAC 600
TTGGAGCAGC AACGAATGCA ACAAGCGCCA ACACCTCCTG TGCAAGTACC GACCATAGAG 660
30 CAAGAATCAA GATTCCTGCTA ACTCTGACAG AGCCCGCTCC TCCTCTCTTC TGCTAGCCTG 720
CTCAAAATCT CTCATTATT CAGAGGGGAA ACCTAGCAAA CTAAGAGTGA TAAGGGCCCT 780
ACTACACTGG CTTTTTATAG CTTAGAGACA GAAACTTTAG CATTGGCCCA GTAGTGGCTT 840
CTAGCTCTAA ATGTTTGGCC CGCCATCCCT TTCCACAGTA TCCTCTCTTC CTCTCCCTCT 900
35 GTCTCTGGCT GTCTCGAGCA GTCTAGAAGA GTGCATCTCC AGCCTATGAA ACAGCTGGGT 960
CTTTGGCCAT AAGAAGTAAA GATTTGAAGA CAGAAGGAAG AACTCAGGA GTAGCTTCT 1020
AGACCCCTTC AGCTTCTACA CCTTCTGCC CTCTCTCCAT TGCCCTGACC CCACCCAGC 1080
CACTCAACTC CTGCTTGTTT TTCTTCTGGC CATAGGAAGG TTTACCACTA GAATCTCTGC 1140
TAGGTGATG TGGGCCATAC ATTCTTTAA TAAACCATG TGTACATAAG AAAAAAAAAA

Seq ID NO: 138 Protein sequence

Protein Accession #: NP_114433.1

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1 11 21 31 41 51
MASRSMRLLL LLSCLAKTGV LGDIIMRPS APGWVYHKN CYGYFRKLRN WSDAELEQCS 60
YGNGAHLASI LSLKEASTIA EYISGYQRS PIWIGLEDPO KRQWQWIDG AMYLRSWSG 120
KSMGGRKHA EMSNNNNFLT NSSNECNKRO HFLCKYRP

Seq ID NO: 139 DNA sequence

Nucleic Acid Accession #: XM_051860.2

Coding sequence: 52..3042

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1 11 21 31 41 51
GCTCACCAG GAAAAATATG CAATCGTCCC ATTGATATAC AGGCCACTAC AATGGATGGA 60
GTTAACTCA GCACCGAGGT TGTCTACAAA AAAGGCCAGG ATTATAGGTT TGCTTGCTAC 120
GACCGGGCA GAGCTGCGCG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG 180
CCCAAACTCA CAGTCACCAT TGACACCAAT GTGAACAGCA CCATTCTGAA CTTGGAGGAT 240
AATGTACAGT CATGGAACCT TGGAGATACC CTGGTCATTG CCAGTACTGA TTAATCCATG 300
TACCAGGCAG AAGAGTTCCA GGTGCTTCCC TGACATCTCT GCGCCGCCAA CCAGGTCAAA 360
GTGGCAGGGA AACCAATGTA CCGTGCATC GGGGAGGAGA TAGACGGGCT GGACATGCGG 420
GCGGAGGTTG GCTTCTGAG CCGGAACATC ATAGTGATGG GGGAGATGGA GGACAAATGC 480
TACCCCTACA GAAACCATC CTGCAATTTC TTTGACTTGG ATACCTTTGG GGGCCACATC 540
AAGTTTGCTC TGGGATTAA GGCAGCACAC TTGGAGGGCA CGGAGCTGAA GCATATGGGA 600
CAGCAGCTGG TGGGTCACTA CCGATTAC TTTCACTGG CCGGTGATGT AGACGAAAGG 660
GGAGGTTATG ACCCAACCCAC ATACATCAGG GACCTCTCCA TCCATCATA ATTCTCTGCG 720
TGCGTCAAG TCCATGCTC CAATGGCTTG TTGATCAAGG ACGTTGTGGG CTATAACTCT 780
TTGGGCCACT GCTTCTTAC GGAAGATGGG CCGGAGGAAC GCAACACTTT TGACCACTGT 840
CTTGGCTCTC TTGTCAAGTC TGGAAACCTC CTCCCTCGG ACCGTGACAG CAAGATGTGC 900
70 AAGATGATCA CAGGAGACTC CTACCCAGGG TACATCCCCA AGCCAGGCA AGACTGCAAT 960
GCTGTGTCCA CCTTCTGGAT GGCCAAATCCC AACAACAACC TCATCAACTG TGCCTGTGCA 1020
GGATCTGAGG AAACCTGATT TTGCTTTATT TTTCAACAG TACCAAGCGG CCCCTCGGTG 1080
GGAATGTACT CCCCAGGTTA TTCAGAGCAC ATTCCACTGG GAAATTTCTA TAACAACCGA 1140
GCACATTCCA ACTACGGGGC TGGCATGATC ATAGACAACG GAGTCAAAAC CACGAGGGCC 1200
75 TCTGCGAAGG ACAAGCGGCC GTTCTCTCA ATCATCTCTG CCAGATACAG CCTCAACAG 1260
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TCCAGCAAG AGATAAAGAA CAGCTTGTGT GTTGGCGAGA GTGGCAACGT GGGGACGGAA 1500
80 ATGATGAGCA ATAGGACTCG GGGCCCTGCG GGCTTGGACC ATAGCGGAAG GACCTCTCCT 1560
ATAGGCCAGA ATTTTCCAAT TAGAGGAATT CAGTTATATG ATGGCCCCAT CAACATCCAA 1620
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CGCTGGAATA ATGCTTGCCA GAGCTGCCCC CATAACAACG TGACCGGCAT TGCTTTGAG 1740
GAGCTTCCGA TTACTTCCAG AGTGTCTTTC GGAGAGCCTG GGCCTGTGTT CAACAGCTG 1800

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GACATGGATG GGGATAAGAC ATCTGTGTTC CATGACGTGC ACGGCTCCGT GTCGAGTAC 1860
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 GTCTTCGTGA GGACCTTGCA GATGGACAAA GTGGAGCAGA GCTACCTGG CAGGAGCCAC 2340
 TACTACTGGG ACGAGGACTC AGGGCTGTTG TTCTGAAGC TGAAGCTCA GAACGAGAGA 2400
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 CATTTCTTGG AGGTGAAGAT GGAGAGTTC AAGCAGCACT TCTTCCACT CTGGAACGAC 2640
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 GTGGTGATTG ACGGGAACCA AGGGCGCGTG GTGAGCCACA CGAGCTTCAG GAACTCCATT 2760
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 AAGCTTGGGG CAGACAGGGG TCTCAAGTTG AAAGAGCAAA TGGCATTCTG TGGCTTCAA 2940
 GGCAGCTTCC GGCCCATCTG GGTGACACTG GACACTGAGG ATCACAAGC CAAATCTTC 3000
 CAAGTTGTGC CCATCCCTGT GGTGAAGAAG AAGAAGTTGT GAGGACAGCT GCCGCCCGGT 3060
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 GTCCCCAGC CCCTGCAGC AGCTGCCTGG GAAGGCGGTG TTTCAGCCCT GATGGGCCAA 3180
 GGAAGGCTA TCAAGAGCCC TGGTGTGCTC ACCTGCCCT ACTCAAGTGT TCACTGGAG 3240
 CCCTGGGGC GGTGCTGGCC AATGCTGGA ACATTCACCT TCCTGCAGCC TCTTGGGTGC 3300
 TTCTCTCTTA TCTGTGCTTC TTCAGTGGGG GTTGGGGAC CATATCAGGA GACCTGGGTT 3360
 GTGCTGACAG CAAAGATCCA CTTTGGCAGG AGCCCTGACC CAGCTAGGAG GTAGTCTGGA 3420
 GGGCTGGTCA TTCAAGATC CCCATGTGCT TCAGCAGACA AGTGAGGGTG GTAAATGTAG 3480
 GAGAAAGGCT CTTGGCCTTA AGGAAATCTT TACTCCTGTA AGCAAGAGCC AACCTCAG 3540
 GATTAGGAGC TGGGGTAGAA CTGGCTATCC TTGGGGAAGA GGCAAGCCCT GCCTCTGGCC 3600
 GTGTCCACTT TCCAGGAGAC TTGAGTGGC AGGTTTGGAC TTGAGTAGA TGACTCTCA 3660
 AGGCCCTTTT AGTCTCGAG TTCCAGAAAT CTGCTGCAAT TCACATGGTA CCTGGAAACC 3720
 AACAGTTCAT GGATATCCAC TGATATCCAT GATGCTGGGT GCCCAGGCG ACACGGGATG 3780
 GAGAGGTGAG AACTAATGCC TAGCTTGAGG GGTCTGCAGT CCAGTAGGGC AGGCAGTCAG 3840
 GTCCATGTGC ACTGCAATGC CAGGTGGAGA AATCAGAGG AGGTAAATG GAGGCCAGTG 3900
 CCATTTTACA GGGGAGGCTC AGGAAGGCTT CTGCTTACA GGAAAGAAGG CTGGGGGATG 3960
 TTTGCTGGGG GAGATGAGG CAGCCTCTGG AATGGCTCAG GGATTCAGCC CTCCCTGCCG 4020
 CTGCTGTCTG AAGCTGTGTA CTACGGGTC GCCCTTGTCT CAGCTCTCTC TGGCCCACTC 4080
 ATGATGGAGA AGTGTGCTCA GAGGGGAGCA ATGGGCTTTG CTGCTTATGA GCACAGAGGA 4140
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70 Seq ID NO: 140 Protein sequence
 Protein Accession #: XP_051860.2

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Protein Accession #: Eos sequence

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Seq ID NO: 146 Protein sequence
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Seq ID NO: 148 Protein sequence
Protein Accession #: AAH12089.1

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Nucleic Acid Accession #: NM_033049.1
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Protein Accession #: NP_149038.1

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40 Seq ID NO: 152 Protein sequence
 Protein Accession #: Eos sequence

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50 Seq ID NO: 153 DNA sequence
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Seq ID NO: 154 Protein sequence
Protein Accession #: NP_001423.1

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Seq ID NO: 155 DNA sequence
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Coding sequence: 85..2466

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Seq ID NO: 156 Protein sequence
Protein Accession #: NP_037414.2

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	PECRNDASEV	VLAGERLRES	KKKAKMASAT	SSSQRDWGRG	MACVGRTEKC	TIVPSNHYGP	420
	IPGIPVGTMK	RFRVQVSESG	VHRPHVAGIH	GRSNDGAYSIL	VLAGGYEDDV	DHGNFFTYTG	480
60	SGGRDLSGNK	RTAEQSCDQK	LNTNRLALAL	NCFAPINDQE	GAEAQWRSRG	KPVRVVRNVK	540
	GGKNSKYADA	EGNRYDGIYK	VVKYWPEKGG	SGFLVWRYLL	RRDDEPGPW	TKEGKDRIKK	600
	LGLTMQYPDG	YLEALANRER	EKENSKEEEE	BQSGGCFASP	RTGKGKWKRK	SAGGGPSRAG	660
	SPRRTSKRTK	VEPYSLTAQQ	SSLIREDKEN	AKLMNEVLAS	LKDRPASGSP	PQLFLSKVEE	720
65	TFQCICQCEL	VFRPIITVQ	HNVCCKCLDR	SFRAQVPSCP	ACRYDLGRSY	AMQVNOPLQT	

Seq ID NO: 157 DNA sequence
Nucleic Acid Accession #: NM_000756.1
Coding sequence: 186..776

70	1	11	21	31	41	51	
	AGAAACTCAG	AGACCAAGTC	CATTGAGAGA	CTGAGGGGAA	AGAGAGGAGA	GAAAGAAAAA	60
	GAGAGTGGGA	ACAGTAAAGA	GAAAGGAAGA	CAACCTCCAG	AGAAAGCCCC	CGGAGACGTC	120
	TCTCTGCAGA	GAGGCGGCAG	CACCGGCTC	ACCTGCGAAG	CGCCTGGGAA	GCGAGTGCCC	180
75	CTAACATGCG	GCTGCGCGTG	CTTGTGTCGG	CGGGAGTCCG	GCTGGTGGCT	CTCCTGCCCT	240
	GCCCGCCATG	CAGGGCGCTC	CTGAGCGCGG	GGCCCGTCCC	GGGAGCTCGG	CAGGCGCGCG	300
	AGCACCTCA	GCCCTTGGAT	TTCTTCCAGC	CGCCGCGCGA	GTCCGAGCAG	CCCCAGCAGC	360
	CGCAGGCTCG	TCCGCTGCTG	CTCCGATGG	GAGAGGAGTA	CTTCTCCGCG	CTGGGGAACC	420
	TCAACAGAG	CCCGGCGGCT	CCCTTTCCGC	CGCCCTCTCT	GCTCTCGGCC	GGAGGCAGCG	480
80	GCAGCCGCC	TTCCGCGGAA	CAGGCGACCG	CCAACTTTTT	CCCGTGTGTT	CTGCAGCAGC	540
	TGCTGCTGCC	TGCGGCGCTG	CTCGACAGCC	CGCGGCTCT	CGCGGAGCGC	GGCGCTAGGA	600
	ATGCCCTCGG	CGGCCACGAG	GAGGCAACCG	AGAGAGAAAG	GCGGTCCGAG	GAGCCTCCCA	660
	TCTCCCTGGA	TCTCACCTTC	CACCTCTCTC	GGGAAGTCTT	GGAAATGGCC	AGGGCCGAGC	720
	AGTTAGCACA	GCAAGCTCAC	AGCAACAGGA	AACTCATGGA	GATTATTGGG	AAATAAAGC	780

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GTGCGTTTGG CCAAAAAGAA TCTGCATTTA GCACAAAAAA AATTATAAAA AATACAGTAT 840
TCGTGACCAT AGCGCTGCTC TTATGCCATT TGTTTATTTT TATATAGCTT GAAACATAGA 900
GGGAGAGAGG GAGAGAGCCT ATACCCCTTA CTTAGCATGC ACAAAGTGTG TTCAGGTGCA 960
GCAGCAACAC AATGTTATTC GTTTTGTCTA CGTTTAGTTT CCGTTTCCAG GTGTTTATAG 1020
TGGTGTTTTA AAGAGAATGT AGACCTGTGA GAAAAAGTTT TGTTTGAAAA AGCAGACAGA 1080
AGTCACTCAA TTGTTTITGT TGTGCTCTGA GCCAAAGAGA ATGCCATICT CTTGGGTGGG 1140
TAAGACTAAA TCTGTAAAGT CTTTGAACA ACTTTCTCTT GTAAACGTTT CAGTAATAAA 1200
ACATCTTTCC AGTCTTGGT CAGTTTGGTT GTGTAAGAGA ATGTTGAATA CTTATATTTT 1260
TAATAAAAGT TGCAAAGGT

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Seq ID NO: 158 Protein sequence
Protein Accession #: NP_000747.1

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1      11      21      31      41      51
|      |      |      |      |      |
MRLPLLVSAG VLLVALLPCP PCRALLSRGP VPGARQAPQH PQPLDFFQPP PQSEQPQQPQ 60
ARFVLLRMGE EYFLRLGNLN KSPAAPLSPA SLLLAGSGSG RPSPEQATAN FFRVLLQQLL 120
LPRRLDSPA ALAERGANA LGGHQBAPER ERRSEEPPI S LDLTFHLLRE VLEMARAEQL 180
AQAHSNRKL MEIIGK

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Seq ID NO: 159 DNA sequence
Nucleic Acid Accession #: NM_001200.1
Coding sequence: 325..1514

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1      11      21      31      41      51
|      |      |      |      |      |
GGGGACTTCT TGAACCTGCA GGGAGAATAA CTTGCGCACC CCACTTTGCG CCGGTGCCTT 60
TGCCCCAGCG GAGCCTGCTT CGCCATCTCC GAGCCCCACC GCCCTCCAC TCCTGGCCT 120
TGCCCGACAC TGAGACGCTG TTCCAGCGT GAAAAGAGAG ACTGCGCGCG CGGCACCOGG 180
GAGAAGGAGG AGGCAAGGAA AAGGAACGGA CATTCGTTCC TTGCGCCAGG TCCTTTGACC 240
AGAGTTTTC CATGTGAGCG CTCCTTCAAT GGAOGTGTCC CCGGTGTCTT CTTAGACGGA 300
CTGCGGTCTC CTAAGGTGCG ACCATGCTGG CCGGACCCCG CTGTCTTCTA GCGTGTCTGC 360
TTCCCCAGGT CCTCTGGGCG GCGCGGCTG GCCTGTTTCC GGAGCTGGGC CGCAGGAAGT 420
TGGCGGCGCG GTCTGCGGCG CGCCCTCAT CCCAGCCCTC TGACGAGGTC CTGAGCGAGT 480
TCGAGTTGCG GCTGCTCAGC ATGTTGCGCC TGAAACAGAG ACCCAACCCC AGCAGGGACG 540
CGGTGTGTCG CCCCACATG CTAGACCTGT ATCGCAGGCA CTCAGGTGAG CCGGGCTCAC 600
CCGCCCCAGA CCACCGGTTG GAGAGGCGAG CCAGCCGAGC CAACACTGTG CGCAGCTTCC 660
ACCATGAAGA ATCTTTGGAA GAACCTACCAG AAACGAGTGG GAAAACAACC CGGAGATTCT 720
TCCTTAATTT AAGTTCTATC CCACGAGAG AGTTTATCAC CTCAGCAGAG CTTGAGTTT 780
TCCGAGAACA GATGCAAGAT GCTTTAGGAA ACAATAGCAG TTTCATCAC CGAATTATA 840
TTTATGAAAT CATAAACCT GCAACAGCCA ACTCGAAATT CCCCCTGACC AGACTTTTGG 900
ACACCGAGTT GGTGAATCAG AATGCAAGCA GGTGGGAAAG TTTTGATGTC ACCCCCGCTG 960
TGATGCGGTG GACTGCACAG GGACAAGCCA ACCATGGATT CGTGGTGGAA GTGGCCCACT 1020
TGGAGGAGAA ACAAGGTGTC TCCAAGAGAC ATGTTAGGAT AAGCAGGTCT TTGCACCAAG 1080
ATGAACACAG CTGGTCACAG ATAAGGCCAT TGCTAGTAAC TTTTGGCCAT GATGAAAAAG 1140
GGCATCCTCT CCACAAAGA GAAAAACGTC AAGCCAAACA CAAACAGCGG AAACGCTTA 1200
AGTCCAGCTG TAAGAGACAC CCTTTGTACG TGGACTTCAG TGACGTGGGG TGGAACTACT 1260
GGATTGTGGC TCCCCCGGGG TATCACGCTT TTTACTGCCA CGGAGAATGC CCTTTCTCTC 1320
TGCTGATCA TCTGAATCTC ACTAATCATG CCATTGTGTC GACGTTGGTC AACTCTGTTA 1380
ACTCTAAGAT TCCTAAGGCA TGCTGTGTCC CGACAGAACT CAGTGTCTATC TCGATGCTGT 1440
ACCTGACGCA GAATGAAAG GTTGTATTAA AGAATATCA GGACATGGTT GTGGAGGGTT 1500
GTGGGTGTG CTAGTACAGC AAAATTAAAT ACATAAATAT ATATATA

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Seq ID NO: 160 Protein sequence
Protein Accession #: NP_001191.1

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1      11      21      31      41      51
|      |      |      |      |      |
MVAGTRCLLA LLLPQVLLGG AAGLVPELGR RKFAAASSGR PSSQPSDEVL SEFRLRLLSM 60
FGLKQRPTFS RDAVVPFMYL DLYRRHSGQP GSPAPDHRLE RAASRANTVR SPFHESLEE 120
LPETSGKTTR RFFFNLSIP TEEFITSABL QVPREQWQDA LGNNSSFHHR INIYIHKPA 180
TANSKFPVTR LLDT

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Seq ID NO: 161 DNA sequence
Nucleic Acid Accession #: NM_001999.2
Coding sequence: 1..8736

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1      11      21      31      41      51
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ATGGGGAGAA GACGAGGCT GTGTCTCCAG CTCTACTTCC TGTGGCTGGG CTGTGTGGTG 60
CTCTGGGCGC AGGGCAAGGC CGGCCAGCCT CAGCTCTCTC GSCCAAGACC GCCCCGGCCC 120
CAGCGCGCGC CGCAACAGGT TCGGTCCGCT ACAGCAGGCT CTGAAGCGGG GTTTCTAGCG 180
CCCGAGTATC GCGAGGAGGG TGCCGCACTG GCCAGCCGCG TCCGCGCGCG AGGACAGCAG 240
GACGTGCTCC GAGGGCCCAA CGTGTGCGGC TCCAGATTCC ACTCCTACTG CTGCCCTGGA 300
TGAAGAGCGC TCCTTGGAGG AAACCAAGTC ATTGTCCCGA TTTGTAGAAA TAGTTGTGGA 360
GATGATATTT GTTCCCGTCC TAACATGTGT ACTTGTTCOA GTGGGCAAAAT ATCATCAACC 420
TGTGATCAAA AATCAATTCA GCAGTGCAGT GTGAGATGCA TGAATGGTGG GACCTGTGCA 480
GATGACCATC GCCAGTGCCA GAAAGGATAT ATTGGAACCT ATTGTGGAAC ACCTGTCTGT 540
GAAAATGATG GTCAGAAATG TGGACGTTGC ATGCCCAAC CGTGTGCTTG TGTTTATGGG 600
TTCACTGTGC ATGATGTGTA AAGAGATTAC AGGACAGGCC CGTGTTCAC TCAGGTCAAC 660
AACCAGATGT GCCAAGGGCA GCTGACAGGC ATTTGCTGCA CGAAGACTCT GTGCTGTGCC 720
ACCATCTGAC GGGCGTGGGG CCATCCCTGT GAGATGTGTC CAGCCAGGCC TCAGCCCTGC 780
CGACGGGGTT TCATCCCAAA CATCCGCACT GGAGCTTGCC AAGATGTGTA TGAATGCCAG 840
GCTATCCGAC GGATATGCCA AGGAGGAAAC TGTATCAATA CAGTGGGCTC TTTTGAATGC 900

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	AGATGCCCTG	CTGGTCACAA	ACAGAGTGAA	ACTACTCAGA	AATGTGAAGA	CATTGATGAG	960
	TGCAGCATCA	TTCTGGGAT	ATGTGAAACT	GGTGAATGTT	CCAACACCGT	GGGAAGCTAT	1020
	TTTTGTGTTT	GTCCACGTGG	ATATGTAAAC	TCAACAGATG	GCTCTCGATG	CATCGATCAG	1080
5	AGAACAGGCA	TGTGTTTCTC	GGGCTTGGTG	AATGGCCGCT	GTGCACAAGA	GCTCCCGGGG	1140
	AGAATGACGA	AAATGCACTG	CTGCTGTGAG	CCTGGCCGCT	GCTGGGGCAT	CGGAACCAAT	1200
	CCTGAAGCCT	GTCTGTGTCAG	AGGTTCTGAG	GAATATCGCA	GACTTTGCAT	GGATGGACTT	1260
	CCAATGGGAG	GAATTCACAG	GAGTGTCTGT	TCCAGACCTG	GAGGCACTGG	GGGAAATGGC	1320
	TTTGGCCCAA	GTGGCAATGG	CAATGGCTAT	GGCCAGGAG	GGACAGGCTT	CATCCCCATC	1380
10	CCTGGAGGCA	ATGGCTTTTC	TCTGGGCTTT	GGGGAGCCG	GTGTGGGGC	CGGGGACAG	1440
	GGACCTATCA	TCACTGGACT	AACAATCTG	AACCAGACAA	TAGATATCTG	TAAGCATCAT	1500
	GCTAACCTTT	GTTTAAATGG	ACGCTGTATA	CCAACCTGCT	CAAGCTACCG	ATGTGAATGC	1560
	AACATGGGTT	ATAAGCAGGA	TGCARAATGGA	GATTGTATAG	ATGTTGATGA	ATGCACATCA	1620
	AATCCCTGCA	CTAATGGAGA	TTGTGTTAAT	ACACCTGGTT	CCTATTATTG	TAAATGTCAT	1680
15	CTGGGATTCC	ATGGAGACTCC	TACCAAGCAA	GCATGCAATG	ATATTGATGA	GTGCATCCAG	1740
	AATGGGGTTC	TTGTAAAAA	CGGTGATGTC	GTGAACCTCAG	ATGAAAGTTT	CCAGTGCAAT	1800
	TGCAATGCCG	GCTTTGAATT	AACTACAGAT	GGAAAAAAT	GTGTTGATCA	TGATGAATGT	1860
	ACAACCTACCA	CATGTGTTT	GAATGGAAATG	TGCATCAATG	AAGATGGCAG	CTTCAAGTGC	1920
	ATCTGCAAA	CAGGATTGTG	CTTGCTCCCA	AATGGGGCTT	ACTGTACTGA	TGTTGATGAA	1980
20	TGCCAGACCC	CAGGAATCTG	CATGAATGGG	CACCTGCATCA	ACAGTGAAGG	GTCTTCCCG	2040
	TGTGACTGTC	CCCCAGGCC	GGCTGTGGG	ATGGATGGAC	GTGTGTGTGT	TGATACTCAC	2100
	ATGGCGAGTA	CCTGCTATGG	AGGAATCAAG	AAAGGAGTGT	GTGTGCGTCC	TTTCCCGGTT	2160
	GCAGTGACCA	AGTCGGAATG	CTGCTGTGCC	AATCCAGACT	ATGCTTTTGG	AGAACCCTGC	2220
	CAGCCATGCC	CTGCAAAAAA	TTCACTGAA	TTCCACGGCC	TTTGTAGTAG	TGGAGTAGGT	2280
25	ATCACTGTGG	ATGGAAAGGA	TATCAATGAA	TGTGCTTTGG	ATCTGTATAT	ATGTGCCAAT	2340
	GGGATTGTGT	AAAACTTACG	TGGTAGTTAC	CGTTGTAAAT	GCAACAGTGG	CTATGAACCA	2400
	GATGCTCTG	GAAGAACTG	TATTGACATT	GATGAATGTT	TAGTAAACAG	ACTGCTTTGT	2460
	GATAACGGAT	TGTGCCGAAA	CAOGCCAGGA	AGTTACAGCT	GTACGTGCC	ACCAGGGTAT	2520
	GTGTTCAAG	GTGACACAGA	GACCTGTGAA	GATATAAATG	AATGTGAAG	CAACCCATGT	2580
30	GTCAATGGGG	CCTGCAGAAA	CAACCTTGGA	TCITTTCAAT	GTGAATGTTT	GCCCGGCAGC	2640
	AAACTCAGCT	CCACAGGATT	GATCTGTATT	GACAGCCTGA	AGGGGACCTG	TTGGCTCAAC	2700
	ATCCAGGACA	CGCGCTGTGA	GGTGAATATT	AATGGAGCCA	CTCTGAAATG	TGAATGCTGT	2760
	GCCACCCCTG	AGCCGCGCTG	GGGGAGCCCC	TGTGAGCGGT	GTGAACCTAGA	TACAGCTTGC	2820
	CCAAGAGGGC	TTGCCAGGAT	TAAAGGTGTT	ACGTGTGAAG	ATGTTAATGA	GTGTGAGGTG	2880
35	TTCCCTGGCG	TTGTGCCAAA	TGGACGCTGT	GTCAACAGTA	AGGGATCTTT	TCATTGCGAG	2940
	TGCCCTGAAG	GCCTTACGTT	GGATGGGACT	GGCGGTGAT	GTTTGGATAT	TGCGATGGAG	3000
	CAGTGTACT	TGAAGTGGGA	TGAAGATGAA	TGCATCCACC	CCGTCTCTGG	AAAGTTCCGC	3060
	ATGGATGGCT	CTGTCTGTGC	TGTGGGGGCG	GCTTGGGGCA	CCGAGTGTGA	GGAGTGCCCC	3120
	AAACCTGGCA	CCAAGGAATA	CGAGACACTG	TGCCCCCGCG	GGGCTGGCTT	TGCTAACCGA	3180
40	GGGGATGTTT	TTACTGGGCG	GCCATTTTAC	AAAGACATCA	ATGAATGCAA	AGCATTTCCT	3240
	GGGATGTGCA	CTTATGGGAA	GTGCAGAAAT	ACAATCGGAA	GCTTCAAAATG	CCGTTCGAAT	3300
	AGTGCTCTTG	CTCTAGACAT	GGAGGAAAGA	AACTGCACCG	ACATCGACGA	GTGCAGGATT	3360
	TCTCTGACC	TCTGTGGCAG	TGGAATCTGC	GTCAATACAC	CGGGCAGCTT	TGAGTGGGAG	3420
	TGCTTCGAAG	GCTATGAAG	TGGCTTCATG	ATGATGAAGA	ACTGCATGGA	CATTGAACGA	3480
45	TGTGAACGTA	ACCTCTCTCT	TTGTAGGGGT	GGCACCTGTG	TGAACACTGA	GGGCAGCTTT	3540
	CAGTGTGACT	GCCTTACGTT	ACAAGAGCTG	TCAACATCCC	GTGAGGACTG	TGTGATATT	3600
	AATGAATGCT	CCCTGAGTGA	CAATCTCTGC	AGAAATGGAA	AATGTGTGAA	CATGATTGGA	3660
	ACCTATCAGT	GCTCTTGCAA	TCCTGGATAT	CAGGCTACGC	CAGACCCGCA	GGGCTGTACA	3720
	GATATTGATG	AATGTATGAT	AATGAAACGA	GGCTGTGACA	CCCAGTGCAC	AAATTCAGAG	3780
50	GGAAAGCTAG	AATGCAGCTG	CAGTGAGGGT	TATGCCCTGA	TGCCAGATGG	GAGATGCTGT	3840
	GCAGAGCTAG	ATGAATGTGA	AAACAATCCT	GATATCTGTG	ATGGCGGCCA	GTGTACCAAC	3900
	ATTCTCTGAG	AGTATGCTGT	CCTCTGCTAT	GATGGCTTCA	TGGCTTCCAT	GGACATGAAA	3960
	ACATGCATTG	ATGTCAATGA	ATGTGACCTA	AATTCAAAAT	TCTGCATGTT	TGGGGAATGT	4020
	GAGAACACAA	AGGGATCCTT	CATTTGCCAC	TGTCACTGCG	GTTACTCAGT	GAAGAAGGGG	4080
55	ACCACAGGAT	GTACAGATGT	GGATGAGTGT	GAAATTTGGT	CTCATAACTG	CGACATGCAT	4140
	GCCTCATGTC	TGAATATCCC	AGGAAGCTTC	AAGTGTAGCT	CGAGAGAAAG	CTGGATTGGA	4200
	AAOGGATCA	AGTGTATTGA	TCTGGACGAA	TGTTCTAATG	GAAACCCACA	GTGTAGCATC	4260
	AATGCTCAGT	GTGTAATATC	CCCGGGCTCA	TACCGCTGTG	CCTGCTCCGA	AGGTTTCACT	4320
	GGTGATGGCT	TTACTGTCTC	AGATGTTGAT	GAGTGTGAC	AAAACATAAA	CCTCTGTGAG	4380
60	AAOGGACAGT	GCCTTAATGT	CCCGGGTCCA	TATCGCTGCG	AGTGTGAGAT	GGGCTTCACT	4440
	CCAGCCTCAG	ACAGCAGATC	CTGCCAAGAT	ATTGATGAAT	GCTCCTTCCA	AAACATTTGT	4500
	GTCTCTGGA	CATGTAATAA	CCTGCCTGGA	ATGTTTCATT	GCACTCTGGA	TGATGGTTAT	4560
	GAATTGGACA	GAACAGGAGG	GAACTGTACA	GATATTGATG	AGTGTGACGA	TCCTATAAAC	4620
	TGTGTCAATG	GCCTATGTGT	CAACAACGCT	GGTGGCTATG	AGTGTAACTG	CCCAACCGAT	4680
65	TTTCAGTTGA	ACCCAACTGG	TGTGGGTTGT	GTGACAAAC	GTGTGGGCAA	CTGCTACCTG	4740
	AAGTTTGGAC	CTCGAGGAGA	TGGGAGTCTG	TCTTGCAACA	CCGAGATCGG	GGTGGGCGTC	4800
	AGTGGCTCTT	CATGCTGCTG	CTCTCTGGGA	AAGGCTGGGG	GAAACCCCTG	TGAGACATGC	4860
	CCCCCTGTCA	ATAGCACTGA	ATATTACACC	CTGTGTCGCG	GAGGTGAAGG	CTTCAGACCT	4920
	AAOCCCATCA	CAATCATTTT	AGAAGACATT	GACGAATGCC	AGGAGTTACC	AGGTCTCTGC	4980
70	CAGGGTGGAA	ACTGCATCAA	CACCTTTGGG	AGCTTCCAGT	GTGAGTGGCC	ACAAGGCTAC	5040
	TACCTCAGCG	AGGATACCCG	CATCTGTGAG	GATATTGATG	AGTGTTTTGC	ACATCCTGGT	5100
	GTGTGTGGGC	CTGGGACCTG	CTATAACACC	CTGGGAAATT	ACACCTGCAT	TTGCCACCT	5160
	GAGTACATGC	AGGTCAATGG	AGGCCACAAC	TGCATGGACA	TGAGAAAAAG	CTTTTGCTAC	5220
	CGAAGCTATA	ATGGAAACCC	TTGTGAGAAAT	GAGTTGCCCT	TCAATGTGAC	AAAAAGGATG	5280
75	TGCTGTGCA	CATATAATGT	GGGCAAGCT	GGGAACAAAC	CTTGTGAACC	ATGCCCAACT	5340
	CCAGGAACAG	CTGACTTTAA	AACCATATGT	GGAAATATTC	CTGGATTAC	CTTTGACATT	5400
	CACACAGGAA	AAGCTGTGTA	CATTGATGAA	TGTAAAGAGA	TTCCAGGCAT	TTGTGCAAT	5460
	GGTGTGTGCA	TTAACACAGAT	TGGCAGTTTC	CGCTGTGAAT	GCCCTACAGG	ATTCAATTAC	5520
	AATGACCTGC	TGTTGGTTTG	TGAAGATATA	GATGAGTGCA	GCAATGGTGA	TAATCTCTGC	5580
80	CAGCGGAATG	CAGACTGCAT	CAATAGTCTT	GGTAGTTACC	GCTGTGAATG	TGCCGCGGGT	5640
	TTCAAACCTT	CACCCAAATG	GGCCTGTGTA	GATGCAATG	AATGTTTAGA	AATTCCTAAC	5700
	TTTGCACTG	ATGGCTGTGT	TGTTGATCTG	CAGGAAGATT	ACCAGTGATC	CTGCCCAAT	5760
	GGCTTTAAG	CTTCTCAGGA	CCAGACCATG	TGCATGGATG	TTGATGAGTG	CGAGCGGCAC	5820
	CCATGTGGA	ATGGAACTTG	TAAAAACACC	GTGGATCCT	ATAACTGTCT	GTGCTACCCA	5880
	GGGTTTGAAC	TCACTCATAA	TAATGATTGC	CTGGACATAG	ATGAGTGCAG	TTCTTTTTT	5940

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GGTCAGGTGT GCAGAAATGG ACGTTGTTTT AATGAAATGG GTTCTTTCAA GTGTCTATGT 6000
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GCCCTTCCCG GCTCTTGCTC TCCTGGTACC TGTGAGAAAT TGGAGGGATC CTTCAGATGTG 6120
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GGGCACTACC TGTCACTGGA TACAGAGGTC GATGAGGAAA ATGCTCTGTC CCCAGAAGCA 8280
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GGAATATATG TGTGTTGTTG TGTTTTAAAC CCATTTTTTT TTAGAATTT TCAATTAATC 9840
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CCAAACCTCA TATGTGAAT GGCCAAAGCA CATGCAGGCT CTGTGTTGTT CCTCTCAAAC 10080
CTGTGCTGAC CAAAGATTAG TAACCAAGTA TTTGAGGTTT TATTGTTTTT 10140
TTAATAACTA AAAAAAACT CGTGCC
  
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Seq ID NO: 162 Protein sequence
 Protein Accession #: NP_001990.1

75
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1 11 21 31 41 51
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DGFCRPNMC TCSSGQISST CGSKSIQCCS VRQNGGTCA DDRCCQKGY IGTYCGQFVC 180
ENGQNGGRC IAQPCACVYG FTGPQCERDY RTGPCFTQVN NQMCQQLTG IVCTKTLCCA 240
TTGRAWHGPC EMCPAQPQPC RRGPIFNIRT GACQDVDEQC AIPGICQGGN CINTVGSPEC 300
RCPAGHKVQS TTQKCEIDE CSIIPIQIBT GECSNTVGSY FCVCPRGVYT STDGSRCIDQ 360
RTGCMFSGLV NGRCAQELPG RMTRMQCCCE PGRCMGIGTI PEACPVRGSE EYRRLCMDGL 420
  
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5	PMGGIPGSAG SRPGGTGGNG FAPSGNGNGY GPGGTGFPII PGGNGFSPGV GGAGVGAGGQ 480
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	NPCTINGDCVN TEGSYVCKCH AGFQRTPTKQ ACIDIDECIQ NGVLCKNGRC VNSDGSFQCI 600
	CNAGFELTID GKNCVDHDEC TTTNMCLNGM CINEDGSFKC ICKPGFVLAP NGRYCTDVDE 660
	CQTPGICMNG HCINSEGSFR CDCPPGLAVG MDGRVCVDTM MRSTCYGQIK KGVCVRPFPF 720
	AVTKSECCCA NPDYGFGEPC QPCPAKNSAE FBGLCSSGVG ITVDGRDINE CALDPDICAN 780
	GICENLRGSY RCNCNSGYEP DASGRNCIDI DECLVNRLLC DNGLCRNTPG SYSTCFFPGY 840
	VFRTEETCE DINECESNPC VNGACRNNG SFNCECSPGS KLSSTGLICI DSLKGTCLWN 900
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	CFEGYESGFM MMKNMDIDG CERNPLLCRG GTCVNTGSP QDCDPLGHEL SPSREDCVDI 1200
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	GSYECSCSEB YALMPDGRSC ADIDECENNP DICDGGQCTN IPGEYRCLCY DGFMASSDMK 1320
	TCIDVNECDL NSNIQMFGE ENTKGSFICH CQLGYSVKKG TTGCTDVDEC EIGAHCMDH 1380
	ASCLNIPGSF KCSREGWIG NGIKCIDLDE CSNGTHQCSI NAQCVNTPGS YRCACSEGFT 1440
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20	VSGTCNNLPG MFHCICDDGY ELDRGTGNGCT DIDECADPIN CVNGLCVNTP GRYECNCPFD 1560
	FQLNPTGVGC VDNRVGNCYL KFGPRGDGSL SCNTBIGVGV SRSSCCCSLG KANGNPCETC 1620
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	RSYNGTTCEM ELFPNVTKRM CCCTYNVGA GNKPCFPCPT PGADPKTIC GNIPGPTFDI 1800
25	HTGKAVDIDE KCEIPGICAN GVCINQIGSF RCECPTGFSY NDLLLVCEDI DECSNGDNL 1860
	QRNADCINSP GSYRCECAAG FKLSPNGACV DRNECLEIFN VCSHGLCVDL QGSYQCI 1920
	GFKASQDQTM CMDVDECEH PCNGTCKNT VGSYNCLCYP GFELTHNND LDIDECSFF 1980
	GQVCRNGRC NEIGSFKCLC NEGVELTDPG KNCIDTNECV ALPGSCSPGT CQNLGSPFC 2040
	ICPPGYEVKS ENCIDINECD EDPNICLFPS CTNTPGGPQC LCPFGFVLS NGRRCFDTRQ 2100
30	SFCPTNFENG KCSYVKAFT TKAKCCCSKM PEGEWGDPCE LCPKDEAVP QDLPCFV 2160
	VPSLHDTRED VNECLESEFI CSNGQCINTD GSFRCECPMG YNLDYTGVR VDTDECSIGN 2220
	PCNGTCTNV IGSFECNCE GFEPGPMNC EDINECAQNP LILCALRMT FGSYECTCPI 2280
	GYALREDOQM KDLDECAEG LHDCESRGMM CKNLIGTFMC ICPPGMARRP DGBGCVDENE 2340
	CRTKPGICEN GRCVNIIGSY RCECNEGFQS SSSGTCLDN RQGLCPAEVL QTICQMASS 2400
35	RNLVTKSECC CGGGRGWGHQ CELCPLPSTA QYKKICPHGP GYTTDGRDID ECKVMPNLCT 2460
	NGQCINTMGS FRCFCVGYT TDISGTSCID LDECSQSPKP CNYICKNTBG SYQCSCPRGY 2520
	VLQEDGTCK DLDDEQTKQH NCQFLCVNTL GGFTCKCPPG FTQHTACID MNECSQPL 2580
	CGGKGIQNT PGSFSCBQR GFSLDATGLN CEDVDECDGN ERQHGQCN I LGGYRGCPQ 2640
	GYIQHYQWQV CVDENECSNP NACGSASCYN TLGSYKACAP SGFSFDQFS ACHDVNECSS 2700
40	SKNPNYNGS NTEGGYLCG PPGYRVGQG HCVSGMGPNK GQYLSLDEB DEENALSPEA 2760
	CYECKINGYP KKDSRQKRSI HEPDPTAVEQ ISLESVDMDS PVMKFNLSH LGSKEHILEL 2820
	RFATQPLNNH IRYVISQND DSVFRIHQRN GLSYLHTAK KLMPGTITLE ITSIPLYKK 2880
	ELKKLESENE DDYLLGELGE ALRMRLQQL Y

Seq ID NO: 163 DNA sequence

Nucleic Acid Accession #: NM_013372.1

Coding sequence: 63..617

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		AGCACAATGA CTCAGAGCAG ACTCAGTCGC CCCAGCAGCC TGGCTCCAGG AACCGGGGGC 240
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		AGCAGACCAT CACAGAGGAA GGCTGCAACA GTGCACCAT CATCAACGCG TTCTGTTAAG 420
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60		AACTACAGCC ACCTACCAAG AAGAAGAGAG TCACACGTGT GAAGCAGTGT CGTTGCATAT 600
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		GGGACCCAGA ATCTCCTTTC GGAATGAATG TTCTAGGAAG AGGCTCCTCT GAGGGCAAGA 1020
		GACTGTGTTT AGTGCTGCAT TCGACATGGA AAGTCTCTT TAACCTGTGCT TTGCATCCTC 1080
		CTTCTCCTCT CCTCTCACAT ATCCATCTCT TCTTAAGTTG ATAGTGACTA TGTCACTCTA 1140
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		GACATTGCAG AAGCTTGAAA GGCCAATACC AGAACACAGG CTGATGCTTC TGAGAAAGTC 1380
		TTTTCTAGT ATTTAACAGA ACCCAAGTGA ACAGAGGAGA AATGAGATTG CCAGAAAGTG 1440
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35 Seq ID NO: 164 Protein sequence
 Protein Accession #: NP_037504.1

40 1 11 21 31 41 51
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 QGRGTAMPG BEVLESSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFCYG 120
 QCNFPYIPRH IRKEGSPQS CSFCKPKRPT TMMVTLNCPE LQPPTKKIRV TRVKQCRGIS 180
 IDLD

45 Seq ID NO: 165 DNA sequence
 Nucleic Acid Accession #: CAT cluster

50 1 11 21 31 41 51
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55 Seq ID NO: 166 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1650

60 1 11 21 31 41 51
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 65 CTGAGGCTCT GCAGGAGCTT CTACATCACC TGCGCGCGGC TGCGCTGCTT CCCCCAGCCT 240
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 80 GGGATCTCTT GGAATGCTGT CAATTGGCA AAGTATCCGG AATACAGGA GAAATCCGGA 1140
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 GCGAGTTCG GCGTGTGTG GGCCTAACCA CTGCTACGTT TCGGCTGAG CGTGAGACGA 1560
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Seq ID NO: 167 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
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 VLPPLVLVHP DYIKPLLGAS AAIAPKDDL F YGFLKPWLGD GLLSKGDKW SRHRLTPA 180
 FHFIDILKPYM KIFNQASDIM HAKWRHLAEG SAVSLDMFEH ISLMTLDSLQ KCVFSYNSNC 240
 QEIMSDYISA IIELSALSVR QYRLHHYLD FIYYRSADGR RFRQACDMVH HFTTEVIQER 300
 RRALRQQGAE AWLKAQKGT LDFIDVILLA RDEDEKELSD EDIRAEADTF MFEHDTTSS 360
 GISWMLFNLA KYPEYQSKCR EEIQEVMKGR ELEELWDDL TQLPFTMC I KESLRQYFPV 420
 TLVSRQCTED IKLEPDRIIP KGIIICLVSIY GTHNPTVWP DSKVYNPYRF DPDPQQRSP 480
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Seq ID NO: 168 DNA sequence
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 Coding sequence: 252..1772

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 CCGTGTGGTG GCAAAAGGGC TTGGGAACGG TTGCTGTCT TTTCTCTCT GGTAAATTC 240
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 GCTCAACCAA CCGGTGGCTT TTGCCAAAC AGCCTTTCTC TGGGGAGCTG CTCTCACTTT 360
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 TAAGTTTTCG ATTCATCTTC CCAGCATCTT GACAGTTTCC AGAAGAATCT ATGGGATTTT 1800
 CCCCCACTG GTCTGCATAA AAGAAAATAA AATGACATAA AAGGGAGC

Seq ID NO: 169 Protein sequence
 Protein Accession #: BAB71658.1

1 11 21 31 41 51
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 RELEELLRAQ SPKKTKEKSP AKRIIISLKI NDPLVTKVAF ATALKNLYMS EVEINLEDLL 180
 GVLASAHILQ FSGLFQRCVD VMIA RLKPST IKKPYEAGCK YKEBQLTTCG EKWMENLVP 240
 LGGTQIHLHK IPQDLHLKVL KSPRLPTPSE PHLLKTMLLW VFLQLNYKIQ AIPTYETVMT 300
 FPKSFFPENCC FLDRDIGRSL RPLFLCLRHL GITKGRDLEV LRHLNFFPES WLDQVTUNHY 360
 HALENGSDMV HLKDLNTQAV RFGLLFNQEN TTYSKTIALY GPFPIKGLK HDTTYSYFYM 420
 QRIKHTDLES PSAVYENHNV SLRAARLVKY EIRAEALVDG KWQEPRTNQI KQKPLGLTSS 480
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Seq ID NO: 170 DNA sequence
 Nucleic Acid Accession #: NM_007000.1
 Coding sequence: 1...777

1 11 21 31 41 51
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 GTGACAGCCG ACCAGTACCG TGTATACCA CTGATGGGAG TCTCAGGCAA GGATGACGTC 180
 TTGCTGTGGT CCGTGGATTC CATCTTCTGC GGCTTCTCTT TCTCATGGT AGCCAGTTT 240

5
10
GGTGTGGGTG COGCACTCTG COGCGCCCGG TCCATGGTCC TCACGTACCT GGTGCTCATG 300
CTCATGCTCT ACATCTTCTGA GTGCGCCTCC TGCATCACTG CCTACACCCA COGTGACTAC 360
ATGGTGTCCA ACCCATCCCT GATCACCAAG CAGATGCTGA CCTTCTACAG CGCGGACACC 420
GACCAGGGCC AGGAGCTGAC COGCTCTGG GACCGCGTCA TGATTGAGCA AGAATGCTGT 480
GGCACATCTG GTCCCATGGA CTGGGTGAAC TTCACTGTCAG CCTTCCGGGC GGCACTCCG 540
GAGGTGGTGT TCCCTGGGCC CCCACTGTGC TGTGCGCGGA CGGAAACTT CATCCCCCTC 600
AAGGAGGAGG GCTGCGGCTT GGGGCACATG GACTACCTGT TCACCAAGGG CTGCTTCGAA 660
CACATCGGCC ACGCCATCGA CAGCTACACG TGGGGTATCT CGTGGTTTGG GTTTGCCATC 720
CTGATGTGGA CGCTCCCGGT CATGCTGATA GCCATGTATT TCTACACCAT GCTCTGA

Seq ID NO: 171 Protein sequence
Protein Accession #: NP_008931.1

15
20
1 11 21 31 41 51
MASAAAAEAE KGSFVVVGLL VVGNIIILLS GLSLFAETIH VTADQYRVYP LMVSGKDDV 60
FAGAWTAIPC GFSFFMVASF GVGAALCRRR SMVLTYLVLM LIVYIFECAS CITSYTHRDY 120
MVSNNPSLITK QMLTFYSADT DQGQELTRLW DRVMIEQECC GTSGFMDOWN FTSAFRAATP 180
EVVFPWPLLC CRRTGNFIPL NEBGCRLGHH DYLFKGCFFE HIGHAIDSYT WGISWFGFAI 240
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Seq ID NO: 172 DNA sequence
Nucleic Acid Accession #: NM_006760.1
Coding sequence: 39..593

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TGCCCCCCTG TCACCTCACA GGAGGCAATG CCACACTGAT GGTCCGAGA GCCAATGACA 240
GCAAAGTGTG GACGTCCAGC TTGTGGTGC CTCCGTGCCG TGGGCGCAGG GAACTGGTGA 300
GTGTGGTGA CAGTGGTGT GGTCTCACAG TCATCTGGCT CAGTGCATAC CAGGTGACAA 360
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AGTCCAGCAG AGAGATCCCA ATGTCCACAC TCCCTCGAAG GAACATGGAA TCCATTGGGC 480
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TCTGCTGCT GCTGGGCTTC ATCATTGCCC TGSCACTGGG CTCCCGCAAG TAAGGAGGTC 600
TGCCCGGAGC AGCAGCTTCT CCAGGAAGCC CAGGGCACCA TCCAGCTCCC CAGCCCACT 660
GCTCCAGCCG CCCAGGCCCTG TGGCTCCCTT GGTGCCCTCG CCTCCTCCTC CTGCCCTCCT 720
CTCCCTCAGA GCGCTCTCCT CCGCTGTGCC CTCTCCTTGC CCGCAGTGCC TCACCTTCCA 780
ACACTCCATT ATTCTCTCA CCGCACTCCT GTCAGAGTTG ACTTTCCTCC CATTTTACCA 840
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GCTGAGGCTG CATCTGCCAA AAAAAAAAAA AA

Seq ID NO: 173 Protein sequence
Protein Accession #: NP_006751.1

50
55
1 11 21 31 41 51
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VKKGTATBSS REIPMSTLPR RNMESIGLGM ARTGGMVVIT VLLSVAMFLI VLGFIIIALAL 180
GSRK

Seq ID NO: 174 DNA sequence
Nucleic Acid Accession #: Eos sequence
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25 Seq ID NO: 175 Protein sequence
 Protein Accession #: Bos sequence

30 1 11 21 31 41 51
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 NCYLHTAGAL PSCECHLNL SQSVNFCERT KIWTGFKINE RFTNDLLNSS SAIRYSKYANG 180
 IBIQLKAYE RIQGFESVQV TQFRNGSIVA GYEVVVGSSA SELLSAIEHV AEKAKTALHK 240
 LPFLEDGSRF VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GHQVIRETCV 300
 35 LSLLEELNKN FSMIVGNATE AAVSSPVQNL SVIIRQNPST TVGNLASVVS ILSNISLSL 360
 ASHFRVSNST MEDVISIADN ILNSASVTNW TVLLREEKYA SSRLLTLEN ISTLVPPPAL 420
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 SMASLTGNL LPVSKNGNAQ VNGEVISTVI QNYSINEVFL FFSKIESNLS QPHCVFWDPS 540
 HLQWMDAGCH LVNETQDIVT CQCHLTSTFS ILMSPFPVST IFPVVKWITY VGLGISIGSL 600
 40 ILCLIEALF WKIIRKSQTS HTRRICMVNI ALSLLIADVH FIVGATVDTT VNPBGVCTAA 660
 VFPTTHFFYLS LFWMLMLGI LLAIRIILVF HEMAQHLMA VGFCGLYGCE LIISVITIAV 720
 TOPSNTYKRK DVCWLWNSG SKPLAFVVP ALAIVAVNPV VVLLVLTKLW RPTVGERLSR 780
 DDKATIRVG KSLILITPLL GLTWGPGIGT IVDSQNLAWH VIFALLNAPG GFFILCFGIL 840
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Seq ID NO: 176 DNA sequence
 Nucleic Acid Accession #: AB035089.1
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 60 AATCTCTCTC ACTAACCACT TTCCCTATAG ATTGCCACAA GCACATAATA AGAACAATA 540
 AATAAAATGT TCTCTTGACT TTGTTACTTA ACAATGCTGA GAAACCTTTA CAGCCTTCAT 600
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	GATGATAGCA CAACCTTTGTG AATATAATAA AATCATTGAA TTGTACAGTT GAAATTTATGG	2280
	TATATAAAT ATATGTTAAT AAAAAGGGGG TCCACAAAAC AAACAGCCCC CCACTCTGGT	2340
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Seq ID NO: 177 Protein sequence
 Protein Accession #: BAB21525.1

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YFKGQWENKF KKENTKEEFK WPNKNTYKSV QMRQYNISP FALLEDVQAK VLEIPYKGD 240
LSMIVLLPNE IDGLQKLEEK LTAELKMEWT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300
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Coding sequence: 50..1240

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25 GATGGCTCAG AAGCTGGTGG ACTTGGCGAT GTTTTCTGTC TACATGAGCA GTAACCCAGA 720
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50 Seq ID NO: 179 Protein sequence
Protein Accession #: NP_001901.1

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QPSQSSTYSQ PQQSFSIQYG TGLSLGIIGA DQVSVEGLTV VQQPFGESVT EPGQTFVDAB 180
FDGILGLGVP SLAVGVVTFV FDNMMQNLV DLPMPFSVYMS SNPEGGAGSE LIFGGYDHS 240
60 PSGLANWVYV TKQAYWQIAL DNIQVGGTVM FCSBQQAIV DTGTSBITGP SDKIRQLQNA 300
IGAAPVDGEY AVECANLNVN PDVTFITNGV PYTLSPATYT LLDVFDGMQF CSSGFGGLDI 360
BPPAGPLWIL GDVPIRQFYS VFDRCNNRVG LAPAVP

65 Seq ID NO: 180 DNA sequence
Nucleic Acid Accession #: NM_018058.1
Coding sequence: 319..1575

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80 AAAGTGGACA TCGTCTATGG CAACTGGAAT GGCCGCCACC GCCTCTATCT GCAATGAGC 660
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GTCCGACCGG CATCACCGG CAGACTTGGC AATGACCGAG AGCTGGAGAT CTCTCTCAAC 780
AACATTGCCT ACCGACGCTC CTCAGCCAAC CGCCTCTTCC GCGTCAATCG TAGAGAGCAC 840
GGAGACCCCT TCATCAGGA GCTCAATCCC GCGAGCGCTT TGGAGCCTGA GGGCGGGGGC 900
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GGGCTTTGTC AACACGTG

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Seq ID NO: 181 Protein sequence
Protein Accession #: NP_060528.1

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1 11 21 31 41 51
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PRDIASPKFS MSPSPRTVIT ADFDNDQBLE IFFNNIAYRS SSANRLFRVI RREHGDPLIE 180
ELNPGDALEP EGRGTGGVVT DFDGDMLDL ILSHGSEMAQ PLSVFRGNQG FMNNWLRVVP 240
RTRVGAFARG AKVVLVYTKS GAHLRIIDGG SYLCEMEPV AHFGLGIDEA SSVEVITWPDG 300
KMSVSNVASS EMNSVLEILY PRDEDTLQDP APLETPMNAS SSHSCALETS PYVSTFMEAT 360
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Seq ID NO: 182 DNA sequence
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Coding sequence: 1..1962

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Seq ID NO: 183 Protein sequence
Protein Accession #: CAC08451

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	EIYFLATNNA	FSGVATYTDK	LFKFNNRWE	DILSDENVVA	RGVASLFAGR	SVACVDRKGS	180
	GRYSIYIANY	AYGNVGPDAL	IEMDPEASDL	SRGILALRDV	AAEAGVSKYT	GGRGVSVGPI	240
10	LSSASDIFC	DNENGNPFLP	HNRGDGTFVD	AAASAGVDDP	BQHGRGVALA	DFNRDGVKDI	300
	VYGNWNGPHR	LYLQMSHTGK	VRFRDIASPK	FSMPSPVRTV	ITADFNDQJE	LEIFFNNIAY	360
	RSSSANRLFR	VIRREHGDPL	IEELNPGDAL	EPEGRGTGGV	VTFDGDGML	DLILSHGESM	420
	AQPLSVFRGN	QGFNNNWLVR	VPRTRFGAFA	RGAKVVLVTK	KSGAHLRIID	GGSGYLCEME	480
	PVAHFLGLKD	EASSVEVTWP	DGKMVSRNVA	SGEMNSVLEI	LYPRDEDTLQ	DPAPLECGQG	540
15	FSQQENGHCN	DTNECIQFPF	VCPRDKPVCV	NTYGSYRCRT	NKKCSRGYEP	NEDGTACVGT	600
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	TCACCTACT	ACGCGCTGCG	GGACCGGCAG	GGGAACGCCA	TCCGGGTGAC	AGCCTGCGAC	240
	ATCGACGGGG	ACGCGCGGGA	GGAGATCTAC	TTCTCAACA	CCAATAATGC	CTTCTCGGGC	300
	CACAGCAGCT	CAGCGCAGGT	CCCTTCTGGG	CTCCACAGAA	ACAGGCGCTGT	GCTGAAGCCT	360
30	CCACCTACAA	CCCTCTCAGG	CCTCCTGGGT	CTGCCTCCAC	TCAGCGGAAG	GGACTTTTCC	420
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	TGTGGGGGTG	GACTGAGACC	TACCCATGAA	CCAGAACCAT	TTCTCTGAG	ACCCAATCA	540
	GGGGTGCCCA	CGTACACCGA	CAAGTTGTTT	AAGTTCGCA	ATAACCGGTG	GGAAAGCATC	600
	CTGAGCGATG	AGGTCAACGT	GGCCCGTGGT	GTGGCCAGCC	TCCTTGCCGG	ACGCTCTGTG	660
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	GGTAATGTGG	GCCCTGATGC	CCTCATTGAA	ATGGACCTTG	AGGCCAGTGA	CCTCTCCCGG	780
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	GGAGGAGACC	CAGAGGAGGC	AGATGAGGAG	CACAGTGGGG	ATGGAAGCAC	CAGCCAACCTG	960
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	GAGCTTGGAG	GCTCCCTGAG	CCAAGCCACA	CAGCACTGCG	CTGCTAGAGA	GCTGTATGAC	1500
	CTGGGAGAAC	CTCCCATTTT	ACAAGAAGCA	GACGGAGATC	CAGGGAGGAG	AAGGAGACTCG	1560
50	CCCAAGGTCA	CACAGAGGTC	CCATCTAGTG	GCCAACATGC	CAGCTCTCGG	GGAGCTGAG	1620
	GGCCCGGGGA	GGGTGGCCAA	GCAGAGAGAT	GGGAGAGAGA	CTGGGGCAGT	AGGAAGACCA	1680
	CTCTCCCATC	CCCTGGTCCC	CAACTTCCCC	AGCTGTCTGA	GGCCTCTTGA	AGCCGGGACA	1740
	GTGCGGGGAG	TGCGCCCTGC	TGGGAATCCT	GGGAACCTGG	TTCTGGACAT	GGCCAAGGCC	1800
	CTGGCGTGGA	ACCAGATGGA	AAAAGAGGAG	GGGAAGATTC	ATGGAGACCA	TGAGCCCGGA	1860
55	TTTAGGCTCA	GGAAAGCAAG	GGAAAGCAAA	TTCCCCCAG	GCTCCTCTGA	GGAGCCTCTG	1920
	CTGCACTTCC	CCTCAGGCTC	CAGAGGCAGC	CCTGTCTCTC	AGGTGGGCTC	GGGGCTGTCT	1980
	CTCTGCCATC	ACTGTGGGTC	GATGTCTTTT	CTAGGGGGCC	GAGGCGTCAG	CGTGGGCCCC	2040
	ATTCCTCAGC	CGAGTGCCTC	GGATATCTTC	TGCGACAATG	AGAATGGGCC	TAACTTCTCT	2100
	TTCCACAACC	GGGGCGATGG	CACTTCTGTG	GACGCTGCGG	CCAGTGTCTG	ACGTGCTTTA	2160
60	GCCTTCATCG	TTCACTCAA	ATATCACTTC	TGCAGAGATT	TTCTCACTC	CCTGTGCCAC	2220
	CTAGCAGAAA	CTGGTCTCTC	CTCCTCTGCG	TGCCCGTGGC	ATGCACTGCT	TCTTCAGGCT	2280
	CCACATTGCC	ATCATGTTT	GTCTATGAGC	TTTACAAGGA	CCGGTCAAG	GTTCTATTCA	2340
	TTCTTGAGCG	AAGGCTTGGC	CTCCAGTGCC	CACCGGAGGA	CACCTCAGCT	CCAGGGTTCT	2400
	CAGGGGGCCC	CACCTTGCTC	TCTGGCAAGA	GCTCCTGTG	TCTGGGGTCT	TCTGATCCCC	2460
65	ACTGCCTATT	ACATTGTCTC	GTGGTCTGCC	ATCCAGAGGA	GCCTGATGAC	CCACAGCTAT	2520
	TTGTCTCTG	AAAGATCAA	CGTGGGTGTG	GACGACCCCC	ACCAGCATGG	GOGAGGTGTC	2580
	GCCTGGGCTG	ACTTCAACCG	TGATGGCAAA	GTGGACATCG	TCTATGGCAA	CTGGAATGGC	2640
	CCCCACCGCC	TCTATCTGCA	AATGAGCAAC	CATGGGAAGG	TCCGCTTCCG	GGACATCGCC	2700
	TCACCCAGT	TCTCCATGCC	CTCCCTGTGC	CGCAGGTCA	TCACCGCCGA	CTTTGACAA	2760
70	GACCAAGAGC	TGGAGATCTT	CTTCAACAAC	ATTGCTTACC	GCAGCTCCTC	AGCCAAACCG	2820
	CTCTTCCGAT	GCTTCACTCT	GGCTGGTGGC	TCTTCACTCT	TGACAGCTGG	TGGGAGGAAC	2880
	GTTCAGGGAG	AAGGTTTAAG	AATCAGAAGG	GGAGGGTTCC	CAGGGCCAGG	GGGTGAGGCC	2940
	AAGGTCAAGC	GAGTCCCCCT	GATGAAGAAA	CAGAAAGGAA	GGAAGGACGA	GGACTGGGCA	3000
	AGAGGCTGTG	GGAATGCAGG	GCAAGGCTG	GCCAAGGAGC	CGGCTCTGCG	TATTGCAGGG	3060
75	AAAGGGAAGG	GAAATGTGCG	CCAAAGTGTG	CCAGAAACCC	AAGCGCCACA	AGATACAAAG	3120
	CCACACTACC	TACGGGCTCC	GCTACAGGGT	CCAATCACTA	CCAGGAAAAG	GGGCTACGGG	3180
	GTCCAATCAC	TACCAAGAAA	AGGGGCTACG	GGGTCCAATC	ACTACCAAGG	AAAGGGGCTA	3240
	CGGGGTCCAA	TCACTACCA	GAAAAGGGGC	TACGGGGTCC	AATCACTACC	AGGAAAAGGG	3300
	GCTACGGGCT	CCAAATCACTA	CCAGGAAAAG	GGGCTACAGG	GTCCAATCAC	TACCAAGAAA	3360
80	AGGGGCTACG	GGCTCCAATC	ACTACCAAGG	AAAGGGGCTA	CAGGGTCCAA	TCACTACCA	3420
	AGAAAGGGGC	TACGGGCTCC	AATCACTACC	AGGAAAAGGG	GCTACGGGGT	CCAATCACTA	3480
	CCAGGAAAAG	GGGCTACAGG	GTCCAATCAC	TACCAAGAAA	AGGGGCTACG	GGGTCCAATC	3540
	ACTACCAAGG	AAAGGGGCTA	CGGGCTCCAA	TCACTACCA	GAAAAGGGGC	TACGGGGTCC	3600
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GTCCAATCAC TACCACAGAA AGGGGCTACG GGCTCCAATC ACTACCAGGA AAAGGGGCTA 3720
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AACAACAAC TGGTGGAGT GGTGCCACGC ACCCGGTTTG GGGCCTTTGC CAGGGGAGCT 4140
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AGTGTGGAGG TGACGTGGCC AGATGGCAAG ATGGTGAGCC GGAACTGGC CAGCGGGGAG 4320
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CCCAAAAGG AGCTGCAACT TTCCCAAGGC ATCTGCACCC CGCTCTGGTC CTTTTCCTG 4680
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CAGAAAGCTC CAGGTATTCC AGAAGCCCAA GTGTATGAAC AAGATCAGGA ATAA

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Seq ID NO: 185 Protein sequence

Protein Accession #: FGENESHH

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1 11 21 31 41 51
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PPTTPAGLLG LPPLSGRDFS SSLGQASPDS RQGERVPVPC CRGGLRPTH EPEPFLRPKS 180
GVATYTDKLF KFRNNRWED LSEENVARG VASLFAGRSV ACVDRKSSGR YSIYIANYAY 240
GNVGPDALE MDPASDLER GILALRDVAA EAGVSKYTEG FSHTASPSIG EISGRTEERE 300
GGDFEAEDEE HSGDGSQSL CRLGWDGQF KEBAALVEE QREAGAAGVP RGRVRTALQT 360
SKSHLADKNL PGPPCIYSVC APSAHPFPA RQAPQHYVPA PLVTQLMTHG RLAKGLARSV 420
PHPRAPGMDP KCKGRHAEPG LMAEALGAWP ALSTTVVPGG LRSWEESRQK GQAMSRCLAR 480
ELGGPWSQAT QHLPARELYD LGEPPIQLRT DGDGPRRRDS PKVTQECHLV ATMPALGGLE 540
GPGRVAKREI GRETVAVGRP LSHPLVPNFP SCLRLPEAGT VPGAALPGNP GNWVLDMAKA 600
LAWNQMEKEE KGIHGDHEPR FRLRKAREAE FPPGSSEEP LQFPGLRGS FVLQVGLGLA 660
SATHCGSMSP LGGRGVSVGP ILSSASDIF CDNENGPNFL FHRNGDSTFV DAAASAERRL 720
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RGPITTRKRG YGVQSLPGK ATGNSHYQEK GLQGPITTRK RGYQLQSLPG KGATGNSHYH 1140
RKLRLAPITT RKRGVGVQSL PGKGATGNSH YQEKGLRGPI TTRKRGYGLQ SLPGKGATGS 1200
NHYQEKGLQG PITTTRKRGY VQSLPQKQAT GSNHYQEKGL RGPITTRKRG YGLQSLPGKE 1260
AMGNSHYQEK GLRAPITTRK RGYGVQSLPG KGATGNSVIR REHGDPLEIE LNPGDALPE 1320
GRGTGGVVTD PDGDMLDLI LSHGESMAQP LSVFRGNQGF NNWLRVVRP TRPGAFARGA 1380
KVVLVTKKSG AHLRIIDGGS GYLCEMEPVA HFGLGKDEAS SVEVTNPDGK MVSERNVASGE 1440
MNSVLEILYP RDEDLQDPA PLECGQGFSG QENGHQMOTN ECIQFPFVCP RDKPVCVNTY 1500
GSYRCRTNKK CSRGYEPNED GTACVGTSELG SRHTMTWKPR PKKELQLSQG ICTPVVWSFPL 1560
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Seq ID NO: 186 DNA sequence

Nucleic Acid Accession #: NM_000584.1

Coding sequence: 75..374

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CTGCAGCTCT GTGTGAAGGT GCAGTTTTCG CAAGGAGTGC TAAAGAACT AGATGTGAGT 180
GCATAAAGAC ATACTCCAAA CCTTCCACC CCAAATTAT CAAAGAACTG AGAGTGATTG 240
AGAGTGGACC ACACTGCGCC AACACAGAAA TTATTGTAAA GCTTCTGAT GGAAGAGAGC 300
TCTGTCTGGA CCCAAGGAA AACTGGGTGC AGAGGGTGT GGAGAAGTTT TTGAAGAGGG 360
CTGAGAATTC ATAAAAAAT TCATTCTCTG TGGTATCCAA GAATCAGTGA AGATGCCAGT 420
GAAACTTCAA GCAAACTTAC TTCAACACT CATGTATTGT GTGGGTCTGT TGTAGGGTTG 480
CCAGATGCAA TACAAGATTC CTGGTTAAAT TTGAATTCA GTAAACAATG AATAGTTTTT 540
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CAAAAAACAA CAATAATTTT TTAATATAA GGATTTTCCT AGATATTGCA CGGGAGAATA 660
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GAATGGGTTT GCTAGAAATG GATATTGAA GCATCACAATA AAATGATGS GACAATAAAT 780
TTTGGCATAA AGTCAAAATT AGCTGGAAT CTGGATTTT TTTCTGTAA ATCTGGCAAC 840
CCTAGTCTGC TAGCCAGGAT CCACAAGTCC TTGTTCCTCT GTGCCCTGGT TTCTCCITTA 900
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5 Seq ID NO: 187 Protein sequence
 Protein Accession #: NP_000575.1

1 11 21 31 41 51
 10 MTSKLAVALL AAFILISAALC EGAVLPRSAK ELRCQCIKTY SKPFHPKFIK ELRVIESGPH 60
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15 Seq ID NO: 188 DNA sequence
 Nucleic Acid Accession #: NM_003661.1
 Coding sequence: 1..1152

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 AAGGAAAAG TGAGCACACA GAATCTGCTA CTCCTGCTGA CTGATAATGA GGCTTGGAAC 240
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 25 TACAGAAACT GGTTCCTGAA AGAGTTTCTT CGTTTGAAAA GTGAGCTTGA GGATAACATA 420
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 30 ACACAAGCCC AAGCCACGA CCTGGTCATC AAAAGCCTTG ACAAAATTGA GGAGGTGAGG 720
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 35 ACGGATGTGG CCCCTGTAA GCTTCTTCTT GTGCTGGATG TAGTCTACCT CGTGTACGAA 1020
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40 Seq ID NO: 189 Protein sequence
 Protein Accession #: NP_003652.1

1 11 21 31 41 51
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 YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGSLIS SGILTLVGMG 180
 LAPFTGGSL VLEPGMBLG ITAALTGITS STMDYGKQW TQAQHLVLI KSLDKLKEVR 240
 50 EFLGENISNF LSLAGNTYQL TRGIGKDIRA LRRARANLQS VPHASASRPR VTEPISAESG 300
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55 Seq ID NO: 190 DNA sequence
 Nucleic Acid Accession #: NM_014452.1
 Coding sequence: 1..1968

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 TCTAGTGTGA TGAATGCAA AGCATACACA GACTGTCTGA GTCAGAACCT GGTGTGATC 600
 70 AAGCOGGGGA CCAAGGAGAC AGACAACGTC TGTGGCACAC TCCGTCCTT CTCCAGCTCC 660
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5 AGCCCCATCC CCAGCCCCAA CGCGAAACTT GAGAATTCCG CTCTCCTGAC GGTGGAGCCT 1620
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10 Seq ID NO: 191 Protein sequence
 Protein Accession #: NP_055267.1

15 1 11 21 31 41 51
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 LPCAALTDRE CTCPPGMFQS NATCAPHTVC FVGNGVRKKG TETEDVRCKQ CARGTFSQVP 180
 SSVMKCKAYT DCLSNLVVI KPGTKETDNV CGLTSPFSSS TSPSPGTAIF PRPEHMETHE 240
 VPSSTYVPKG MNSTESNSA SVRPKVLSSI QEGTVPDNTS SARGKEDVNK TLPNLQVNVH 300
 QGGPHRRHIL KLLPSMEATG GEKSSTPIKG PKRGHPQRNL HKHFDINEHL PWMIVLFLLL 360
 20 VLVVIVVCSI RKSSRTLKKG PRQDPSAIVE KAGLKSMTP TQNKREKIYY CNGHGIDILK 420
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 SPQDKNGKFF VDESEPLLRC DSTSSGSSAL SRNGSFITKE KKDITVLRQVR LDPDCLQPIF 600
 25 DDMHLHFNPE ELRVIEEIPQ AEDKLDRLF EIGVKSQEAS QTLSDSVYSH LPDLL

Seq ID NO: 192 DNA sequence
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 65 ACCAGGCGGT GGATCCAGGA CATCGAGGGA GCCAGCGCCA AGGACCTTTG CAGCGGTCTT 1980
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 CTGATCACC GAGGGTACCA GTCCCTGTCA GACAGCCCCC CGGGGTCCCG AGTCTTCACT 2640
 GAGTCAGAGA AGAGGCCACT CAGCATCCAA GACAGCTTCC TGGAGGTATC CCAAGTGTGC 2700
 CCGCGGCCCC GGGTCCGCTT TGGCTCGGAG ATCGGTGACT CTGTGTGTGT AGAGCTGACT 2760
 80 TCCAGAGGAC GCTGCCCTGG CTTACAGGGC TGTGAATGCT CGGAGAGGGT CAACTGGACC 2820
 TCCCTTCGCT TCTGCTCTTC GTGGAACACG ACCGTGTTGC CCGGCCCTTG GGAGCCTTGG 2880
 GGCCAGCTGG CCTGCTGCTC TCCAGTCAAG TAGGGAAGCT CCAACACCCC AGACACCCAA 2940
 ACAGCCGTGG CCGGAGAGGT CCGGCGCAA TATGGGGGCC TGCCTAGGTT GGTGGAAACG 3000
 TGCTCCTTAT GTAAACTGAG CCCTTTGTTT AAAAAACAAT TCCAAATGTG AAAGTGAAT 3060
 GAGAGGGAAG AGATAGCATG GCATGCAGCA CACAAGGCTG CTCAGTTTCA TGGCCTCCCA 3120
 GGGGTGCTGG GGATGCATCC AAAGTGGTTG TCTGAGACAG AGTTGGAAAC CCTCACCAAC 3180

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TGGCCTCTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCCTGTCTC ACTGCAGATT 3240
CAGGACCAGC TTGGGCTGCG TGGGTCTCTG CTGCGCAGTC AGCCGAGGAT GTAGTGTGTT 3300
CTGCCGTCGT CCCACCACCT CAGGGACCAG AGGGCTAGGT TGGCACTGCG GCCCTCACCA 3360
GGTCTTGGGC TGGGACCCAA CTCTGGGACC TTCCAGGCT GTATCAGGCT GTGGCCACAC 3420
GAGAGGACAG CCGAGCTCA GAGAGATTT CGTGACAATG TACGCCTTTC CCTCAGAAAT 3480
CAGGGAAGAG ACTGTGCGCT GCCTTCTCC GTTGTGCGT GAGAACCGT GTGCCCTTC 3540
CCACCATATC CACCTCGCT CCATCTTTGA ACTCAAACAC GAGGAACATA CTGCACCTG 3600
GTCCTCTCCC CAGTCCCAG TACACCTCC ATCCTCACC TTCCTCCAT CTAAGGGATA 3660
TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGTT TTTATACATT TTTTAATAAG 3720
ATGCACCTTA TGTCAATTTT TAATAAAGTC TGAAGAATTA CTGTTT

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Seq ID NO: 193 Protein sequence
Protein Accession #: XP_044533.3

15
20
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30

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1 11 21 31 41 51
| | | | |
MLRTAMGLRS WLAAPMGALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60
RFEAEHISNY TALLLSRDGR TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEKKQQC 120
SFKGKDPORD CQNYIKILLP LSGSHLFTCG TAAPSPMCTY INMENFTLAR DEKGNVLEED 180
GKGRCPDFPN FKSTALVVDG ELYTGTVSF QGNDPAISRS QSLRPTKTS SLNWLQDPAP 240
VASAYIPESL GSLQGDDEKI YFPFSETGQS FEFFENTIVS RIARICKGDE GGERVLQQRW 300
TSFLKAQLLC SRPDGPPFN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV 360
FTMKDVQRVF SGLYKEVNRLE TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420
NFLKDHPLMD GQVRSRMLLL QPQARYORVA VHRVPLHHT YDVLPLGTGD GRLHKAHSV 480
PRVHIIEBLO IFSSGQPVQN LLLDTHRGLL YAASHGVVQ VPMANCSLYR SCGDCLLARD 540
PYCAWSSGSC KHSVLYQPL ATRPWQDIE GASAKDLCSA SSVVSPSFVP TGEKPCQVQ 600
FQPNVTNLA CPLLSNLATR LMLENGAPVN ASASCHVLP GDLLLVGTQQ LGFQCHSLE 660
EGFQQLVASY CEVVEDGVA DOTDEGGSVP VIISTSRVSA PAGGKASWGA DRSYWKFLV 720
MCTLFVLAVL LFLVPLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNLGLPFPST 780
PLDHRGYQSL SDSPGSRVP TESEKRPLSI QDSFVEVSPV CPRPRVRIGS EIRDSVV

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Seq ID NO: 194 DNA sequence
Nucleic Acid Accession #: NM_022819.1
Coding sequence: 1..635

35
40
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50

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1 11 21 31 41 51
| | | | |
ATGGCAGATG GGGCAAAGGC CAACCCCAAA GGGTTCAAAA AGAAGGTGCT GGATAGATGC 60
TTCTCTGGGT GGAGGGGCC ACCTCTCGGG GCCTCTCTGT CTCAAGAAC CTCAGGCTCT 120
AGCCTGGGTA TGAAGAAGTT CTTCACCGTG GCCATCCTTG CTGGCAGCGT TCTGTCCACA 180
GCTCAGCGCA GCCTGCTCAA CCTGAAGGCC ATGGTGGAGS CCGTCACAGG GAGGAGCGCC 240
ATCTGTCTCT TCGTGGGCTA CGGTTGCTAC TGTGGGCTGG GGGGCCGTGG CCAGCCCAAG 300
GATGAGGTGG ACTGTGTGCT CCACGCCAC GACTGCTGCT ACCAGGAAC CTTTGACCAA 360
GGCTGTACCC CCTATGTGGA CCACTATGAT CACACCATCG AGAACAACAC TGAGATAGTC 420
TGCAGTGACC TCACACAAGC AAGTGTGAC AAGCAGACAT GCATGTGTGA CAAGAACATG 480
GTTCTGTGCC TCATGAACCA GACGTACCGA GAGGAGTACC GTGGCTTCTT CAATGTCTAC 540
TGCCAGGGCC CCACGCCCAA CTGCAGCATC TATGAACCGC CCCCTGAGGA GGTCACTCTG 600
AGTCACCAAT CCCAGCGGCC CCCGCCCCCT CCCTAG

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Seq ID NO: 195 Protein sequence
Protein Accession #: NP_073730

55
60

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1 11 21 31 41 51
| | | | |
MADGAKANPK GKPKKVLDR C FSGWRGPRFG ASCPSRTSRS SLGKKKFTV AILAGSVLST 60
AHGSLNLNKA MVEAVTGRSA ILSFVGYGCV CGLGGRGQPK DEVDCCHAH DCCYQELFDQ 120
GCHPYVDHYD HTIENNTIIV CSDLNKTECD KQTCMCDKNM VLCLMNQTYR EBYRGFLAVY 180
CQGPTFNCIS YEPFPEVTC SHQSPAPPAP P

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Seq ID NO: 196 DNA sequence
Nucleic Acid Accession #: XM_028196.1
Coding sequence: 1315..1791

65
70
75
80

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1 11 21 31 41 51
| | | | |
GGCATTGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60
GTGTGTGTGT GTCTGAGATC ATGGCAGGCT CCCTTTCTGT CTGTCTCCTT GCTCTGCCCC 120
AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180
ATGGCCTGGG CTGGGCCCTT GAGGCGAGGC TGACTGGAC ATGGCAAGAG GGGTCCAGG 240
CTCTTGTGGG CAAGCAGGG GAGGCGCCAA TGTGAGGAA CAGAGTCTCC TGGCTGGCTG 300
CTGCTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCTG 360
GGGTACCCCT AGGCCCATG TAGCACCTG GTTCCCTCG CTGTAGGTGA CAGGAGCCAG 420
CCAGCCAGG TGTGCTCCTT CCCCAGGCC TAGGCAGGCG GGTACAGGGG CCAGCAGCTG 480
GGCCCGCCCC ACCTTCTCTT CCACCCACAT GCGCAAGGGT GGCCAGGCAG CAGGTGGAC 540
GAGTCCAGGC AGCGGCTGAG TCAGTGTGTG TGAATGTTT TGGCCGCTCC CAGCTGCACC 600
CTGCCCTTAC CTGACACAC CACACCTTCA TCCTCAGGCG CTGGGCGCTT GAGCCCTGCG 660
CAGGAATGCA CCTTTAGCCC AGGCCCTGCT AGTGAGCTCC GCGCAGACCC AGCCCTGCTC 720
CTCCCGCAT GACCTGACAG ACCCTCTGCG GCTTCAAGT TCCTGGGGGC TGCAGTGAAC 780
ATGCTCCACC TGCAATGCTG GCAAAACATG GTGGGCCCCA CCTGTGTGTC GTGCTGGGGT 840
AGAGGCAAGG AAGTGATGGG ACCGCAGAGA TGAGACCCCC AGGATATGAG TGGGACCCCC 900
AGGCAGGGCC CAGGGTCCAG GGCCAGGAG AGAGAAGCAG GGAGGAGAG AGCTTCTGG 960
TGGAGGACGC ATCTACAGT GGGGCAAGG GTGCTCTGAG GTCCGCTGAA GGCAGGGACT 1020
AGGCTGCCCA GGCCTGCGCT GCTTGGCTGG GGCTGGGGGC TGCTGGGAGG TGGCTGGGAG 1080
GCTGGGCGCT GGCAGCTAAG CTGGAGCTTT GGCCAGGGTC CAGAGCCTCC CTCCTTTCAG 1140

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5 CTTCTGCTG CACAGAACCC TCGCCCTG CACCCCGTG CTGCTCTCTT GCCCTGGCAG 1200
 ACCCAGCACT GGCTGCTGCT AGTCAGATGG GGTAGCCGGC AGGGGCCGGA GGGGCCACCC 1260
 TCCCAGCTGA CCGAGCCTCC TGGGCCGCTT CTTCACAAAC AGCAGGGTAG AAAGATGGGG 1320
 CACCCACAGG TCTCTCCAG TGCCTCCGCT CCAGCTGGCA CCACAGCTAT ACCTGGGCTT 1380
 ATTCCAGACC TTGTGCGCGG GACCCCTGT GAGTTGTGGG ATTCACAGA GGGGTGTGGG 1440
 GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCTCTACC 1500
 CCAGGGCCCC GCTGGGCTCT CATTGCCGGC GCCCTTGCGG CGGGCGTCTT CCTCGTCTCC 1560
 TGCTCTCTCT GTGCTGCTG CTGCTGCTGC CGCCGCCACA GGAAGAAGCC CAGGGACAAG 1620
 10 GAGTCCGTGG GTCTGGGCGG TGCCCGCGGC ACCACCAACA CCCACTGGT GAGGAGCGGC 1680
 TCCTTGCTCA CTCAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA 1740
 GCGCAGTTCA GCCCCAGGGA TGGTTTAAAC CCCACAGAGG CAGGGGTTG AGGACCTTCC 1800
 TGGCAGGGAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCAT 1860
 GGGCCCGAGG GAGCCACAGC GGGTCTTGA GGAAGGCAGG GGGTACCCCA GATGCCACGT 1920
 15 TTTGGGTGGG TTTGGCGGT CTCACAGAGC GAAGCCGAGG ATTTGTGCTT GTTGGGTGGC 1980
 CTGGCTGGA GCGGGGGGT CTTGAACCAT GTCATGCAAG GGCTGCCCGG GAGCCACAGG 2040
 CTCTGATGAG GCATGATGTC AGCACCACT GCCCTTGTC CCACTCACT CCAGGTGCAA 2100
 CCTGATGTGG ATGGCTGGA GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCTGCGAG 2160
 CTCTCCCTGG AGTTGCACTT TGAAGCCAG GAGGTGAAG GCCCGCTGCG GCAGGACAG 2220
 20 CGGTCTGCGG AGTTTCCGGA AAGGGTGAGC GGGGAAGGGC AGACCCATG CCTGGGTGG 2280
 TGGGAGCTG ACAGGGCAGG GGCCTTGGC TGAGCCACCC CGCTGGCTC CCAGATCAGG 2340
 GTGGGCTGAG GGCAGGCAGC CGACCTGAGG CCTGGGGCA CGTGGAGCC CTATGCCCGG 2400
 GTCAGCGTCT CCACCCAGGC CGACACAGA CATGAGACAA AAGTGACCG AGGCACGCTC 2460
 TGCCCGTGT TTGACAGAGC CTGCTGCTTC CAGCTGAGTC AGGGATGCTC GGCTGGGTGG 2520
 25 GCTGCGTGG CTGATGGG CTGGGCTGGG TGGGCTGGG CAGCTGGGTG GGCTGGGCA 2580
 GCTGGGTGG CCTGAGCTAG GGCAGCAGGG CCTGGCTCAC GCGCTGCTT CAGATCCCGC 2640
 AGGCGGAGCT GCCAGGGGCC ACCCTGCAGG TGACGCTTT CAACTTCAAG CGCTTCTCGG 2700
 GGCATGAGCC CCTGGGTGAG CTCGCTGTC CACTGGGCAC CGTGGATCTG CAGCATGTTT 2760
 TGGAGCACTG GTACCTGCTG GGCCTGCGG CTGCCATCA GGTGAGGTGC TGGTCAACAG 2820
 30 GCCACAGCCC AAGGCAGAGC TGGCAGGGAC CCTGCCCTAT GGGCCATCGG AAAGACAGGC 2880
 CTGATGGGCA GCATTTTCGG GGTCTGAGC CCCAACTCGG CCAGAATCAC CCTCCCGGGC 2940
 TGAAGCCCTT CTGCTGCCC ACAGCCCGAG CAGGTCCGGG AGCTGTGCTT CTCTCTCCGG 3000
 TACGTGCCCA GCTCAGCCG GCTGACCGTG GTGGTGTGAG AGGCTCGAGG CCTGGTCCA 3060
 GGACTTGCAG AGCCCTACGT GAAGGTCCAG CTCATGCTGA ACCAGAGGAA GTTCAAGAG 3120
 35 AGAAAGACAG CCACCAAAA GGCACCGCG GCCCCTACT TCAATGAGGC CTTCACCTTC 3180
 CTGGTGCCCT TCAGCCAGGT CCAGAATGTG GACCTGGTGC TGGCTGTCTG GTTACCGCAGC 3240
 CTGCCGCTCC GAATCAGACC CGTAGGCAAG GTGCACCTGG GTGCCCGGGC CTCGGGGCAG 3300
 CCCCCTGACG ACTGGGCAAG CATGCTGGCC CAOCGCGGC GGCCCATTTG CCAGCGGCAC 3360
 CCCCCTGCGC CAGCCAGGGA GTTGGACCGC ATGCTGGGCC TGACGCCCG CCTTCGCTG 3420
 40 CGCTGCGCTT TGCCCACTC CTGAATGCAC CACATGCCTC TGTCTCCCGG CTGAGCCAG 3480
 GCATTTGCCC AGGCGGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCTT GCC

Seq ID NO: 197 Protein sequence

Protein Accession #: XP_028196.1

45 1 11 21 31 41 51
 MGHPVPSPSA PAPAGTIAIP GLIPDLVAGT PCELNDSQEG CGENPAKWGL QLSTDALSLA 60
 STGPFRWALL AGALAAGVLL VSCLLCAACC CRRHRKRPK DKESVGLGSA RGTTHLVR 120
 50 SGLLTQSRE GLKSLQSPG QRGESPRDG LTPTEAGR

Seq ID NO: 198 DNA sequence

Nucleic Acid Accession #: NM_000612.2

Coding sequence: 553..1095

55 1 11 21 31 41 51
 TTCTCCGCA ACCTTCCCTT CGCTCCCTCC GGTCCCGCCC AGCTCCTAGC TTCGACTCC 60
 CTCCTCCCTT CAGCCCGGCC CTCTGCTCTT CGCCGAACCA AAGTGGATTA ATTACAGCT 120
 60 TTCTGTTTCT CTCGTGCTG TTCTCTCCCG CTGTGCGCTT GCCCGCTCT CGCTGTCTCT 180
 TCTCCCTCTT GCCCTCTCTT CGGCCCGCCC CTTTCAAGTT CACTCTGTCT CTCCACTAT 240
 CTCTGCCCTT CTCTATCCTT GATACACAG CTGACCTCAT TTCCGATAC CTTTCCCCC 300
 CCGAAAGTA CACATCTGG CCGGCCCGAG CCGCAAGACA GCCCTGCTC CTTGGACAAT 360
 CAGACGAAT CTCCTCCCTT CCCCACCAAA AAAAGCCATC CCCCCTCTT GCCCGTCTC 420
 65 ACATTGCGCC CCGCGACTC GGCAGAGCG GCGCTGGCAG AGGAGTGTCC GGCAGGAGG 480
 CCAACGCGCG CTGTTCGTT TGGACACGC AGCAGGAGG TGGGCGGCG CGTCCCGGC 540
 TTCCAGACAC CAATGGGAAT CCAATGGGG AAGTGGATGC TGGTGTCTT CACCTTCTT 600
 GCTTTCGCTT CGTGTGCTT TGCTGCTTAC CGCCCGAGT AGACCTGTG CCGCGGGGAG 660
 CTGTTGGACA CCTCCAGTT CGTCTGTGG GACCCGGCT TCTACTTCA CAGGCCGCA 720
 70 AGCGGTGTA GCGCTGCGG CGTGGCATC GTTGGAGAGT GCTGTTCGG CAGCTGTGAC 780
 CTGGCCCTCC TGGAGAGTA CTGTGTACC CCGCCAAAT CCGAGAGGGA CGTGTGAGC 840
 CCTCCGACCG TGCTTCGGA CAATTTCCCT AGATACCCCG TGGGCAAGTT CTTCAATAT 900
 GACACCTGGA AGCAGTCCAC CCAGCGCTG CGCAGGGGCC TGCTGCTCT CTTGCTGCT 960
 CGCGGGGCTC ACGTGTCTCG CAAGGAGCTC GAGGCGTTCA GGGAGGCCAA ACCTCACCT 1020
 75 CCCCCTGATT CTCTACCCAC CCAAGACCCC GCGCCCGGGC GCGCCCGCCC AGAGATGGCC 1080
 AGCAATCGGA AGTGAGCAA ACTGCGCAA GTCTGCAGC CGGCGCAC ATCTGCAGC 1140
 CTCCTCTGTA CCAAGACCT TTCCATCAGG TTCCATCCCG AAAATCTCTC GGTTCACGT 1200
 CCCCCTGGGG CTCTCTCTGA CCAAGTCCCG GTGCGCGGCC TCCCGGAAC AGGCTACTCT 1260
 80 CCTCGGCCCG CTTCATCGGG CTGAGGAAGC ACAGCAGCAT CTTCAAACAT GTACAAAATC 1320
 GATTGGCTTT AAACACCTT CACATACCT CCCCC

Seq ID NO: 199 Protein sequence

Protein Accession #: NP_000603.1

1 11 21 31 41 51

MGIPMGKSM L VLLTFLAFAS CCIAAYRPSE TLGGELVDVT LQFVCGDRGF YFSRPASRVS 60
 RRSRGIVEEC CFRSCDLALL ETYCATPAKS ERDVSTPPTV LPDNFPRYPV GKFFQYDTRK 120
 QSTQRLRRGL PALLRRRHH VLAKLEAFR EAKRHRPLIA LPTQDPAHGG APPENASNRK

Seq ID NO: 200 DNA sequence
 Nucleic Acid Accession #: AK057131.1
 Coding sequence: 61..1146

1 11 21 31 41 51
 AGTCTGGGCG TTTAGGTCAG AACTACCCCG GTAGCCTGAC AGCAGGAGCT CGAGAGAAGC 60
 ATGGCTCAGC GGTGCGTTTG CGTCTGGGCC CTGGTGGCTA TGCTGCTCCT AGTTTTCCTT 120
 ACCGCTCCA GATCGATGGG CCGAGGAGC GGGGAGCATC AAAGGGGCTC GCGAATCCCT 180
 TCTCAGTTCA GCAAAGAGGA ACGCGTCGCG ATGAAAGAGG CGCTGAAAGG TGCCATCCAG 240
 ATTCCAACAG TGACTTTTAG CTCTGAGAAG TCCAATACTA CAGCCCTGGC TGAGTTCGGA 300
 AAATACATTC ATAAAGTCTT TCCTACAGTG CTCAGCACCA GCTTTATCCA CATGAAAGTC 360
 GTGGAAGAGT ATAGCCACT GTTCACTATC CAAGGCTCGG ACCCCAGCTT GCAGCCCTAC 420
 CTGCTGATGG CTCACTTTGA TGTGTTGCTT GCCCTGGAAG AAGGCTGGGA GGTGCCCTCA 480
 TTCTCTGGGT TGGAGCGTGA TGGCGTCATC TATGGTTGGG GCACACTGGA CGACAAGAAC 540
 TCTGTGATGG CATTACTGCA GGCCTTGGAG CTCTGCTGTA TCAGGAAGTA CATCCCCGA 600
 AGATCTTTCT TCATTCTCTT GGGCCATGAT GAGGAGTCAT CAGGGACAGG GGCTCAGAGG 660
 ATCTCAGCCC TGCTACAGTC AAGGGGCGTC CAGCTAGCCT TCATTGTGGA CGAGGGGGG 720
 TTCATCTTGG ATGATTTTCA TCCTAACTTC AAGAAGCCCA TCGCCTTGAT TGCAGTCTCA 780
 GAGAAGGGTT CCATGAACCT CATGCTGCAA GTAAACATGA CTTCAGGCCA CTCTTCAGCT 840
 CCTCCAAAGG AGACAGCAT TGGCATCCTT GCAGCTGCTG TCAGCCGATT GGAGCAGACA 900
 CCAATGCTTC TCATATTGGG AAGCGGGACA GTGGTGAAGT TATTGCAGCA ACTGGCAAAT 960
 GAGGTTTATG GAGAGAAATC CCTTAACCAA TGCAATAATC AGGACCAACA CGGCACTCAC 1020
 CATATTCAAA GCAGGGGTCA AGTTCAATGT CATCCCCCA GTGGCCGAGG CCACAGTCAA 1080
 CTTCCGGATT CACCTGGGAC AGACAGTCCA AGAGGTCTTA GAACTCAGCA AGAACATTGT 1140
 GGCTGATAAC AGAGTCCAGT TCCATGTGTT GAGTGCTCTT GACCCCTCC CCGTCAGCCC 1200
 TTCTGATGAC AAGGCTTGG GCTACCAGCT GCTCCGCGAG ACCGTACAGT CCGTCTTCCC 1260
 GGAAGTCAAT ATTACTGCC CAGTTACTTC TATTGGCAAC ACAGACAGCC GATTCTTTAC 1320
 AAACCTCACC ACTGGCATCT ACAGGTTCTA CCCCCTCTAC ATACAGCCTG AAGACTTCAA 1380
 ACGCATCCAT GGAGTCAACG AGAAATCTC AGTCCAAGCC TATGAGACCC AAGTGAAATT 1440
 CATCTTTAGG TTGATTCAGA ATGCTGACAC AGACAGGAG CAGTTTCTC ACCTGCACAA 1500
 ACTGTGAGGT CAAGGGGCTT GCTGGGTTAG GCATGCCGGA CCGCGGACA GCACTAACCC 1560
 AAGGGGGAAG GCTAGTGTG ATGAAACTTT TGATCAAAAC CACATTGTAA AACATTGCC 1620
 ATCTGTCTTG CTCACTCTTA AACTCTCCCA AGAACAGGC CGGGTAAGG TAAAGTCAGC 1680
 AGAAATCTGG CTCTCTCCCT CTTCCGACA TCTGCATCCC TTGATCCACT GGCATTGCT 1740
 GCCCTCTGTT CCCTTATCTG TCTTATGCTG GTTATTTCAC TGCTTCACCT TCCAGGCTTG 1800
 ACTTAACAAA TGTATGTTG AGAAATCTCA ACCAGTTGTT ACCTGATAGG AGTCTTTAAT 1860
 TTAGGGCACT CTGTCTGGGA TGCTTTCTCC AGAGCTTATA TATTTCTTCT TACTAGAACT 1920
 TTCTTCCCCC TTTTATTTCC CTCTCTCTT GAGCTCATGA GCTGTCTCTT CATCTCTCCT 1980
 CTCCTCTCTG CATCTCTCCC CTTACTCTTC AATTATTCTT ACTTCTGGAC CTGCACTTAC 2040
 CCAACTGTG ATACTACCAT AATTGTCACC ATAATCAGTC AAATAAAGTG ATCTGTGCAT 2100
 C

Seq ID NO: 201 Protein sequence
 Protein Accession #: BAB71368.1

1 11 21 31 41 51
 MAQRVCVLA LVAMLLLVFP TVSRSMGPRS GEHQASRIP SQFSKEERVA MKEALKGAIQ 60
 IPTVTPSSEK SNTTALAEPG KYIHKVFPPTV VSTSPQHEV VEEYSHLEFI QGSDPSLQFY 120
 LLMAHFEDVVP APEEGWEVPP FSGLERDGI YGWGTLDDKN SVMALLQALE LLLIRKYIPR 180
 RSFFISLGHQ EBSSSGTAGR ISALLQSRGV QLAIFVDEGG FILDDFIPNF KKPIALIAVS 240
 EKGSMMLMLQ VNMTSGHSSA PPKETISGIL AAASRLBQT PMPIIFGSGT VVTVLQQLAN 300
 EVYGEKSLNQ CNNQDHHGTH HIQSRGQVQC HPPSGPQHSQ LPDSFWTDSR RGRPTREHEC 360
 G

Seq ID NO: 202 DNA sequence
 Nucleic Acid Accession #: NM_004217.1
 Coding sequence: 58..1092

1 11 21 31 41 51
 GGCCGGGAGA GTAGCAGTGC CTTGGACCCC AGCTCTCCTC CCCCTTCTC TCTAAGGATG 60
 GCCCAGAAGG AGAACTCCTA CCCCTGGCCC TACGGCGGAC AGACGGCTCC ATCTGGCCTG 120
 AGCACCCCTGC CCCAGCAGT CCTCCGAAA GAGCCTGTCA CCCATCTGAC ACTTGTCTCT 180
 ATGAGCCGCT CCAATGTCCA GCCCAGAGCT GCCCTGGCC AGAAGGTGAT GGAGAAATAGC 240
 AGTGGGACAC CCGACATCTT AACCGGCGAC TTCACAATTG ATGACTTTGA GATTGGGCGT 300
 CCTCTGGGCA AAGGCAAGTT TGGAAAAGTG TACTTGGCTC GGGAGAAGAA AAGCCATTCT 360
 ATCGTGGCGC TCAAGGTCTT CTTCAAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG 420
 CTGCGCAGAG AGATGGAAT CCAGGCCAC CTGACCATC CCAACATCTT CGGTCTCTAC 480
 AACTATTTT ATGACGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGGAG 540
 CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTTGACGAGC AGCGAACAGC CAOGATCATG 600
 GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTCA CAGAGACATA 660
 AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTGGCCTG 720
 TCTGTGCATG CGCCCTCCCT GAGGAGGAAG ACAAATGTGT GCACCCCTGA CTACCTGCC 780
 CCAGAGATGA TTGAGGGGCG CATGCACAAT GAGAAGGTGG ATCTGTGGTG CATTGGAGTG 840
 CTTTGTCTAT AGCTGTCTGT GGGGAACCCA CCTTTTGA GAATCATACA CAACGAGACC 900
 TATGCCGCA TGTCAAGGT GAGCTCAAG TTCCCGCTT CTGTGCCAC GGGAGCCGAG 960
 GACCTCATCT CCAAACTGCT CAGGCATAAC CCTCGGAAC GGCTGCCCTT GGCCAGGTC 1020

TCAGCCACC CTGGGTCG GGCACACTCT CGGAGGGTGC TGCCCTCCCTC TGCCCTTCAA 1080
 TCTGTGCGCT GATGTGCCCT GTCAATCACT CGGGTGCCTG TGTGTGTATG TCTGTGTATG 1140
 TATAGGGGAA AGAAGGGATC CCTAAGCTGT CCCTTATCTG TTTTCTACCT CCTCCTTTGT 1200
 TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 203 Protein sequence
 Protein Accession #: NP_004208

1 11 21 31 41 51
 MAQKENSYPW PYGRQTPSPG LSTLPQRVLR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN 60
 SSGTDPDILTR HFTIDDFEIG RPLGKKGKFGN VYLAREKKSH FIVALKVLFK SQIEKEGVEH 120
 QLRREIEIQA HLHHPNILRL YNYFYDRRRI YLILEYAPRG ELYKELQKSC TFDQRATATI 180
 MEELADALMY CHGKVKIHRD IKPENLLGLL KGELEKIADFG WSVHAPSLRR KTMCGTLDYL 240
 PPEMIEGRMH NEKVDLWICG VLCYELLVGN PPFESASHEH TYRRIKVDL KFPASVPTGA 300
 QDLISKLLRH NPSEKPLAQ VSAHPWVRAN SRRVLPPSAL QSVV

Seq ID NO: 204 DNA sequence
 Nucleic Acid Accession #: AK055663
 Coding sequence: 38..1423

1 11 21 31 41 51
 AGAAGCGCTT CCGGCGGGAG CTGTGCAGCT CCTTATCATG GGGACAATTC ATCTCTTTCTG 60
 AAAACCACAA AGATCCTTTT TTGGCAAGTT GTTACGGGAA TTTAGACTTG TAGCAGCTGA 120
 CGGAAGGTCC TGAAGATAC TGCTCTTTGG TGAATAAACC TTGATATGTA CTGGCTTCCT 180
 GCTTATGTGG TGCAGTTCTA CTAAATAGTAT AGCTTTAACT GCCTATACCT ACCTGACCAT 240
 TTTTGAATCT TTTAGTTTAA TGACATGTTT AATAAGTTAC TGGGTAAACAT TGAGGAAACC 300
 TAGCCCTGTC TATTCATTTG GGTITGAAAG ATTAGAAGTC CTGGCTGTAT TTGCCTCCAC 360
 AGTCTTGCCA CAGTTGGGAG CTCTCTTTAT ATTAAGAAAG AGTGCAGAAC GCTTTTGGGA 420
 ACAGCCCGAG ATACACACGG GAAGATTATT AGTTGGTACT TTTGTGGCTC TTTGTTTCAA 480
 CCTGTTCAG ATGCTTTCTA TCGGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG 540
 TAGGAGCTGG CTCAAGAGC ATGTTGCAGA TCTTAGTCGA AGCTTGTGTG GAATTAATCC 600
 GGGACTTAGC AGTATCTTCC TTCCCGCAAT GAATCCATTT GTTTTGAATT ATCTTGCTGG 660
 AGCATTGTCT CTTTGTATTA CATATATGCT CATTGAAATT AATAATTATT TTGCGTAGA 720
 CACTGCTCTG GCTATAGCTA TTGCTTGAT GACATTTGGC ACTATGTATC CCATGAGTGT 780
 GTACAGTGGG AAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATTGGTC AGTTGGACAA 840
 ACTCATCAGA GAGGTATCTA CCTTAGATGG AGTTTTAGAA GTCCGAAATG AACATTTTGT 900
 GACCCTAGGT TTTGGCTCAT TGGCTGGATC AGTGCATGTA AGAATTGAC GAGATGCCAA 960
 TGAACAAATG GTTCTTGCTC ATGTGACCAA CAGGCTGTAC ACTCTAGTGT CTAECTTAAC 1020
 TGTTCAAATT TTCAAGGATG ACTGGATTAG GCTGCTCTTA TTGCTCGGGC CTGTTGCAGC 1080
 CAATGTCCTA AACTTTTCTG ATCATCACT AATCCCAATG CCTCTTTTAA AGGGTACTGA 1140
 TGATTTGAAC CCAGTTACAT CAATCCAGC TAAACCTAGT AGTCCACCTC CAGAATTTTC 1200
 ATTTAACTCT CCTGGGAAAA ATGTGAACCC AGTTATTCTT CTAAACACAC AAACAAGGCC 1260
 TTATGTGTCT GTTCTTCAAT ATGGACACAC ACCTTACAGC AGCATGCTTA ATCAAGGACT 1320
 TGGAGTTCCA GGAATTGGAG CAATCAAGG ATTGAGGACT GGTTTTACAA ATATACCAAG 1380
 TAGATATGGA ACTAATAATA GAATTGGACA ACCAAGACCA TGATAGACTC TAACCTATT 1440
 TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTTAG TAATCCAACT TTGCATTGAC 1500
 TGTTTAATCA TTTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCACATT TCATGAAACC 1560
 TATGAACTAA TTTTCTTGA AAATGTATTT GTGACAGTGA AATCCTGCTA AATGTTAAAG 1620
 GCTTTAATAA GGCTTCTTCT AGAAAATGTG TTTCTTTTAA TTTGATTTT GGTATCTTTG 1680
 GTTTTGTAGT TGACTGCACT GTGATGTGAC CTTACCTTTA TAAGAGCCAC TTGATGGAGT 1740
 AGATCTGTCA CATTACTAAG ATACGATATT TCTTTTCTTT TCGAGACGG AGTCTTGCTC 1800
 TGCCACTGTG CCGGCGCAAT ACATTATTAT TAACTTAAGG CTGTACTTTA TTAAGGCTTC 1860
 CTTAGTTTCT GTTTTGTGTT GTTTTGTGAG ATGGAGTCTC ACTCTGTGCG CCAGGCTGGA 1920
 ATGCACTGGC ATGATCTCAG CTCACCTCAA CCTCTGCTCT CTGAGTTCAA ATGATCTCTC 1980
 TGCCCTCAGC TCCCGAGTAG CTGGGATTAC AGGCACCTGC CACCAAGCCC AGCTAATTTT 2040
 TGTATTTTTA GTAAAGACGG GGGATTTCAC CATGTTGGCC AGGCTGTGCT TGAACCTCTG 2100
 ACCTCATGAT CCACCCACCT TAGCCTCCCA AAGTGTCTGG ATTAGGTGTG AGCCACCGCA 2160
 CCTGGCGGAT ATTTTCTTTA ATGAAATTTA TAAATATGCT TCTTGAATAA TACACATTTT 2220
 GGGAAAGGGA AAAATGTCTG TTCAAAAAGT AAAGTCTCTT TTTATAGCTT TTCCAACTT 2280
 AATGTCTAAA TTTTCTTTTG AGGTCTCTCT GAATATATGCT TTACAACTA AAAGCAAAA 2340
 TTTTATGACG AAATTTTGA ATACATTCTA TCTAGCACAA TTTGAATTTT TAATTATCAA 2400
 GATTTTGTGT AAAGTTCTCT TCTTTTAAAT ATTTTAGTAC ATTTGTAAAT

Seq ID NO: 205 Protein sequence
 Protein Accession #: BAB70980.1

1 11 21 31 41 51
 MGTIHLFRKP QRSFFGKLLR EFRVLAADRR SWKILLFGVI NLICTGFLLM WCSSTNSIAL 60
 TAYTYLTIFD LFSIMTCLIS YMTLRKPSF VYSFGFERLE VLAVFASVTL AQLGALFILK 120
 ESAERFLEQP BIHTGRLVQ TFVALCPNLF TMLSIKNKPF AYVSEAASTG WLQEHVADLS 180
 RSLCGIIPGL SSIFPLRMNP FVLIDLAGAP ALCITYMLIE INNYFAVDTA SAIAIALMTF 240
 GTMYFMSVYS GKVLQITPP HVIGQLDKLI REVSTLDGVL EVRNEHFWTL GFGSLAGSVH 300
 VRIIRDANQ MVLARVINRL YTLVSTLTQV IFKDDWIRPA LLSGPVAANV LNFSDHVVIP 360
 MPLLKGTDLD NPVTSTPAKP SSPPEPSFN TPGKNVNPVI LLNTQTRPYG FGLNHGHTPY 420
 SSMNLQGLGV PGIGATQGLR TGFTNIPSRV GTNNRIGQRP P

Seq ID NO: 206 DNA sequence
 Nucleic Acid Accession #: NM_016361.1
 Coding sequence: 397..1662

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	GGA	ACT	CAGG		GCC	GGT	CTCT		GTT	CCT	TCAA		GAG	TGT	CTGA		GGC	CAA	ACTT		GAA	TACA	AG	60
	TTT	AAT	GTTC		CTC	GT	CGGG		AAA	AGAT	AAAG		GAT	CCG	ATCT		CCC	CGG	CCCC		GGT	GTG	CAGC	120
	AGG	AGC	GAC		AAC	CCG	AGCC		CGG	TTA	AAAA		CTC	CC	AGGG		CTC	TTG	CTG		CTG	CC	ACCT	180
	TTG	TTCT	CTC		CCCC	GT	TCCC		ACT	CGG	GGTC		TCC	CT	CAGG		CCG	GG	AGG		CAG	CGG	TCCC	240
	TGCT	TGCTGA		AGG	GCT	GGAT		GT	AGC	ATCC		GC	AGG	TTCC		GCG	GACT	TGG		GGG	CG	CCCC	300	
	TGAG	CCCCGG		CGC	CCG	CAGA		AG	ACT	TGTGT		TTG	CT	CTCTG		CAG	CT	CAAC		CCG	GAG	GCG	360	
	CGAG	GGCTA		CC	ACCA	TGAT		CAC	TGG	TGTG		TT	CAG	ATGC		GCT	TGT	GGAC		CCC	AGT	GGG	420	
	GTCT	GACCT		CG	CTGG	CTA		CTG	CT	GCAC		CAG	CGG	CGGG		TGG	CCCT	TGGC		CG	AGC	TGC	480	
	GAGG	CCGATG		GCC	AGT	GTCC		GGT	OGA	CCGC		AGC	CTG	CTGA		AGT	TG	AAAAAT		GGT	GC	CAGG	540	
	GTG	TTTGAC		ACG	GGG	CTCG		GAG	TCT	CTC		AAG	CCG	CTCC		CG	CTG	AGGA		GC	AGG	TAG	600	
	TGGA	ACCC		AGC	TTT	TAGA		GGT	CCC	ACCC		CAA	ACT	CAGT		TTG	ATT	TACAC		AGT	CAC	CAAT	660	
	CTAG	CTGGT		GTC	CGA	AAAC		AT	ATT	CTCCT		TAC	GACT	CTC		AAT	ACC	TAGA		GAC	CA	CCCTG	720	
	AAG	GGGGG		TG	TTT	GCTGG		GC	AGC	TGACC		AAG	GTG	GGCA		TG	CAG	CAAAAT		GTT	TG	CCCTT	780	
	GGAG	AGAG		CT	ATG	TGGAA		GAC	ATT	CCCT		TT	CTT	TCAAC		AAC	CTT	CAAC					840	
	CC	ACAGG		TCT	TTA	TTCG		TT	CC	ACTA	AAAC		ATT	TTT	CGGA		AT	CTG	GAG		CAC	CGT	TGT	900
	TTG	CTCC		AGC	TTT	TCCA		GTG	TC	AGAAA		GA	AGG	ACCCA		TC	AT	CAT	CCA		CAC	TG	GAA	960
	GC	AGATT		CAG	AAG	CTTGA		TCC	CA	ACTAC		CAA	AGC	TGCT		GG	AGC	CTGAG		GC	AG	AACC	1020	
	AG	AGG		CCG	GA	GGAG		CT	CTT	TACAG		CC	AGG	AATCT		CAG	AGG	AATTT		G	AAAA	AGGTG	1080	
	AAG	GA		CAG	GA	ATTGA		CAG	TAG	TGAT		AA	AGT	GGACT		TCT	T	CAT	CTC		CCT	GG	ACAAC	1140
	TG	GGCTG		CCG	AG	CAG		CA	ACCT	CCCCA		AG	CTG	CCCCA		TG	CT	G	AAG		ATT	TG	CA	1200
	ATG	ATG		CAAC	AG	AGC		TGT	TAC	ATAC		TG	CC	CAAGGA		AG	CA	GGG	GAA					1260
	AGT	CTT		CAGA	TGG	CAGTAG		CCC	ATT	CCCTC		CAC	AT	CCCTAG		AG	AG	CAACCT		GCT	G	AAAGCC	1320	
	ATG	GACT		CTG	CCA	CTGCCC		CG	CA	AGATC		AG	AA	AGCTGT		AT	CT	CTATGC		GG	CT	CAT	GAT	1380
	GTG	ACCTT		CA	TACG	CTCT		AAT	G	ACCCCTG		GGG	AT	TTTTG		ACC	CA	AAATG		GCC	AC	CGTTT	1440	
	GCT	GTTG		ACC	TG	ACCATGGA		ACT	TTA	CCAG		CAC	CT	GGAAT		CTA	AGG	AGTG		GTT	TG	TG	CAG	1500
	CTC	TATT		ACC	ACG	GAAGGA		GC	AGG	TGCG		AG	AGG	TGCC		CTG	AT	GGGCT		CTG	CCG	CGCTG	1560	
	GAC	ATG		TCT	TGA	ATGCCAT		GT	CAG	TTTAT		AC	CTT	AAAGCC		CAG	AAAA	AATA		CC	ATG	CACTC	1620	
	TGCT	CTCA		AA	CTC	AGGTGAT		GGA	AGT	TGGA		AAT	G	AAAGAGT		AAC	T	GATT	TA		TAA	AA	AGCAGG	1680
	ATG	TGTTGAT		TTT	AAAA	ATAA		AGT	G	CCCTTA		TAC	AAAA	AAAAA		A								

Seq ID NO: 207 Protein sequence
Protein Accession #: NP_057445.1

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	1		11		21		31		41		51	
	MRL	WTF	VGVL		TSL	AYC	LHQR		RVA	LAE	LQEA	60
	LPL	EEQ	VEWN		QFD	YTV	TNLA		GGP	KPY	SPYD	120
	GMQ	MFAL	GE		RLR	KNY	VEDI		PFL	SPT	FNPG	180
	PII	IHT	DEAD		SEV	LYP	NYQS		CNS	LRQ	RTRG	240
	DFI	ILL	DNVA		AEQ	AHN	LPSC		PML	KRP	PARMI	300
	LBS	NLL	KAMD		SAT	APD	KIRK		LYL	YAA	HDVT	360
	ESK	EW	FWQLY		YHG	KEQ	VPRG		CPD	GLC	PLDM	420
	E								FLN	AMS	VYTL	
									SPE	KYH	ALCS	
									QTV	M	EVGN	

Seq ID NO: 208 DNA sequence
Nucleic Acid Accession #: CAT cluster

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	1		11		21		31		41		51	
	TTT	GAGG	GGG		TGGT	GGGG	GGG		AGT	TTA	ATTC	60
	TAA	CAGC	CTG		CCCT	TGG	AGA		GAA	GT	CCTTC	120
	TGCT	GGGG	GGC		CAGT	GT	TAGG		CTT	CAG	GCCA	180
	TAGT	GGC	AGA		GCCT	TGG	AGTG		ATG	AGT	GGGA	240
	TCTG	GTG	CT		CTTG	CA	TTTG		CA	TTT	GCAC	300
	GGAG	CCCT	CC		GCAG	AT	CAGT		CGC	GT	CAGCT	360
	CGT	CTTT	ATT		GGCA	AA	TGGG		TC	ATT	TGGCTT	420
	GCAG	GT	TCT		CACT	GT	CTCT		TC	ACC	AGTGT	480
	TGAG	CT	GGCA		GCG	CAG						

Seq ID NO: 209 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..564

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	1		11		21		31		41		51		
	ATG	GAG	CCCT		GGG	CGT	GGCT		GC	AGG	GT	TTA	60
	TC	AGAT	CCGT		TCT	CTG	CGCT		GCC	AGC	TC	CAG	120
	CAG	AGT	CA		CAG	TG	GGCT		GAC	ACT	GGTG		180
	GAT	CCCT	TCT		ACT	AT	GACTG		GAA	AA	ACCTG		240
	CTG	GC	CA		TTG				AGT	GG	CAAAAT		300
	AAG	CAG	CA		GT	CT	GTACC		TG	AGA	AGG	CC	360
	AC	CTT	GG		CA	AA	AT		AT	CC	CACT	CA	420
	AG	T	CA		CA	CT	CTCG		AGT	GC	CTCT		480
	GAT	G	CTG		CC	CT	CACTC		AGG	CC	ATCCA		540
	GG	AA	CGA		GG	CT	ACCTA		AT	G			

Seq ID NO: 210 Protein sequence
Protein Accession #: FGENESH predicted

80

	1		11		21		31		41		51	
	MEP	WAN	LQGL		KSR	PT	CPAAS		SDP	F	SALPAQ	60
	DPF	YD	WKNL		QLS	GLI	CGGL		LAI	AGI	AAVL	120
									SGK	CK	KSSQ	
									QHS	PV	PEKA	
									IPL	IT	PGRFL	

TLAKSNKPLS PSTFVLVFGI SYTSVFRVPL SASLYPAIPG DAAALTSQHP SMQNISMQNT 180
GKKGCT

5 Seq ID NO: 211 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..318

1	11	21	31	41	51	
10	ATGCCCGGCC	ACCCCGTCTG	TGAAGTGAGG	AGCACCTCTG	CCCGGCTGCC	CCGCTCGGGA 60
	AGTGAGGAGC	GGCTCTGCCC	GGCTGCCACC	CCGTCTGTGA	GTGCTGCTG	CGCTGGGCCC 120
	AGGCCGCGCG	TGCCCTGCCA	GGCCCTCCGG	CCCCCACT	TCCACCCAG	GGCTGCTCC 180
	TCACCCAGG	GTTCATCTC	CCTAGTTTCC	ACCAGAGACT	GGGTCTTCAT	TCTCACCTG 240
15	CTACACAGCC	CCTACCAGAA	CGTTCTGAAA	TGCAACCTA	ACAACTGTCT	CACCCAGCA 300
	GGAAACTCCC	CAGGGTCCCG	GGCCCCCTGC	GGGTTCAG	GCCTCACTCT	TGCGCCCAT 360
	CCCTCCGCCC	TGACCGCCCT	GAGCTCGCCC	CCAGTGTGG	CCCTCAOGT	CCAGTTATCC 420
	CTCCAGCCT	CCAAGGTCCC	CGTTACCGAA	GACCGCCACC	ATCAGACAT	AGCGCAGCAC 480
	ATATGGGACA	CTGGTGAAGG	AGCAGTGAGG	AACCTGCAGA	GTCAACAGT	TGGCCTGACT 540
20	GCCTTGGAAG	CCAATGACCC	ATTGCCAAT	AAAGAAGATC	CCTTCTACTA	TGACTGGAAA 600
	AACCTGCAGC	TGAGCGGACT	GATCTGCGGA	GGGTCTCTGG	CCATTGCTGG	GATCGCGGCA 660
	GTCTTGAGTG	GCAAAATGCA	ATGCAAGAGC	AGCAGAAGC	AGCAGAGTCC	TGTACCTGAG 720
	AAGGCCATCC	CACATCATCAC	TCCAGGCAGA	TTTCTCACCT	TGGCCAAATC	AAATAAACCT 780
	TTATCTCAA	GCACCTTTGT	CTTGGTGTGT	GGCATCAGCT	ACACATCAGT	CTTCCGAGTG 840
25	CCTCTTTCTG	CGTCCCTGTA	CCCTGCCATT	CCTGGTGATG	CTGCTGCCCT	CACATCAGGC 900
	CATCCAGCA	TGCAGACAT	AAGCATGCAG	AACACTGGAA	CGAAGGGCTG	TACCTAA

Seq ID NO: 212 Protein sequence
Protein Accession #: FGENESH predicted

30	1	11	21	31	41	51	
	MPGHPVCEVR	STSAIRLRLG	SEERLCPAAT	PSVSACCAGP	RPPVPCQALR	PPTFHPRACS	60
	SPQSGISLVS	TRDWVFILTL	LHSPYQNVLK	CKFNNCLTPA	GNSPFSRAPC	GVAGLTLRAH	120
35	PSALTALSSP	PVALALHVLQ	LPASKVPVTE	DRHHHDIAQH	IWDTEGAVR	NLQSHTVGLT	180
	ALEANDPFAN	KDDPFYDWMK	NLQSLGLICG	GLLAIAAGIA	VLSGKCKCKS	SQKQHSVPVE	240
	KAIFLITPGR	FLTLAKSNKP	LSPSTFVLVF	GISYTSVFRV	PLSASLYPAI	PGDAAALTSQ	300
	HPSMQNISMQ	NTGKKGCT					

40 Seq ID NO: 213 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..1758

45	1	11	21	31	41	51	
	ATGATGGGGT	CTCATGTTGC	CCAGGCTGGT	CTTGAACCTC	TGGGCTCGAG	TGACCCCTCCT	60
	GCCTTGGCCT	CCGAAAGTGC	TGGGATTACA	GGACTGTTAT	TACAGGAATC	CATAACACTG	120
	GAGGATGTGG	CTGTGGACTT	CACCTGGGAG	GAGTGGCAAC	TCCCTGGGCG	TGCTCAGAA	180
	GACCTGTACC	GGGATGTGAT	GTGGAGAAC	TACAGCAACC	TGGTGGCAGT	GGGGTATCAA	240
50	GCCAGCAAAC	CGGATGCACT	CTTCAAGTTG	GAACAAGGAG	AACAACCTGT	GACAATTGAA	300
	GATGGAATCC	ACAGTGGAGC	CTGTTCAGGT	TCTCCAAAGG	TCCCGTTCTC	CATTTTCTCA	360
	TCTGTGCCCT	TCACTCTTCA	AAATGSCCTT	CATTCTAACA	TATGGAAAGT	TGATCATGTG	420
	CTGGAGCGCT	TGCAGAGTGA	AAGCCTGGTG	AACAGAAGGA	AACCATGTCA	TGAACATGAT	480
	GCATTTGAAA	ATATTGTTCA	TTGCAGCAAA	AGTCAGTTTC	TGTTAGGGCA	AAATCATGAT	540
55	ATATTTGACT	TACGTGGAAA	AAGTTTGAAA	TCCAATTAA	CTTTAGTTAA	CCAGAGCAAA	600
	GGCTATGAAA	TAAAGAACTC	TGTTGAGTTT	ACTGGAAATG	GGGACTCCTT	TCTTCATGCT	660
	AACCATGAAC	GACTTCATAC	TGCAATTAAA	TTCCCTGCAA	GTCAAAACTC	CATCAGCACT	720
	AAGTCCCAAT	CATCATGTC	CAAGCATCAG	AAAACACGAA	AATTAGAGAA	GCATCATGTG	780
	TGCAGTGAAT	GTGGGAAAGC	CTTCATCAAG	AAGTCTTGCC	TAACTGATCA	CCAGGTAATG	840
60	CATACAGGAG	AGAAACCCCA	CAGATGTAGT	CTATGTGAGA	AAGCCTTCTC	CAGAAAGTTC	900
	ATGCTTACTG	AACATCAGCG	AACTCATACA	GGAGAAAAAC	CTTATGAATG	CCCTGAATGT	960
	GGCAAGCCCT	TTCTCAAGAA	ATCAGCGCTC	AACATACATC	AGAAACACAC	TACCGGAGAG	1020
	AAACCCCTATA	TATGCAGTGA	ATGTGGAAAA	GGCTTCATCC	AGAAAGGAAA	TCTCATTTGA	1080
	CACCAGCGAA	TTTCATACAGG	TGAGAAACCT	TATATATGCA	ATGAATGTGG	AAAAGGCTTC	1140
65	ATTCAGAAGA	CGTGTCTCAT	AGCAGATCAG	AGATTTCACA	CAGGAAAGAC	GCCCTTTGTG	1200
	TGCAGTGAAT	GTGGAAAAATC	CTGTTCTCAG	AAATCAGGTC	TCATTAAACA	TCAAGAAATG	1260
	CACACAGGAG	AGAAACCCCT	TGAATGTAGT	GAATGTGGGA	AAGCCTTTAG	CACAAAGCAA	1320
	AAGCTCATTT	TCCATCAAAG	GACTCATACA	GGAGAGAGAC	CCTATGGCTG	TAACGAGTGT	1380
	GGGAAAGCGT	TTGCGTATAT	GTGTTGCTG	GTTAAGCATA	AGAGAAATCA	CACAAGGGAG	1440
70	AAACAAGAGG	CAGCCAGGCT	GGAAAACTCT	CCTGCAGAGA	GGCAGAGCTC	ATTACACACC	1500
	AGTGATGTCA	TGCAGGAGAA	AAACTCTGCT	AACGGGGCGA	CTACACAAGT	GCCTTCTGTG	1560
	GCCCTCAGA	CATCATTTAA	CATCAGCGGC	CTCCTGCGAA	ACAGGAACGT	AGTCCTTGTG	1620
	GGACAGCCAG	TGGTCAGATG	TGCAGCCTCA	GGAGATAACA	GAGGATTTGC	ACAGGACAGA	1680
75	AACCTGTGTA	ATGCAGTGAA	TGTGTTGTG	CCTTCCTGTA	TCAATTATGT	CTTATTTTAT	1740
	GTTACAGAAA	ACCCATAG					

Seq ID NO: 214 Protein sequence
Protein Accession #: FGENESH predicted

80	1	11	21	31	41	51	
	MMGSEVAQAG	LELLGSSDPF	ALASESAGIT	GLLLQESITL	EDVAVDPTWE	EWQLLGAAQK	60
	DLVYRDVMLEN	YSNLVAVGVQ	ASKPDALFKL	BQGEQLWTIE	DGIHSGACSG	SPKVPPSIFS	120
	SVPPTLQNCIL	HSNIWKVDHV	LERLQSESLV	NRKRPCHERD	AFENIVHCSK	SQPLLQONHD	180
	IFDLRGRSLK	SNLTLVNQSK	GYEIKNSVEF	TGNGDSFLHA	NHERLHTAIK	FPASQRLIST	240

5 KSPFISPKHQ KTRKLEKHHV CSECGKAFIK KSWLTDHQVM HTGEKPHRCS LCEKAPSRKF 300
 MLTEHQRTHT GEKPYBCPEC GKAFLEKSR LNIHQRTHTGE KPYICSECGK GPIQKGNLIV 360
 HQRHTEGKFP YICNECGKGF IQKTCLIAHQ RFHTGKTPFV CSECGKSCSQ KSLGIKHQRI 420
 HTGKPFECES ECGKAFSTKQ KLIVHQRTHT GERPYGCNEC GKAFAYMSCL VHKRIHTRE 480
 RQEAARKVENP PAERHSSSLHT SDVMQEKNSA NGATTQVPSV APQTSNLISG LLANRNVVLV 540
 GQPVVRCAS GDNRGFAQDR NLVNAVNVVV PSVINYVLFY VTENP

Seq ID NO: 215 DNA sequence
 Nucleic Acid Accession #: NM_032190.1
 Coding sequence: 502..1332

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 1 11 21 31 41 51
 | | | | |
 GATTCCGTGT TCTTGCCCAT GTTAGCCATA ATATCCTGTG CAGTAIGTTT TCTCTGTGCA 60
 GAGGCAAAAA CATATTGGGC ATATGTTCOC AAGCCOCCAG CAGTATGACC CATACTTTGG 120
 AGTGACACTC CTCTTAAGAT TTATCATGAT TAAGGAGCAT GGGCTCCAGC ACCCTTAACT 180
 CCACCTGACA TAGAACAGTT AGACTCTCAG AATAATGTCA TTAATTATAC CGCTCCATTG 240
 GAAGGACTTC CTTTGTGTGT CACCACAAAG ACATCACTCA GCCATAGCTG TCTTACAGTT 300
 CAAGCTCACA CATGGTTGAG TCACATAGGG AAAATCATGT ACTTATTAAG TCTTGGTTAT 360
 ATTAATGTAA CCGGTGTGCT AACCAACCAT TCCTGGCCCA ATGCGCTTCA TTGTGCTGAC 420
 TATACAGAAAT GGATTCCCTT CAATAGTTCC TACCCOCCCT CATAGACCCA GTGTCTTGGC 480
 CCACCTGGCTA GAAAACAATC TATGTTAACT GGAGACATTG TGGATTGGGG ACCTAAAGGC 540
 CAATTAGATG GAAAAGAAGA AAATCAGAAA TCGTGGCACA AACTTTGCTG GCATTGGTGG 600
 CAAGCTTTTA ATGCTTCTTC TTTATATAAC ACTGGGATCC AATCCAGTC GGCOCGCCAG 660
 ATTGCTTGGC ATGGAGCAGG CTTTAGCCCG CCTCTTCTC AGTGGCATT TCTAGGGAGG 720
 AAAGGACCAA TTCAAAGAT GATATGGAAG GCAGCATTC CAITTTATGA TGGCAACATC 780
 TGGGTTGCCA TAATACTATC CAATAATAGC AATAGTAAGC AACACAGTCT TAATGTTACA 840
 TTTGTAAAGA ATATCACCAC TCAATTACA GTTGTGTTT TTAATCCTTA TGTGTTTTTG 900
 GCAGCTAAGA AGGACAGCT CCAGGTAAC AATACCCAAT TGACCTGTAA ATCTTGCCAG 960
 TTATATCACT GATTAATCA TAGCACATTG CAACACATA ATATCTTAC TTTGATGATT 1020
 TTAGGTTGCA TCCTGGGCT ATGGAATCCT GTTAATCTGT CTGAGCCATG GGCTGCCACA 1080
 ATTGCTTAC ATTTGTGAA ACTTCTTCTA ACTCAGTTA CTCATTGTGT CCGTAGAGGC 1140
 TTAGGCTAGA TAATTTTTC TATTGTTTAC TTGCTCACAC TAATAATTTC TGTGTGATG 1200
 TCCTCTGTAG CTTTGCATAG TTCTATTCAA ACAGCTCAGT ATGTGGAGAA CTGGACACGC 1260
 ACAGTCAACC AAGGTGGCT ACTTGGAAT AAAAATTAACA CTGAGTTACA AACTGAAAGT 1320
 GCAGTGTAT ATCCACGAT TCTATGGTTA GGGGAACAAG TACAAAGCTT GCAATTGCAG 1380
 CAGTAATGT GTTGTCATT TAATCACACT CATATTGTG TAACCAACTT AGAATATAAC 1440
 CAAAGTAGAT ATCCATGGGA TCTTGTAAGA GCCCATTGCG AGGGAGCTTT CACATCCGAC 1500
 ATCACTCTTG ATATTGGTGA ATTACAAAAC AAAATTCTTG ATTTAAATAA ACAAATTCCA 1560
 GAGTTTCAGC CTCTTTAGA AGACTGGACT GAATCCAGC AAGGCCTGGA GAGCGTCAAC 1620
 CCTTGGACCT ATCTAAGCA CCACATTAC ATCTTATATA TAGTCTTGG AATAATGTTG 1680
 TTTTGTCTCT GTCTTCTGTT CATAGTCTGT AAAATCGGAT GGACTGCCAA TCGGAGAAATG 1740
 AAAGCTACCC AGCCTGGCCT TACATTCTTT CACTTAATAC ATAAACAAGA AGGGGGAAT 1800
 GTTGGGAGCC AAAAAGGCCA AAGGGATGGT GACCAACTCA GCATTCCACT GGAGGCTACA 1860
 TGATCAAAAC GAAACTGTT TATCATGAAT ACAGAATGTG GGCAAACTCG CTCTGTGACC 1920
 TGCCCAGAAG GTTGTCTGAG GGCCATGCT COCTGGCCCC GGCTCCTTGA GGTATATCTAC 1980
 TGGGACATCT AGAGCCTATT GTTCGAGGAA TGCAGTCTG CAAGCCTACT CTGGACCCAG 2040
 CAGCTCACT CTCTTCCAC ACCOCTTCT ACTATCTCT TTGCTTAATA AATATGGAGG 2100
 GCTGTGAAA GCTCAGGGCC CTTGTCCACT AGAGGCAAGG TGTCCCTGA CCCCTCTTCC 2160
 AAACAT

Seq ID NO: 216 Protein sequence
 Protein Accession #: NP_115566.1

55 1 11 21 31 41 51
 | | | | |
 MLTGDIVDWG PRGQLDGKEE NQKSWHLKCN HWQAFNASS LYNTGSIQSQ AAQIAWHGAG 60
 FSPPLQWYH LGRRKPIQRM IWKAAFFPMN GNIWVAILLS NNSNSKQSL NVTFTVKNIT 120
 QFTVCFNFPY VFLAAKRDQL QVNNYQLTCK SQQLVHCINL STLQENIST LMILGCIPGL 180
 WIPVNLSEPW AATIALHFVK LLLTQFTHCV RRLGLMIIPA IVLYLVTLLS VVMSSVALHS 240
 SIQTAYQVEN WRTTVNQGWL LENKINTELQ TEVAVL

Seq ID NO: 217 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1566

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 1 11 21 31 41 51
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 ATGGTGAACC CCAAAATCCAC TTCTCCCTC TTCAGGTTAT GTTTTTTGCT CTGAGGAGT 60
 CAGAACCTGT GGGTTGAAGA GCAAAATCAA TGCAAAAACA TATTGGGCAT ATGTTCCCAA 120
 TCCOCCAGCA GTATGGGCTA TACTTTGGAG CTCACCTCTC CTGAGATTTA TCAAGATCAG 180
 GGAGAGTGGG CTCCAGGACC CCTAACTCCC CGTGACATAG AAAAGTTAGA CTCTCAGAAC 240
 AATGTCATTA ATTAATACCAC TCCACTGGAA GGACTCCCTT TGTATTATCAC CACAAGAGC 300
 TCGCTCAGCC ATGACTGTCT TGCAATTCAA GCTCAAAACAT GGTGAGTCA CTATGGAAAA 360
 ATTATGTACT TATTAGTCTT TGGTCTTATT AATGTAACTG GTGTGCTAAC CAATCATTCC 420
 CAGTCCAGT ACCCTAATTG TGCTGATTAT ACAGAATGGA TTCCATTCAA TAGTCTCTAC 480
 CCCACTCTGT GGACCCAGTG TCTTGATCCA CTGGCTAGTA AACAATATAT GTCAACTGAA 540
 GACACTGTGG ATTGGGAACC TAAAGGTCAA TTAGATGGAA AAGGTGAAAG TCAGAAATCA 600
 TGGCACAAC TCTACTGGCA TTGGGGGCAA GCTTTTAATG CTTCTTCTT ATACAACAGC 660
 AGAATCCAAT CCCAGTCTGC TGCTCAGATT GCTTGGCATG GAGCAGGCTT TAGCCCACT 720
 CTCTCTCAGT TGCATTATCT GGGGAGGAAA GGACCAATTC AAGAACTAT ATGGAAGGCA 780
 GCACTCCCAT TTATGAATGG CAACATCTGG ATTGGAACAC TGTCTAATAA TAGCAATAGT 840
 AAGCAACACA GTCTTAATGT TGCAATTGTA AAGAATATCA CCACTCAGTT TACAGTTTGT 900
 GTTTTAAATC CTTATGCCCT TTTGGCAGCT AAGAAGAAC AGCTCAGGT GGAGAACTGG 960

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ACACGACAG CTGACCAAGC GAGGCTACTT CAGAATAAAA TTAACACTGA GTTACAAACT 1020
GAAGTGGCAA TGTGAAATC CATGGTCTTG TGGTAGGAG AACAGGTACA AAGCTTGACG 1080
TTGCAGCAGC AATTGCGTCA TCATTTTAAT CACATTCATA TTTGCGTAAC TAACTCAGAA 1140
TATAACCAA GTGAGTATCC GTGGGACCTT GTGAAAGCCC ATTTGCAAGG AGCTTTCACA 1200
TCCAACATCA CCTTTGATAT TGGTGAATTA CAAAACAAA TTATTGATTT AAATAGGCAA 1260
ACTCAAGAAT TTCAGCCTTC TTTAGAAGAC TGGACCGAAT TCCAGGAAGG CCTGGAGAGC 1320
CTCAACCCCTT GGACCTATCT AAGGCACCAC ATTAACATCT TATATGTAGT TCTTGGAATA 1380
ATGTTGTTTT GTCTCTGTCT TCGGTTTATA GTCTGTAAAA TCGGATGGAC CACCAATTGG 1440
AGAAATGAGAG CCTCCAGCC CAGCCTTACA TTCTTTCAAT TAATACATAA ACAGAAAGGG 1500
GGATATGCAG GGAGCCAAAG GCCTGTGGGA CGTGACCAAC TCAGCATCTCT GCTGGAGGCT 1560
ATATGA

Seq ID NO: 218 Protein sequence

Protein Accession #: FGENESH predicted

1 11 21 31 41 51
MVNPKSTSSL FRLCFLLLRS QNLWVEBQIQ CKNILGICSQ SPSSMAYTLE LTPPEIYHDQ 60
GEWAPGPLTP RDEKLDSDQN NVINYTTPLF GLPLFITTKT SLSSHCLAIQ AQTWLSHYGK 120
IMYLLGLGSI NVTVGLTNHS QSSHPCADY TEWIPFNSSY PTLWTQCLDP LASKQYMSTE 180
DTVDWEPKQK LDGKGESQKS WHKLHWHWRQ AFNASSLYNS RIQSQSAQI AWHGAGFSPP 240
LPQLHVLGRK GPIQETIWA ALPFMNGNIW IGTLSNNSNS KQHSNLNAPV KNITTOFTVC 300
VFNPYAFLLA KKNQLQVENW TRTADQARLL QNKINTELQT EVAMLKSMVL WLGEQVQSLQ 360
LQQQLRHFFH HIHICVTNSE YNQSEYPWDL VKAHLQGAFT SNITFDIGEL QNKIIDLNRR 420
TQEFQPSLED WTEFQEGLES LNPWTYLRHH INILYVVLGI MLFCLCLRFI VCKIGWTTNW 480
RMRASQPSLT FFLIHKQKG GYAGSQRPVG RDQLSILLEA I

Seq ID NO: 219 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..900

1 11 21 31 41 51
ATGCCCGCGC GGGAGCTGAG CGAGGCGGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
CCGCGCGCGC GTAGCGCGCC CCGAGAGCTG GGCATCAAGT GCGTGTGGT GGGCGACGGC 120
GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
CGGCCCACTG CGCTGGACAC CTCTCTGTGT ACGTACGTTT AATCGCCCGT CGCGCCGCGT 240
GGCTGCGGCG GGGCTGTGCA CCGGGGAGCT GGGCGGGGCG TCTCGCGCGG AGGGCGCAGA 300
GSACCCCGGG GAGGAGACTG GAGCAGGCCC CGAGGTGGCG CTGGTGGCGG CCAGGACGCT 360
CTTCCTAACT CAGGCTCTCC CCGCCCCGCC CCGCAGTGC AAGTCTGCTT GGATGGAGCT 420
CCGGTGGGCA TTGAGCTCTG GGACACAGCG GGACAGGAGG ATTTTGACCG ACTTCGTTCC 480
CTTTGCTACC CGGATACCGA TGTCTCTCTG GGTGTCTTCA GCGTGTGTGA GCCAGCTCC 540
TTTCAAAACA TCAAGAGAAA ATGGCTGCCC GAGATCCGCA CGCACAAACC CCAGGCGCCT 600
GTGCTGCTGG TGGGACCCCA GGCAGACCTG AGGAGCATG TCAACGTACT AATTACGCTG 660
GACCAGGAGG GCGCGGAGGG CCGCGTGCCC CAACCCAGG CTCAGGCTCT GCGCGAGAAG 720
ATCCGAGGCT GCTGCTACCT TGAGTGTCTA GCCTTGACGC AGAAGAACTT GAAGGAAGTA 780
TTTGACTCGG CTATTCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840
GCCAAAGGTG TGCGCACCCCT CTCCCGCTGC CGCTGGAAGA AGTTCTTCTG CTTCGTTTGA

Seq ID NO: 220 Protein sequence

Protein Accession #: FGENESH predicted

1 11 21 31 41 51
MPPRELSEAE PPPLRAPTPP FRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
RPTALDTPSG TYVQSPVRPR GCGGAVHRGA GAGVSAGGRR GPRGGWDRP RGGAGAAQDA 120
LFGSGSPRPA PAVQVLVDGA FVRIELWDTA GQEDFDRLRS LCYPDIDVFL ACFSVVQFSS 180
FQNIETKWL P EIRTHNPQAP VLLVGTQADL RDDVNLIQL DQGGREGPVP QPQAQGLAEK 240
IRACCYLECS ALTQKNLKEV FDSAILSAT E HKARLEKKIN AKGVRTLSRC RWKKPFCFV

Seq ID NO: 221 DNA sequence

Nucleic Acid Accession #: XM_063832.2

Coding sequence: 1..711

1 11 21 31 41 51
ATGCCCGCGC GGGAGCTGAG CGAGGCGGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
CCGCGCGCGC GTAGCGCGCC CCGAGAGCTG GGCATCAAGT GCGTGTGGT GGGCGACGGC 120
GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
CGGCCCACTG CGCTGGACAC CTCTCTGTGT CAAGTCTCTG TGGATGGAGC TCCGCTGCGC 240
ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTTTGACC GACTTCGTTT CCTTTGCTAC 300
CCGATACCG ATGTCTCTCT GCGGTGCTTC AGCGTGTGTC AGCCAGCTC CTTTCAAAC 360
ATCACAGAGA AATGGCTGCC CGAGATCCGC ACGCACACC CCGAGGCGCC TGTGCTGCTG 420
GTGGGCAACC AGGCCGACCT GAGGGACGAT GTCAAGCTAC TAATTGAGCT GGACGAGGG 480
GGCGGGAGG GCCCGTGCC CCAACCCAG GCTCAGGGT TGGCGGAGAA GATCCGAGCG 540
TGCTGCTACT TTGAGTGTCT AGCCTTGACG CAGAAGAACT TGAAGGAAGT ATTTGACTCG 600
GCTATTCTCA GTGCCATTGA GCACAAAGCC CGGCTGGAGA AGAACTGAA TGCCAAAGGT 660
GTGGGCAACC TCTCCGCTG CCGCTGGAAG AAGTTCTTCT GCTTCGTTTG A

Seq ID NO: 222 Protein sequence

Protein Accession #: XP_063832.1

1 11 21 31 41 51

MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
 RPTALDTFSV QVLVDGAPVR IELWDTAGQE DFDRLRLCY PDTDVFLACF SVVQPSFQON 120
 ITEKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGPVFPQP AQGLAEKIRA 180
 CCYLECSALT QKHLKEVFDS AILSAIEHKA RLEKLNNAKG VRTLSRCRWK KFFCFV

Seq ID NO: 223 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1161

1	11	21	31	41	51	
ATGAATCGGC	ACCATCTGCA	GGATCACTTT	CTGGAAATAG	ACAAGAAGAA	CTGCTGTGTG	60
TTCOGAGATG	ACTTCATTGC	CAAGGTGTGT	COGCOGGTGT	TGGGGCTGGA	GTTTATCTTT	120
GGGCTTCTGG	GCAATGGCCT	TGCCCTGTGG	ATTTTCTGTT	TCCACCTCAA	GTCTGGGAAA	180
TCCAGCCGGA	TTTTCTCTGT	CAACCTGGCA	GTAGCTGACT	TTCTACTGAT	CATCTGCCTG	240
CCGTTCTGTA	TGGACTACTA	TGTGCGGCGT	TCAGACTGGA	AGTTTGGGGA	CATCCCTTGC	300
CGGCTGGTGC	TCCTTCATGT	TGCCATGAAC	CGCCAGGGCA	GCATCATCTT	CCTCACGGTG	360
GTGGCGGTAG	ACAGGTATTT	CCGGGTGGTC	CATCCCCACC	ACGCCCTGAA	CAAGATCTCC	420
AATTGGACAG	CAGCCATCAT	CTCTTGCCCT	CTGTGGGGCA	TCAGTGTGTG	CCTAACAGTC	480
CACCTCCTGA	AGAAGAAGTT	GCTGATCCAG	AATGGCCCTG	CAAAATGTGT	CATCAGCTTC	540
AGCATCTGCC	ATACCTTCCG	GTGGCAGCAA	GCTATGTTCC	TCCTGGAGTT	CCTCTGCCCC	600
CTGGGCATCA	TCCTGTCTCT	CTCAGCCAGA	ATTATCTGGA	GCCTGCGGCA	GAGACAAATG	660
GACCGCATG	CCAGATCAA	GAGAGCCATC	ACCTTCATCA	TGGTGGTGGC	CATCGTCTTT	720
GTCACTGTCT	TCCTTCCAG	CGTGGTGTG	CGGATCCGCA	TCTTCTGGCT	CCTGCACACT	780
TCGGGCACGC	AGAATGTGTA	AGTGTACCGC	TCGGTGGACC	TGGCGTTCTT	TATCACTCTC	840
AGCTTCACTT	ACATGAACAG	CATGCTGGAC	CCCGTGGTGT	ACTACTTCTC	CAGCCCATCC	900
TTTCCCAACT	TCCTTCTCCAC	TTTGATCAAC	CGCTGCCTCC	AGAGGAAGAT	GACAGGTGAG	960
CCAGATAATA	ACCGCAGCAC	GAGCGTCGAG	CTCACAGGGG	ACCCCAACAA	AACCAGAGGC	1020
GCTCCAGAGG	CGTTAATGGC	CAACTCCGGT	GAGCCATGGA	GCCCCCTCTA	TCTGGGCCCA	1080
ACCTCAAATA	ACCATTCCAA	GAAGGGACAT	TGTCAACCAAG	AACCAGCATC	TCTGGAGAAA	1140
CAGTTGGGAT	GTTGCATCGA	G				

Seq ID NO: 224 Protein sequence
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MNRHQLQDHF	LEIDKKNCCV	PRDDPIAKVL	PPVLGLEFIF	GLLGNGLALW	IFCFHLKSWK	60
SSRIFLENLA	VADFLLIICL	PFVMDYYVRR	SDWKFGDIPC	RLVLFMPFAMN	RQGSIIPLTV	120
VAVDRYFRVY	HPHHAANKIS	NWTAIIISCL	LWGITVGLTV	HLKKKLLIQ	NGPANVCISF	180
SICHTFRWHE	AMFLEFFLEP	LGIIILFCSAR	IWSLRQRQM	DRHAKIKRAI	TFIMVVAIVF	240
VICFLPSVVY	RIRIFWLLHT	SGTQNCSEVYR	SVDLAPFITL	SPTYMNSMLD	PVVYFSSPS	300
FPNPFSTLIN	RCLQRKMTGE	PDNNRSTSV	LTGDPNKTRG	APEALMANS	EPWSPSYLGP	360
TSNNHSGKGH	CHQEPASLEK	QLGCCIE				

Seq ID NO: 225 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1092

1	11	21	31	41	51	
ATGAATCGGC	ACCATCTGCA	GGATCACTTT	CTGGAAATAG	ACAAGAAGAA	CTGCTGTGTG	60
TTCOGAGATG	ACTTCATTGT	CAAGGTGTGT	COGCOGGTGT	TGGGGCTGGA	GTTTATCTTC	120
GGGCTTCTGG	GCAATGGCCT	TGCCCTGTGG	ATTTTCTGTT	TCCACCTCAA	GTCTGGGAAA	180
TCCAGCCGGA	TTTTCTCTGT	CAACCTGGCA	GTGGCTGACT	TTCTACTGAT	CATCTGCCTG	240
CCCTTCTCTA	TGGACAACCTA	TGTGAGGCGT	TGGGACTGGA	AGTTTGGGGA	CATCCCTTGC	300
CGGCTGATGC	TCCTTCATGT	GGCTATGAAC	CGCCAGGGCA	GCATCATCTT	CCTCACGGTG	360
GTGGCGGTAG	ACAGGTATTT	CCGGGTGGTC	CATCCCCACC	ACGCCCTGAA	CAAGATCTCC	420
AATCGGACAG	CAGCCATCAT	CTCTTGCCCT	CTGTGGGGCA	TCATATTGGA	CCTGACAGTC	480
CACCTCCTGA	AGAAGAAGAT	GCCGATCCAG	AATGGCGGTG	CAAAATTTGTG	CAGCAGCTTC	540
AGCATCTGCC	ATACCTTCCA	GTGGCAGCAA	GCCATGTTCC	TCCTGGAGTT	CTTCTGCCCC	600
CTGGGCATCA	TCCTGTCTCT	CTCAGCCAGA	ATTATCTGGA	GCCTGCGGCA	GAGACAAATG	660
GACCGCATG	CCAAGATCAA	GAGAGCCATC	ACCTTCATCA	TGGTGGTGGC	CATCGTCTTT	720
GTCACTGTCT	TCCTTCCAG	CGTGGTGTG	CGGATCCGCA	TCTTCTGGCT	CCTGCACACT	780
TCGGGCACGC	AGAATGTGTA	AGTGTACCGC	TCGGTGGACC	TGGCGTTCTT	TATCACTCTC	840
AGCTTCACTT	ACATGAACAG	CATGCTGGAC	CCCGTGGTGT	ACTACTTCTC	CAGCCCATCC	900
TTTCCCAACT	TCCTTCTCCAC	TTTGATCAAC	CGCTGCCTCC	AGAGGAAGAT	GACAGGTGAG	960
CCAGATAATA	ACCGCAGCAC	GAGCGTCGAG	CTCACAGGGG	ACCCCAACAA	AACCAGAGGC	1020
GCTCCAGAGG	CGTTAATGGC	CAACTCCGGT	GAGCCATGGA	GCCCCCTCTA	TCTGGGCCCA	1080

Seq ID NO: 226 Protein sequence
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MNRHQLQDHF	LEIDKKNCCV	PRDDFIVKVL	PPVLGLEFIF	GLLGNGLALW	IFCFHLKSWK	60
SSRIFLENLA	VADFLLIICL	PFLMDNYVRR	WDWKPGDIPC	RLMLFPLAMN	RQGSIIPLTV	120
VAVDRYFRVY	HPHHAANKIS	NRTAAIIISCL	LWGITIGLTV	HLKKKMPPIQ	NGGANLCSSP	180
SICHTPQWHE	AMFLEFFLEP	LGIIILFCSAR	IWSLRQRQM	DRHAKIKRAI	TFIMVVAIVP	240
VICFLPSVVY	RIRIFWLLHT	SGTQNCSEVYR	SVDLAPFITL	SPTYMNSMLD	PVVYFSSPS	300
FPNPFSTLIN	RCLQRKMTGE	PDNNRSTSV	LTGDPNKTRG	APEALMANS	EPWSPSYLGP	360
TSP						

Seq ID NO: 227 DNA sequence
Nucleic Acid Accession #: NM_006018
Coding sequence: 61..1224

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      CGCCACTTTG CTGGAGCATT CACTAGGCGA GGCGCTCCAT CGGACTCACT AGCCGCACTC 60
      ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAATAG ACAAGAAGAA CTGCTGTGTG 120
      TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCGGTGTG TGGGCTGGA GTTTATCTTT 180
10     GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCTGGAAA 240
      TCCAGCGGGA TTTTCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG 300
      CGGTTCTGTA TGGACTACTA TGTGCGGCGT TCAGACTGGA ACTTTGGGGA CATCCCTTGC 360
      CGGCTGGTGC TCTTCATGTT TGOCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG 420
      GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 480
15     AATTGGAGAG CAGGCATCAT CTCTTGCCCT CTGTGGGGCA TCACTGTGG CCTAACAGTC 540
      CACCTCCTGA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 600
      AGCATCTGCC ATACCTCCG GTGGCAOGAA GCTATGTTCC TCCTGGAGTT CCTCTGCCCC 660
      CTGGGCATCA TCTCTTCTG CTCAGCCAGA ATTATCTGGA GCCTGGCGCA GAGACAAATG 720
      GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATGCTCTTT 780
20     GTCATCTGCT TCCCTCCGAG CGTGGTTGTG CGGATCOGCA TCTTCTGGCT CCTGCACACT 840
      TCGGGCAGCG AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTTCTT TATCACTCTC 900
      AGCTTCACCT ACATGAACAG CATGCTGGAC CCGTGGTGT ACTACTTCTC CAGCCCATCC 960
      TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 1020
25     CCAGATAATA ACOGCAGCAC GAGCGTCCAG CTCACAGGGG ACCCCAACAA AACCCAGAGG 1080
      GCTCCAGAGG CGTTAATGGC CAACTCOGCT GAGCCATGGA GCCCCTCTTA TCTGGGCCCA 1140
      ACCTCAAATA ACCATTCCAA GAAGGGACAT TGTCAACAAG AACCCAGCAT TCTGGAGAAA 1200
      CAGTTGGGCT GTTGACTCGA GTAAATGTAC TGGACTCGGC CTAAGGTTTC CTGGAACCTC 1260
      CAGATTGAGA GAATCTGATT TAGGGAAACT GTGGCAGATG AGTGGGAGAC TGGTTGCAAG 1320
      GTGTGACCAC AGGAATCTCT GAGGAACAGA GAGTAAAGCT TCTAGGCATC TGAAACTTGC 1380
30     TTCACTCTCG ACGCTCGCAG GACTGAAGAT GGGCAAAATG TAGGOGTTTC TGCTGAGCAG 1440
      AGTTGGAGCC AGAGATCTAC TTGTGACTTG TTGGCTTCT TCCACATCT GCCTCAGACT 1500
      GGGGGGGGCT CAGCTCCTCG GGTGATATCT AGCCTGCTTG TGAGCTCTAG CAGGGATAAG 1560
      GAGAGCTGAG ATTGGAGGGA ATTGTGTTGC TCTGGAGGA AGCCAGGCA TCATTAAACA 1620
      AGCCAGTAGG TCACCTGGCT TCCGTGGACC AATTCATCTT TCAGACAAGC TTTAGAGAAA 1680
35     TGGACTCAGG GAAGAGACTC ACATGCTTTG GTTAGTATCT GTGTTTCCGG TGGGTGTAAT 1740
      AGGGGATTAG CCCCAGAAGG GACTGAGCTA AACAGTGTTA TTATGGGAAA GGAATGGCA 1800
      TTGCTGCTTT CAACCAGCGA CTAATGCAAT CCATTCCTCT CTGTGTTATA GTAATCTAAG 1860
      GGTGAGCAG TTAAGAACGG TTCAGGATAG AAAGCTGTTT CCCACCTGTT TCGTTTAAAC 1920
40     ATTAAGAGGG AAACGTGCCT CTGCCCAACG GGTAGAGGGG GTGCAAGTTC CTCTGCTTC 1980
      CTTCGCTTGT GTTCTGTGAC TTACCAAAAA TCTACCACCT CAATAAATTT TGATAGGAGA 2040
      CAAAAAATA A

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Seq ID NO: 228 Protein sequence
Protein Accession #: NP_006009.1

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45     1      11      21      31      41      51
      |      |      |      |      |      |
      MNRHHLQDHP LEIDKKNCCV FRDDPIAKVL PFVLGLEFIF GLLNGNLALW IFCFHLKSWK 60
      SSRIFLFLNA VADFLLIICL PFVMDYVVR SDWNFGDIPC RLVLFMFAMN RQGSIIFLT 120
50     VAVDRYPRVV HPHHLLNKIS NWTAAIISCL LWGITVGLTV HLLKKLLIQ NGPANVCISF 180
      SICHTRFMHE AMFLLEFLLP LGIILFCSAR IIWSLRQRQM DRHAKIKRAI TFIMVVAIVF 240
      VICFLPSVVV RIRIFMLLHT SGTQNCVYR SVDLAPFITL SFTYMNMLD PVVYFSSPS 300
      FPNFSTLLN RCLQRMTGSE PDNMRSTSV LITGDPNKTG APEALMANS EPWSFSLG 360
55     TSNHNSKKGH CHQEPASLEK QLGCCIE

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Seq ID NO: 229 DNA sequence
Nucleic Acid Accession #: NM_014398.1
Coding sequence: 64..1314

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60     1      11      21      31      41      51
      |      |      |      |      |      |
      GGCACCGATT CGGGGCTGCG CGGACTTCTG CGGCACGCTG CAGAACCTCG CCCAGOGCCC 60
      ACCATGCCCC GGCAGCTCAG CGGGGCGGCC GCGCTCTTGG CGTCCCTGGC CGTAATTTTG 120
      CACGATGGCA GTCAATAGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT 180
65     ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACAGC TAAGCAAGCA 240
      CCTCACAAA CTTTAGCAGC AAGATTATCG GATGTCATA TCACTTTCA AACAGCGGCC 300
      ACAGTAAAAA TTCCAACAC TACCCAGCA ACTACAAAA AACTGCAAC CACCAGCCCA 360
      ATTACTACA CCTGTGTCAC AACCCAGGCC ACACCCAACT ACTCACAC AGCTCCTCCA 420
70     GTTACTGAAG TTACAGTCGG CCTAGCTTA GCCCCTTATT CACTGCCACC CACCATCACC 480
      CCACAGCTC ATACAGCTGG AACCACTTCA TCAACCGTCA GCCACAAC TGGGAACACC 540
      ACTCAACCCA GTAAACAGAC CACCTTCCA GCAACTTTAT CGATAGCACT GCACAAAAGC 600
      ACACCGGCTG AGAAGCTGTA TCAACCCACC CATGCCCGAG GAACAAGGCG AGCTGCCAC 660
      AATACACACC GCACAGCTGC ACCTGCCCTCC ACGGTTCCTG GGCCACCCCT TGCACTCAG 720
      CCATGTCAG TCAAGACTGG AATTATCAG GTTCTAAAG GAAGCAGACT CTGTATAAAA 780
75     GCAGAGATGG GGATACAGCT GATTGTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA 840
      TACTTCAACA TCGACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CGGAAAATCC 900
      AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTTACCAA GGATGAAGAA 960
      TCATATTATA TCAGTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
80     CAAGGAATCA AACATGCGGT GGTGATGTTT CAGACAGCAG TCGGGCATTC CTTCAAGTGC 1080
      GTGAGTGAAC AGAGCCTCCA GTTGTCAAGC CACCTGCAGG TGAACAACAC CGATGTCCAA 1140
      CTTCAAGCCT TTAGTTTGA AGATGACCAC TTTGGAATG TGGATGAGTG CTGCTCTGAC 1200
      TACACAAATG TGCTTCTCTG GATTGGGGCC ATCGTGGTGT GTCTCTGCCT TATGGGTATG 1260
      GGTGTCTATA AAATCCGCTT AAGGTGTCAA TCATCTGGAT ACCAGAGAAT CTAATTGTTG 1320
      CCGGGGGGGA ATGAATAATA TGGAAATTAG AGAACTCTT CATCCCTTCC AGGATGGATG 1380

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5 TTGGGAAATT CCCTCAGAGT GTGGGTCCTT CAAACAATGT AAACCACCAT CTTCTATTCA 1440
 AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACTTTTT 1500
 GTTTATTTTA TGAAAGATAT AGTGAGCTGT TTATTTTCTA GTTTCCTTTA GAATATTTTA 1560
 GCCACTCAAA GTCAACATTT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620
 AGCCTTCAAA TTATAAACCA AGGGTCAATT GTAACATAA CTACTGTGTG TGCAATTGAAG 1680
 ATTTTATTTT ACCCTTGATC TTAACAAAGC CTTTGCTTTG TTATCAAAATG GACTTTTCAGT 1740
 GCTTTTACTA TCTGTGTTTT ATGGTTTCAT GTAACATACA TATTCTGTGT GTAGCACTTA 1800
 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGTAGAC GGAGTTTCAC TCTTGTCCAC 1860
 CAGGCTGGAG TACAGTGGCA CGATCTCGGC TTATGGCAAC CTCGCGCTCC CGGGTTCAG 1920
 TGATTCTCCT GCTTCAGCTT CCGAGTAGC TGGGATTACA GGCACACACT ACCACGCTCG 1980
 GCTAATTTTT GTATTTTAT TATAGACGGG TTTCACCATG TTGGCCAGAC TGGTCTTGAA 2040
 CTCTTGACCT CAGGTGATCC ACCCACTCA GCTCCCAA GTGTGGGAT TACAGGCATG 2100
 AGCCATTGCG CCGGCGCTTA AATGTTTTTT TTAATCATCA AAAAGAACA CATATCTCAG 2160
 GTTGTCTAAG TGTTTTTATG TAAACCAAC AAAAGAACA AATCAGCTTA TATTTTTTAT 2220
 15 CTGTATGACT CCTGCTCCAG AATTGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280
 CTAAACATA AGCAAGAGAC AATAATAATG GCGCTTAATT ATTAACAAAG TGCCAGAGTC 2340
 TAGGCTAAGC ACTTTATCTA TATCTCATTT CATCTCACA ACTTATAAGT GAATGAGTAA 2400
 ACTGAGACTT AAGGGAACAG AATCAGCTAA ATGTCACCTG GCTAAGTATG GGCAGAGCCA 2460
 GAGCTTGAA TCAATGTTGT CTGACATCAA GGTCTTTTGT CTCTCCCTA CACCAAGTTA 2520
 20 CTTACAAGAA CAATGACACC ACACTCTGCC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580
 TCACTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640
 AGCTTTGCG ATAACAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700
 TGAGGGGCTT TGTAAACAT TAGTCAGTTG CTCATTTTTA TGGGATTTGT TAGCTGGGCT 2760
 GTAAAGATGA AGGCATCAAA TAAACTCAAA GTATTTTTTA ATTTTTTGA TAATAGAGAA 2820
 25 ACTTGCTTAA CCAACTGTTT TTTCTTGAGT GTATAGCCCC ATCTGTGTGT AACTTGCTGC 2880
 TTCTGCACCT CATATCCATA TTTCTTATG TTCACTTTAT TCTGTAGAGC AGCCTGCCAA 2940
 GAATTTTATT TCTGCTGTTT TTTTGTCTGC TAAAGAAAGG AACTAAGTCA GGATGTTAAT 3000
 AGAAAAGTCC ACATAACCCCT AGAATTTCTA GTCAAGGAAT AATTCAGTC AGCCTAGAGA 3060
 30 CCATGTTGAC TTTCCTCATG TGTTCCTTA TGACTCAGTA AGTTGGCAAG GTCCTGACTT 3120
 TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAAACT TACTTTGG

Seq ID NO: 230 Protein sequence

Protein Accession #: NP_055213.1

35 1 11 21 31 41 51
 MPRQLSAAAA LFASLAVILH DGSQMRKAF PETRDYSQPT AAATVQDIKK PVQPPARQAP 60
 HQTLAARFMD GHITTFQTAAT VKIPTTTPAT TKNTATTSP I TYTLVTTQAT PNNSHAPPV 120
 40 TEVTVGPSLA PYSLPPTITP PAHTAGTSSS TVSHTTGNT QPSNQTLLPA TLSIALHKST 180
 TGQKPDQPTH APGTTAAAHN TTRTAAPAST VPGPTLAPQP SSVKGTIYQV LNSRLCIXA 240
 EMGIQLIVQD KESVFSPPRY FNIDPNATQA SGNGCTRKN LLLNFQGGFV NLTFTKDEES 300
 YYISBVGAYL TVSDPETVYQ GIKHAVVMFQ TAVGHSFKCV SEQSLQLSAH LQVKTIDVQL 360
 QAFDFEDDFH GNWDECSSDY TIVLPVIGAI VVGLCLMGMG VYKIRLRCQS SGYQRI

Seq ID NO: 231 DNA sequence

Nucleic Acid Accession #: NM_005409.3

Coding sequence: 94..378

50 1 11 21 31 41 51
 TTCTTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
 TTGGCTGTGA TATGTGTGTC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 55 TGCTTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCTT GAAAGAAAAA 300
 AAAGGACAAC GATGCCATAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTT 360
 GAAAGAAAGA ATTTTAAAA ATATCAAAC ATATGAAGTC CTGGAAGAGG GCATCTGAAA 420
 AACCTAGAAG AAGTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAACTG 480
 60 AGACTTTTCT ATGGTTTGT GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAGG ACCAAAAACA GAAATACAGT CTCTCTGAAT GAATGACAAAT CAGAAATCCA 600
 CTGCCCAAAG GAGTCCAGCA ATTAAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 GGTACCATC GAGATTACA AAGTGCTTTC ACGTTCTTAC TTGTGTATT ATACATTCTAT 720
 GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 65 GAGAACATTT CTGTCTTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTC TGTAAAGCA TTCTCAAAC ATTTTTCAT GCAAAATACAC ACTTCTTCC 960
 CCAAAATACA TGTAGCATAT CAATATGTAG GAAACATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAAATCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
 TGGGATACTG GCAACAGTGC ACATATTTCA TAACCAAATT AGCAGCACCG GTCTTAATTT 1140
 70 GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 TGTACTTTTT GTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGAC ACATTGAAA 1260
 TACAAAATGT TTTTGTCTAC CAAGAAAAA TGTGAAAAA TAAGCAAAATG TATACCTAGC 1320
 AATCATTGTT ACTTTTGTGA ATCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
 75 TGTTCATGC CTATATCTG TAAAAATTAG GTATACTCAA GACTAGTTTA AAGAATCAAA 1440
 GTCATTTTTT TCTTAATAA ACTACACAA CCTTCTTTT TAAAAAAA AAA

Seq ID NO: 232 Protein sequence

Protein Accession #: NP_005400.1

80 1 11 21 31 41 51
 MSVKGMAIAL AVILCATVVQ GPFMPKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF

Seq ID NO: 233 DNA sequence
Nucleic Acid Accession #: NM_000577.1
Coding sequence: 41..520

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COGACCTCTT GGGAGAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAAACA 120
GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCOGGA TACTTGCAAG GACCAATGT 180
10    CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
CCATGGAGGG AAGATGTGCC TGTCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
GGAGGAGGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTGGCCTT 360
CATCGCTCA GACAGTGGCC CCACCACCAG TTTTGAAGT GCGCCTGCC CCGGTTGGTT 420
CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG 480
15    CGTCATGGTC ACCAAATTCT ACTTCCAGGA GGACGAGTAG TACTGCCAG GCCTGCCTGT 540
TCCCATTCTT GCATGGCAGG GACTGCAGGG ACTGCCAGTC CCCCTGCCCC AGGGCTCCCG 600
GCTATGGGGG TACTGAGGAC GAGCCATTGA GGGGTGGACC CTCAGAAGC GTCACAACAA 660
CCTGTGCACA GACCTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCCAGAATG 720
GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCTCGCA CAAAGCCCTT CCATGTGGCC 780
20    TCTGCATTCA GGATCAAAAC CGAACCACTT GCCCAACTCT CTCTCTCTT GCCACTGCCT 840
CTTCTCTCCT CATTCACATC TCCCATGCC TGGATCCATC AGGCCACTTG ATGACCCCCA 900
ACCAAGTGGG TCCCAACCCC TGTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
TTTAAGGGTT TGTGAAAAT GAAAATTAGG ATTTTCATGAT TTTTCTTTT CAGTCCCGT 1020
25    GAAGGAGAGC CCTTCATTG GAGATTATGT TCTTTCGGGG AGAGGCTGAG GACTTAAAT 1080
ATTCCTGCAT TTGTGAATG ATGTTGAAAG TAAGTGGTAG CTTTCCCTT CTTTCTTCT 1140
TTTTTTTGTG ATGTCCCAAC TTGTAAAAAT TAAAGTTAT GGTACTATGT TAGCCCATTA 1200
ATTTTCTTTT TCCTTTTAAA ACACCTCCAT AATCTGGACT CCTCTGTCCA GGCAGTCTG 1260
CCCAGCCTCC AAGTCCATC TCCACTCCAG ATTTTCTACA GCTGCTGCA GTACTTTACC 1320
TCCATACAGA AGTTTCTCAG CTCCTAAGGC TCTGAGCAA TGTGGCTCT GGGGGTCTT 1380
30    TCTTCTCTG CTGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTTCTG GCACCTGGAG 1440
ACTGTATGA AAGATGGCTG TGCTCTGCC TGTCTCCCC ACCAGGCTGG GAGCTCTGCA 1500
GAGCAGGAAA CATGACTCTG ATATGCTCA GGTCCCTGCA GGGCCAAAGC CTAAGCTCG 1560
CTCTTGGCAG GTACTCAGCG AATGAATGCT GTATATGTT GGTGCAAGT TCCCTACTTC 1620
35    CTGTGACTTC AGCTCTGTT TACAATAAAA TCTTGAAGT GCCTAAAAA AAAAAAATA 1680
AAAAAATAAA AAAAAAATA AAAAAAATA AAAAAA

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Seq ID NO: 234 Protein sequence
Protein Accession #: NP_000568.1

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MALETICRPS GRKSSRMQAP RIWDVNQKTF YLRNNQLVAG YLQGPVNMLE EKIDVPIEP 60
HALFLGIHGG KMCLSCVKSQ DETRLQLEAV NITDLSENRR QDKRFAPIRS DSGPTTSFES 120
45    AACPGWFLCT AMEADQFVSL TNMFDEGVMV TKPYFQED

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Seq ID NO: 235 DNA sequence
Nucleic Acid Accession #: NM_001840.1
Coding sequence: 149..1567

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TCCGAGGAGC CAGGGAGATG GAAGGGATTG CCCCCTGTGG GTCACCTTCT CAGTCAITTT 120
GAGCTCAGCC TAATCAAGA CTGAGGTAT GAAGTCGATC CTAGATGGCC TTGCAGATAC 180
55    CACCTTCGCG ACCATCACCA CTGACCTCCT GTACGTGGGC TCAATGACA TTCAGTACGA 240
AGACATCAAA GGTGACATGG CATCCAAATT AGGGTACTTC CCACAGAAAT TCCCTTTAAC 300
TTCTCTTAGG GGAAGTCCCT TCCAGAGAA GATGACTGCG GGAGACAACC CCCAGCTAGT 360
CCGAGCAGAC CAGGTGAACA TTACAGAATT TTACAACAAG TCTCTCTGCT CCTTCAAGGA 420
GAATGAGGAG AACATCCAGT GTGGGGAGAA CTTTCATGAC ATAGAGTGT TCATGGTCT 480
60    GAACCCAGC CAGCAGCTGG CCATTGCAGT CCTGTCCCTC ACGCTGGGCA CTTTCAAGGT 540
CCTGGAGAAC CTCCTGGTGC TGTGCGTCAT CCTCCACTCC CGCAGCCTCC GCTGCAGGCC 600
TTCTTACCAC TTATCGGCA GCCTGGCGGT GGCAGACCTC CTGGGGAGTG TCAITTTTGT 660
CTACAGCTTC ATTGACTTCC ACGTGTTCOA CGCAAGAT AGCCGCAACG TGTTTCTGTT 720
65    CAACTGGGT GGGGTCAAGG CCTCTTCAC TGCTCCGTG GGCAGCCTGT TCCTCACAGC 780
CATCGACAGG TACATATCCA TTCACAGGCC CCTGGCCTAT AAGAGGATTG TCACCAGGCC 840
CAAGGCCGTG GTGGCGTTTT GCCTGATGTG GACCATAGCC ATTGTGATG CCGTGTCTGC 900
TCTCTGGGG TGGAACTGCG AGAAACTGCA ATCTGTTTGC TCAGACATTT TCCACACAT 960
TGATGAACCC TACCTGATGT TCTGGATCGG GGTCAACAGC GTACTGCTTC TGTTCATGCT 1020
70    GTATGOSTAC ATGTATATTC TCTGGAAGGC TCACAGCCAC GCCGTCCGCA TGATTACAGC 1080
TGGCACCCAG AAGAGCATCA TCATCCACAC GTCTGAGGAT GGGAAAGGTAC AGGTGACCCG 1140
GCCAGACCAA GCCCGCATGG ACATTAGGTT AGCCAGAGCC CTGTCCTCTA TCCTGGTGGT 1200
GTGTATCATC TGCTGGGGCC CTCGCTTGC AATCATGGTG TATGATGTCT TTGGGAAGAT 1260
GAACAAGCTC ATTAAGACGG TGTTTGCATT CTGCAATATG CTCGCTCGC TGAACCTCAC 1320
75    CGTGAACCCC ATCATCTATG CTCTGAGGAG TAAGGACCTG CGACAGCTT TCCGGAGCAT 1380
GTTTCCCTCT TGTGAAGGCA CTGCGCAGCC TCTGATTAAC AGCATGGGGG ACTCGGACTG 1440
CCTGCACAAA CACGCAACCA ATGCAGCCAG TGTTCACAGG GCGCAGAAA GCTGCATCAA 1500
GAGCAGGGTC AAGATTGCCA AGGTAACCAT GTCTGTGTCC ACAGACAGCT CTGCCGAGGC 1560
TCTGTGAGCC TGATGCCTCC CTGGCAGCAC AGGAAAAGAA TTTTCTTTT TAAGCTCAA 1620
80    ATCTAGAAGA GCTCTATGTT TCCTTGGTTA TATTTTCTTA ACTTTACCAT GTCAATGAA 1680
AAGGTGATTG CCACATGTCA CTTAATTGCT TAGTTTCTGT TTGGGCTAAT CTTCGGGGT 1740
TCGTAGGAAA CCTTT

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Seq ID NO: 236 Protein sequence
Protein Accession #: NP_001831.1

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5	MKSILDLGLAD	TFTRITITDL	LYVGSNDIQY	EDIKGDMSK	LGYPPOKFPL	TSFRGSPFOE	60
	KMTAGDNPOL	VPADQVNITE	PYNKSLSSFY	ENEENIQCGE	NFMDIECFMV	LNPSQQLAIA	120
	VLSLTLTGTFT	VLENLLVLVC	ILHSRSLRCR	PSYHFIGSLA	VADLLGSVIF	VYSFIDFHPV	180
	HRKDSRNVEL	FKLGGVTASF	TASVGSFLFT	AIDRYISIH	PLAYKRIVTR	PRAVVAFLM	240
	WTIAIVIAVL	PLLGWNCEKL	QSVCSDFPH	IDETVLMFWI	GUTSVLLLP	VYAYMYILWK	300
10	AHSHAVRMIQ	RGTKSIIIIH	TSEDGKVQVT	RPDQARMDIR	LAKTLVLILV	VLIIICWGPLL	360
	AIMVYDVFGK	MNKLKIVFA	PCSMCLLNS	TWNPIIYALR	SKDLRHAFRS	MFPSCGTAQ	420
	PLDNSMGDS	CLHKHANNAA	SVHRAESCI	KSTVKIAKVT	MSVSTDTSAE	AL	

Seq ID NO: 237 DNA sequence

Nucleic Acid Accession #: NM_016083.2

Coding sequence: 64..1482

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	GTTATGAGAT	CGATCCCTAGA	TGGCCTTGCA	GATACCACT	TCCGCACCAT	CACCACTGAC	120
	CTCCTGTACG	TGGGCTCAAA	TGACATTGAG	TACGAAGACA	TCAAAGGTGA	CATGGCATCC	180
	AAATTAGGGT	ACTTCCACACA	GAAATTCCCT	TTAACTTCCT	TTAGGGGAAG	TCCCTTCCAA	240
	GAGAAGATGA	CTGGGGGAGA	CAACCCCCAG	CTAGTCCAG	CAGACCAGGT	GAACATTACA	300
25	GAATTTTACA	ACAAGTCTCT	CTGCTCCTTC	AAGGAGAATG	AGGAGAACAT	CCAGTGTGGG	360
	GAGAAGTTCA	TGGACATAGA	GTGTTTCATG	GTCTGTAACC	CCAGCCAGCA	GCTGGCCATT	420
	GCAGTCTCTG	CCCTCAGCCT	GGGCACCTTC	ACGGTCCCTG	AGAACCTCCT	GGTGTCTGTC	480
	GTCACTCTCC	ACTCCGCGAG	CCTCCGCTGC	AGGCCTTCCT	ACCACTTCAT	CGGCAGCCTG	540
	GCGGTGGCAG	ACCTCTCTGG	GAGTGTCTAT	TTTGCTTACA	GCTTCATTGA	CTTCCACGTG	600
30	TTCCACCGCA	AAGATAGCCG	CAACGTGTTT	CTGTTCAAA	TGGGTGGGGT	CACGGCCTCC	660
	CTCACTGCTC	CCGTGGGCGA	CCTGTTCTCT	ACAGCCATCG	ACAGGTACGT	ATCCATTAC	720
	AGGCCCTCTG	CCATTAAGAG	GATTGTCAAC	AGGCCCAAGG	CCGTGGTGGC	GTTTTGCCTG	780
	ATGTGGACCA	TAGCCATTGC	GATGCGCTG	CTGCTCTCC	TGGGCTGGAA	CTGCGAGAAA	840
	CTGCAATCTG	TTTGCTCAGA	CATTTTCCCA	CACATTGATG	AAACCTACCT	GATGTTCTGG	900
35	ATCGGGGTCA	CCAGGGTACT	GCTTCTGTTT	ATCGTGTATG	CGTACATGTA	TATTCTCTGG	960
	AAGGCTTCA	GCCAGCGCGT	CGCATGATT	CAGCGTGGCA	CCAGAAAGAG	CATCATCATC	1020
	CACACGCTCT	AGGATGGGAA	GGTACAGGTG	ACCGGCCAG	ACCAAGCCCG	CATGGACATT	1080
	AGGTTAGCCA	AGACCCCTGT	CCTGATCTCT	GTGGTGTGTA	TCATCTGCTG	GGGCCCTTTG	1140
	CTTGCAATCA	TGGTGTATGA	TGTCTTTGGG	AAGATGAACA	AGCTCATTAA	GACGGTGTCT	1200
40	GCATTCTGCA	GTATGCTCTG	CCTGCTGAAC	TCCACCGTGA	ACCCCATCAT	CTATGCTCTG	1260
	AGGAGTAAGG	ACCTGCGACA	CGCTTTCCGG	AGCATGTTTC	CCTCTTGTGA	AGGCACTGGC	1320
	CAGCCTCTGG	ATAACAGCAT	GGGGGACTCG	GACTGCTCTG	ACAAACACGC	AAACAATGCA	1380
	GCCAGTGTTC	ACAGGGCGCG	AGAAAGCTGC	ATCAAGAGCA	CGGTCAAGAT	TGCCAAGGTA	1440
	ACCATGTCTG	TGTCACAGCA	CACGCTGCGC	GAGGCTCTGT	GAGCCTGATG	CCTCCCTGGC	1500
45	AGCACAGGAA	AAGAATTTTT	TTTTTTAAGC	TCAAAATCTA	GAAGAGTCTA	TGTCTCTCTT	1560
	GGTTATATTT	TTTTTAACCTT	ACCATGCTCA	ATGAAAAGGT	GATTGTCAAC	ATGATCATTT	1620
	ATCAGTTTGC	TAAATGTTCC	ATAGTTTAGG	TACTCAAAT	CCATTCTCCA	GGGTTTACA	1680
	GTGAAGAAAG	CCTGTTGTTT	AAGTGACTGA	ACGATCTCTC	AAAGTCTCAA	TGAATAGGTA	1740
	GGGAACCTTT	TGGCTACACA	ATTGGAAGTC	TAAGAAACCA	TGGAAAAATG	CCATCAAAATG	1800
50	AATAATGCCT	TTGTAAACCA	AACTTTCACT	ATAATGTGAA	ATGTAACGTG	CCGTAGTATC	1860
	AGAGATGTCC	ATTTTACAA	GTTATAGTAC	TAGAGATATT	TTGTAATAATG	TATTATGTCC	1920
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	TTTCTATATT	ATGCCCCATG	ATATAACTTT	AGAAATAAAC	CTTAATATTT	CTTCAAAAT	2100
	CTCTATTATA	TTTTGACACT	GAAATAACCG	TAAAGGTTTA	TTTTTCTGTT	ACCTCAACAA	2160
55	GAAGAATTGG	AAGACTTCAA	AATATTGAGC	AGAATTCATT	CTACTTAAA	AATTTATTAG	2220
	CCCTGCATT	TCATAGGAAG	ACACATTATC	TTCTGGACTA	TAGCTGTTCT	AATGGATTAT	2280
	AATCAGAAATG	GAAGAGAGAA	AGCATATTGA	CTTTTTTTGA	GCGACATCTC	TGACTTTCTT	2340
	TAGTCTTTAG	TATTACTTGG	ATCTCTTAAG	ACAGCATGTG	TTAATCTTAA	TGTATATGCT	2400
60	TATCAGTGTG	CAGTTGCTGT	TTACTTGAAT	AGTATTGTGT	TCCTATATTC	CAGGTTTAAG	2460
	TAGATTTCAT	GCCTGGGTGG	CCAAACAACA	GTCTTCATT	TTTTTAATTG	AAAAGAAGTA	2520
	GTGCTGAGAT	CAGTAAAAAT	ATACTGTGTG	TGAGTGTGAA	TATAAATGTG	TGTATGTGTG	2580
	TTTCTGTCCG	TAACTGTTAC	AGTAATGTCA	TAAAGTGAGA	AACTGTGAC	CAAGTATAAA	2640
	CTTTTACCAC	TGCTGCACT	CTTGCACTG	GATTCACTTT	CTAAATTTGA	GTCTCTCTGT	2700
65	TAATCTTGTT	GATAAAAAATA	CTGACTCCAA	CCATTCAAAA	ATTTCAACCC	ATCCCTCTCT	2760
	AAGAGATTGG	ATCAAGTATT	ACTAAATTGA	CCTTTAGGTA	TTACACAAGA	CCAGTGCTTA	2820
	GCAAAAAATA	ATGACAGGCA	TCCAAGGAAG	GGATGTATTT	GTAGTGTAT	TGCCAGGAAA	2880
	GGAGAGTACT	TTGTTTCTG	AGCACCGAAT	ATTGAGCAAT	ATGTCACTCA	CTAAAAGGAA	2940
	GACAGTTCTA	CAGAAAAACA	AATGGTAACA	TTTTTCAATA	GCGTGTGTAG	ATAGTATGCA	3000
70	CTATATACAT	CACGTTAAAG	TAGGACTATC	ACACCCAGCC	CATGTGGCTA	AAAAAGCTGA	3060
	ATCAGACAGT	GGATGAGACA	CACAACGGCA	GTGAAGAACC	GATACACTTG	GCATTGAAGT	3120
	CTAGCTATGC	TGTTATCTGT	CTTTGCCAC	ATGCCCTTGG	TGACAGCTGA	GCACCCAGCT	3180
	CTGTCTTGGT	AGGTTTGGGC	TAAGGAACAA	ATCTCTCTCT	TGCTCGTGGT	TAGCAAGATA	3240
	CACCTAAGCA	TGAAGATAAA	CACAGCTGCT	TTCTTCTTAC	ACCCCGGTCT	CATGCTCTCT	3300
75	AATGGCGCCA	TGGGTGCTGT	TTGGGCTTT	TTCCAGTAAG	GAATGATATT	GCTGAAGAA	3360
	CTACTTAACC	CTGACAAATT	TTAATTATAA	TCTCTTCTTA	TACAGATAAA	ACATGACTCC	3420
	TACAAGGCC	CAAGGTTTAC	ATAGTCTGAA	GTGAAGTACA	GAGCTGGCAT	CTATCTGGTG	3480
	ATTCTTAGCT	CTGAGATAC	CCAAGCAGCC	TGATGGGGCA	GTCCCTCTTC	TTACGTTTCA	3540
	CGCTCTAAG	CAGGATGTGG	CTTATGAGAT	ACTTTGCATT	GTCTGTCTGC	ACACCTTGAA	3600
80	TCTGCTGTCT	GGCTCCCTTA	CTTTACCTCT	CTGTCACTGT	CAGATGAAGG	CTCAGGGTGC	3660
	TAGAGGATTA	GTAAGATCTC	TTTCTAAAGA	CAGGAGAGAT	TATTTACAAG	AAGAATCTAC	3720
	CAGGGTTTAG	TTTGCAATTA	AGAATTGCCA	GTCTTTTGTG	CTGCATCATC	TTGAACATTA	3780
	ATCCACATGT	TTCAAGCTCT	ACCAGGCAGT	ACCAATGCTC	TTTTTACAGC	TATGAAGAGC	3840
	TAGAGAAATT	CTTGTTATGG	TAGAAAAATT	TCACGGTTCA	TTTTTGAAAC	TGCATTGTGT	3900
	CGTATGCACT	GTAGATTTTA	TAGTGTGTGT	TGCTTTCAAG	ATCTAAATCA	TATATAATAA	3960

5 ATTAAGGGAC AATGGGGCTG ACAGCACTAA ACTTGGTGCT TATTGATATT CTAAGAAATA 4020
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 20 AGCGGGAAC ATGACTCTTT ATTGTCTGTA AATCTAACAT TATTACTTTT CCTCTTAGAA 5160
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 25 TTAAGCCAC AGTATATTTT ATTTCAATGT AATTAAACTG TTAACTTATT CAAAGAGAAA 5400
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 ATGAAGAACA TA

Seq ID NO: 238 Protein sequence
 Protein Accession #: NP_057167.1

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 KMTAGDNPQL VPADQVNITE FYNKSLSSFK ENEENIQCGE NFMIDIECFMV LNPSQQLAIA 120
 35 VLSLTGLTFT VLENLVLVCF ILHSRSLRCR PSYHFIGSLA VADLLGSVIF VYSFIDFHFV 180
 HRKDSRNVEL FKLGGVTASL TASVGSLEFLT AIDRYVSIHR PLAYKRIVTR PKAVVAFCLM 240
 WTAIAIAVL PLLGWNCEKL QSVCSDFPHI IDETYLMFWI GVTSVLLLFV YAYMYILWK 300
 AHSNAVRIHQ RGQKSIILH TSEDGKVQVT RPDQARMDIR LAKTLVLILV LIICWGPLL 360
 40 AIMVYDVFGK MNKLIKTVFA PCSMLCLLNS TVNPIIYALR SKDLRHAERS MPFSCGTAQ 420
 PLDSMGDSDD CLHKHANNA SVHRAAESCI KSTVKIAKVT MSVSTDTSAE AL

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 CGGCAGCCTG GCGGTGGCAG ACCTCCTGGG GAGTGTCTAT TTTGCTACA GCTTCATTGA 360
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 ATCCATTCAC AGGCCCTCTG CCTATAAGAG GATTGTCTAC AGGCCCAAGG CCTGTGTGGC 540
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 CTGCGAGAAA CTGCAATCTG TTTGCTCAGA CATTTCCTCA CACATTGATG AAACCTACCT 660
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 TGCCAAGGTA ACCATGCTCTG TGTCCACAGA CAGCTCTGCC GAGGCTCTGT GA

70 Seq ID NO: 240 Protein sequence
 Protein Accession #: NP_149421.1

75 1 11 21 31 41 51
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 MALQIPPSAP SPLTSCWQA MTFSTKTSKE NEENIQCGEN FMDIECFMVL NPSQQLAIAV 60
 LSLTGTFTV LLENLVLVCF ILHSRSLRCR SYHFIGSLAV ADLLGSVIFV YSFIDFHFVH 120
 RKDSRNVELF KLGGVTASPT ASVGSLEFLTA IDRYISIHRL LAYKRIVTRP KAVVAFCLMW 180
 TTAIVIAVLP LLGWNCEKLQ SVCSDFPHI DETYLMFWIG VTSVLLLFV YAYMYILWKA 240
 80 HSHAVRMIHQ GTQKSIILH SEDGKVQVTR PDQARMDIR AKTLVLILV LIICWGPLLA 300
 IMVYDVFGKM NKLIKTVFAP CSMLCLLNST VNPPIIYALRS KDLRHAFRSM FPFSCGTAQP 360
 LDNSMGDSDC LHKHANNAAS VHRAAESCIK STVKIAKVTM SVSTDTSAEA L

Seq ID NO: 241 DNA sequence
 Nucleic Acid Accession #: NM_003596.1

Coding sequence: 82..1194

	1	11	21	31	41	51	
5	GTAGACTGTC	CATGGCCTGA	ACATTITTCG	AAAATCATT	TGAGCAAAT	ATCTGTTTAA	60
	TAACAAGATA	ACCACATCAA	GATGGTTTGA	AAGCTGAAGC	AGAACTTACT	ATTGGCATGT	120
	CTGGTGATTA	GTTCGTGTAC	TGTGTTTTAC	CTGGGCCAGC	ATGCCATGGA	ATGCCATCAC	180
	CGGATAGAGG	AACGTAGCCA	GCCAGTCAAA	TTGGAGAGCA	CAAGGACCAC	TGTGAGAACT	240
10	GGCTTGGACC	TCAAAGCCAA	CAAAACCTTT	GCCTATCACA	AAGATATGCC	TTTAATATTT	300
	ATTGGRGGTG	TGCTCGGAG	TGGAACCA	CTCATGAGGG	CCATGCTGGA	CGCACATCCT	360
	GACATTGCT	GTGGAGAGGA	AACCAGGTC	ATTCCCCGAA	TCCTGGCCCT	GAAGCAGATG	420
	TGGTCACGGT	CAAGTAAAGA	GAAGATCCG	CTGGATGAGG	CTGGTGTAC	TGATGAAGTG	480
	CTGGATTCTG	CCATGCAAGC	CTTCTTACTA	GAAATTATCG	TTAAGCATGG	GGAGCCAGCC	540
15	CCTTATTTAT	GTAATAAAGA	TCCTTTTGCC	CTGAAATCTT	TAACTTACCT	TTCTAGGTTA	600
	TTCCCCAATG	CCAAATTTCT	CCTGATGTC	CGAGATGGCC	GGGATCAGT	ACATTCAATG	660
	ATTCTCGAA	AAGTTACTAT	AGCTGGATT	GATCTGAACA	GCTATAGGGA	CTGTTTGACA	720
	AAGTGAATC	GTGCTATAGA	GACCATGTAT	AACCAAGTGA	TGGAGGTGG	TTATAAAAG	780
	TGCATGTGG	TTCACTATGA	ACAACTGTG	TTACATCCTG	AACGGTGGAT	GAGAACACTC	840
20	TTAAAGTTCC	TCCAGATTCC	ATGGAACCA	TCAGTATTGC	ACCATGAAGA	GATGATTGGG	900
	AAAGCTGGGG	GAGTGTCTCT	GTCAAAAGTG	GAGAGATCTA	CAGACCAAGT	AATCAAGCCA	960
	GTCAATGTAG	GAGCTCTATC	AAAATGGGTT	GGGAAGATAC	CGCCAGATGT	TTTACAAGAC	1020
	ATGGCAGTGA	TTGCTCCTAT	GCTTGCCAAG	CTTGATATG	ACCCATATGC	CAACCCACCT	1080
	AACTACGGAA	AACTGATCC	CAAAATTAT	GAAAACACTC	GAAGGCTCTA	TAAGGGAGAA	1140
25	TTCCAACTAC	CTGACTTTCT	TAAAGAAAA	CCACAGACTG	AGCAAGTGG	GTAGCAGAAC	1200
	CAGGAGCCTC	TTCCATACAT	GAGGAAAGAT	TGCTGCCTTT	TCAGCAGAA	GGAAATTCCT	1260
	AGGATTGGCT	GTCCCTTGCC	AAGCTTGGTG	GAGCGTCTGC	ACCTTGGCTG	CGCCGCTGT	1320
	GCATTTGCCA	GTTTCTCCTC	ACTGAGAGGA	TGGAGGTGTC	CGCACAGCTT	TGGGCTCTGT	1380
	GAGGGATCTG	CCTCTGAGC	AAAGAGCTCT	TGATCCCGAT	TTCTATGACA	GCCTGTCAGT	1440
30	AAGGAGCCCA	GAAGGAACAT	GTGTTTCCCT	TTAAACTCC	TCTTGTCTC	TTTTCTTACA	1500
	TTATGACGTT	TGTTTTCAG	GAGAGGTTT	AAAAATGGGA	TCCTGTAAGC	AGACTTGGGC	1560
	AGTCTCTCTT	TGAAATAGGT	TGCTGTGACA	TGTTCTAATG	TTTGTAGAA	CACGTGTGCC	1620
	TGTTTAAGTG	TATTGATGTG	AATAATATTA	AATATCTTAA	TTATTTAATT	CATGTATTG	1680
35	TTTCTGAGAA	GTTGGGAAAT	TACCATTATA	CATTTACAAC	CTAATGACTT	TTGTATTTTA	1740
	TTTTTCAAAA	TAAAGCTTT	CAATGTGA				

Seq ID NO: 242 Protein sequence
Protein Accession #: NP_003587.1

	1	11	21	31	41	51	
40	MVGLKQNL	LACLVISST	VFYLGQHAME	CHHRIBERSQ	FVKLESTRIT	VRTGLDLKAN	60
	KLIFAYHKDMP	LIFIGVPR	GTLLMRMLD	AHPDIRGEE	TRVIPRILAL	KQMSRSSEKE	120
	KIRLDEAGVT	DEVLDASMQA	FLLEIIVKHG	EPAPYLKND	PFALKSLTYL	SRLFPNAKFL	180
45	LMVRDGRASV	HSMSIRKVTI	AGFDLNSYRD	CLTRWNRAIE	TMYNQCMVEG	YKKCMVLVHYE	240
	QLVLMPEERWM	RTLLKFLQIP	WNHSLVHHEE	MIGKAGGVSL	SKVERSTDQV	IKPVNVGALS	300
	KWVGKIPPDV	LQDMAVIAPM	LAKLGYDPYA	NPPNYGKPD	KIIENTRRVY	KGEFQLPDFL	360
	KEKPQTEQVE						

Seq ID NO: 243 DNA sequence
Nucleic Acid Accession #: NM_001492.3
Coding sequence: 1395..2513

	1	11	21	31	41	51	
55	ACGCGGGGGG	CGCGGCTCOG	TCGGCTACCG	CGGGCGGGCG	CAGGCGACCG	GCACGGCGGG	60
	CGAGCGGGCG	GTATGGCGCG	GGCGGGGCC	GCGCGGGGCG	CGACGGGGCC	CGAGCCCATG	120
	CGAGCTACG	CGCAGCTAGT	GCAGCGCGGC	TGGGGCAGCG	CGCTGGCGGC	GGCGGGGGCG	180
	TGCACGGACT	GCGGCTGGGG	GCTGGCGCGT	CGCGGCGCTG	CTGAGCACCG	GCACCTGGCG	240
	CGCGCGAGC	TGCTGCTGCT	GGCGCTCGGC	GCGCTGGGCT	GGACCGCGCT	GCGCTCGCGG	300
60	GCCACTGGCG	GCCTCTTTG	GCCCTGGCG	AAGCGTGCT	GCCTCCAGCC	CAGAGATGCC	360
	GCCAAGATGC	CGAGAGCGCG	TTGGAAGTTT	CTCTTCTACC	TGGGCAGCTG	GAGCTACAGT	420
	GCCTACCTGC	TGTTTGGCAC	CGACTACCCC	TTCTTCCATG	ACCCACCATC	TGCTTCTAC	480
	GACTGGACGC	CGGGCATGCG	AGTGCCACCG	GACATTGCAG	CGGCTACCT	GCTCCAGGGA	540
65	AGCTTCTATG	GCCACTCCAT	CTACGCTACG	CTATACATGG	ACACCTGGCG	CAAGGACTCG	600
	GTGGTCAATG	TGCTCCACCA	CGTGGTCACT	CTCATCTCTA	TGCTCTCTC	CTACGCTTTC	660
	CGGTACCACA	ATGTGGGCAT	CCTTGTGCTC	TTCTGTCACG	ATATCAGTGA	CGTGACAGTT	720
	GAGTTACCCA	AGCTCAACAT	TTACTTCAAG	TCCCGCGGCG	GCTCTTACCA	TGGCTGCTAT	780
	GCCTTGGCAG	CAGACTTGGG	CTGCTCAGC	TTGGGCTTCA	GCTGGTTCTG	GTTCCGCTTC	840
70	TACTGGTTCC	CGCTCAAGGT	CCTGTATGCC	ACCACTCACT	GCAGTCTGGG	CACGGTGCCT	900
	GACATGCCCT	TCTACTTCTT	CTTCAATGCG	CTCTGCTGCG	TGCTCACCTT	TATGAACCTC	960
	TACTGGTTCC	TGTACATCGT	GGCGTTTGCA	GCCAAGGTGT	TGACAGGCCA	GGTGACGAG	1020
	CTGAAGGACC	TGGCGGAGTA	TGACACAGCC	GAGGCCACGA	GCTGAAGGCC	CAGCAAAAGC	1080
	GAGAAGCCAC	TAGAGAACCG	CCTGGTGAAG	GACAAGCGCT	TCTGAACCCC	TGGCCCGGCG	1140
75	CCCGTGGAC	CGGCCCCAC	CCGGAATACC	CGGCCACGCG	TCCCCGTCTT	TGGCGGCCCG	1200
	TCCACCCCTT	CCAACTCTGC	TCCTCTAGGG	CGCGCGCCAC	CTCCCTGGG	ACCCCGCCCC	1260
	CTCATCTGCT	CTCCATTTCC	CGGCAAGGCC	CCCCAGGACC	CCTGCCCTTC	CGGGGACACC	1320
	GGCCCCGCCC	TCAGCCCATC	GGTCCCGGGC	CGCGCGGACG	CCTGCGCACT	CTCTGCTCAT	1380
	CGCTTGGGAG	GAAGATGCCA	CGCGCGCAGC	AAGTTCCTGT	CGGCCACACC	CTCTCTCTCC	1440
80	TCCTGGCCCT	GCTGCTGCC	TGCTGCCCC	TGACCCGCGC	CCCCGTGCCC	CCAGGCCAG	1500
	CGCGCGCCCT	GCTCCAGGCT	CTAGGACTGC	GCGATGAGCC	CCAGGGTGCC	CCAGGCTCC	1560
	GGCGGTTTCC	CGCGGCTCATG	TGGCGCTGT	TTGACGCGCG	GGACCCGAG	GAGACAGGT	1620
	CTGGCTGGCG	GCGGAGCTCC	CCAGGGGTCA	CCCTGCAACC	GTGCCACGTG	GAGGAGCTGG	1680
	GGGTGGCGGG	AAACATCGTG	CGCCACATCC	CGGACCGCGG	TGCGCCACCC	CGGGCTCGG	1740
	AGCCTGTCTC	GGCGCGGGG	CATTGCCCTG	AGTGAGCAGT	CGTCTTGAC	CTGTGGCTG	1800

5 TGGAACCCCG TGAGCGCCCG AGCCGGGCCC GCCTGGAGCT GCGTTTCGG GCGGCGGCGG 1860
 CGGCAGCCCC GGAGGGCGGC TGGGAGCTGA GCGTGGCGCA AGCGGCCAG GCGCGGGCGG 1920
 CGGACCCCGG GCGGTGCTG CTCCGCCAGT TGGTGCCCGC CTGGGGCCCG CCAGTGGCGG 1980
 CGGAGCTGCT GGGCGCGCT TGGGCTCGCA ACGCTCATG GCGCGCAGC CTCGCGCTGG 2040
 CGCTGGCGCT AGCCCCCGG GCCCTGCGG CCTGCGCGGG CCTGGCCGAG GCCTCGCTGC 2100
 TGCTGGTGAC CCTCGACCG CGCTGTGACC ACCCCCTGGC CCGGCGCGGG CCGGAGCGCG 2160
 AACCGGTGTT GGGCGGCGGC CCGGGGGGCG CTTGTGCGCG GCGGCGGCTG TACGTGAGCT 2220
 TCCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGGCGCGG CGGCTTCCTG GCCAACTACT 2280
 GCCAGGCTCA GTGCGCGCTG CCGCTGCGGC TGTGCGGGTC CCGGGGGCGG CCGGCGCTCA 2340
 10 ACCAGCTGCT GCTGCGCGCG CTGATGCAGC CGGCCGCCCG GGGAGCGCGC GACCTGCCCT 2400
 GCTGCGTGCC CCGCGCGCTG TCGCCCATCT CCGTGTCTTT CTTTGACAA AGCGACAAAG 2460
 TGGTGTGCG CGAGTATGAG GACATGGTGG TGAACGAGTG CGGCTGCGCG TAACCCGGGG 2520
 CCGGCGAGGA CCGGGGCCCA ACAATAAATG CCGGTGGTTC TGCTC

15 Seq ID NO: 244 Protein sequence
 Protein Accession #: NP_001483.2

20 1 11 21 31 41 51
 MPPFPQGGPCG HLLLLLLALL LPSLPLTRAP VPPGPAAALL QALGLRDEPQ GAPRLRPVPP 60
 VMWRLFRRRD PQETRSRGR TSPGVTLQPC HVEELGVAGN IVRHI PDRGA PTRASEFVSA 120
 AGHCEPWTVV FDLSAFEPAE RPSRARLELR FAAAAAFAPE GGWELSVQAQ GQAGADPGP 180
 VLLRQLVPAE GPVRAELLG AAWARNASWP RSLRLALALR PRAPAACARL AEASLLLVTL 240
 25 DPRLCHPLAR PRDAEPVLG GPPGGACRAR RLYVSPREVQ WHRWIAPRG FLANYCQGCQ 300
 ALPVALSGSG GPPALNHAVL RALMHAAAPG AADLPCCVPA RLSPISVLFV DNSDNVVLQR 360
 YEDMVVDECG CR

30 Seq ID NO: 245 DNA sequence
 Nucleic Acid Accession #: NM_021267.1
 Coding sequence: 17..1125

35 1 11 21 31 41 51
 ACGCGGGGCG CGCGGCTCCG TCGGCTACCG CGGGCGGGCG CAGGCGACGG GCAACGGGGG 60
 CGAGCGGGCG GTATGGCGGC GGCGGGGCCG GCGGCGGGCG CGACGGGGCC CGAGCCCATG 120
 CCGAGCTACG CGCAGCTAGT GCAGCGCGCG TGGGGCAGCG CGCTGGCGGC GCGCGGGGCG 180
 TGCACGAGCT GCGGCTGGGG GCTGGCGCGT CGCGGCTTGG CTGAGCACGC GCACCTGGCG 240
 CGCGCCGAGC TGCTGCTGCT GGCGCTCGCG GCGCTGGGCT GGACCGCGCT CGCTCCGCGG 300
 40 GCCACTGGCG GCCTCTTTCG GCCCTGGGCG AAGCGGTGCT GCCTCCAGCC CAGAGATGCC 360
 GCCAGATGCG CCGAGAGGCG TTGGAAGTTT CTCTTCTACC TGGGCGAGTG GAGCTACAGT 420
 GCCTACCTCG TGTTTGGCAC GCACTACCCC TTCTTCCATG ACCCAACATC TGTCTTCTAC 480
 GACTGGACCG CGGCGATGCG AGTGCCACCG GACATTGCAG CGGCTACCT GCTCCAGGGA 540
 AGCTTCTATG GCGACTCCAT CTACGCTACG CTATACATGG ACACCTGGCG CAAGGACTCG 600
 GTGGTCAATG TGTCCACCA CGTGGTCACT CTCATCTCTA TGTCTCTCTC CTACGCTTTC 660
 45 CGGTACCACA ATGTGGGCGT CCTTGTGCTC TTCTGCAAG ATATCAGTGA CGTGCACTT 720
 GAGTTCACCA AGCTCAACAT TTACTTCAAG TCCCGGGCGG GCTCTTACCA TGGGCTGCAT 780
 GCCTTGGGAG CAGACTTGGG CTGCGCTCAG TTGCGCTTCA GCTGTTCTCG GTTCCGCTTC 840
 TACTGTGTTCC GCTCAAGGT CTTGTATGCC ACCAGTCACT GCAGTCTGCG CAAGTGTGCT 900
 50 GACATCCCTC TCTACTTCTT CTTCATGCG CTCTGCTGCG TGCTCACCTT TATGAACCTC 960
 TACTGTTTCC TGTACATCGT GCGGTTTGCA GCCAAGGTGT TGACAGGCCA GGTGCACGAG 1020
 CTGAAGGAGC TGCGGGAGTA TGACACAGCC GAGGCCGAGA GCCTGAAGCC CAGCAAAGCC 1080
 GAGAAGCCAC TGAGGAACCG CCTGGTGAAG GACAAAGCGT TCTGAACCCC TGGGCCCGCG 1140
 CCGCGTGGAC CCGGCCCCAC CCGGAATACC CCGGCCAGCG TCCCGTCTCT TGGCGGCCCC 1200
 55 TCCACCCCTT CCAACTCTGC TCCTCTAGGG CCGCGGCCAC CTCCCTTGGG ACCCGGCCCC 1260
 CTCATCTTGC CTCATTTTCC CGGCCACGCG CCGCAGGACC CTGCGGCTTC CCGGGACACC 1320
 GGCGCGCGCC GCGGCCACT GGTCCCGGGC CGCGCGGAGC CCGCGGCTCT CTCCTGCTAT 1380
 CGCTGGGAGG GAGGATGCCA CCGCGCGAGC AAGGTCCCTG CGGCCACCAT CTCCTCTCTC 1440
 60 TCCTGGCCCT GCTGCTGCCG TGGCTGCCCG TGAACCGCGC CCGGCTGCCC CAGGCGCCAG 1500
 CCGCGGCCCT GCTCCAGGCT CTAGGACTGC GCGATGAGCC CCAGGCTGCC CCCAGGCTCC 1560
 GCGCGGTTCC CCGGCTCATG TGGCGGCTGT TTGAGCGCGG GAGCCCGCAG GAGACAGGAT 1620
 CTGGCTCGCG GCGGACGCTC CCAGGGGTCA CCTGCAACC GTGCCAAGTG GAGGAGCTGG 1680
 GGGTCCGCGG AAACATCGTG CGCCACATCC CGGACCGCGG TGGCGCCACC CCGGCTCTGG 1740
 AGCTGTGCTC GCGCGCGGGG CATTGCCCTG AGTGGACAGT GGTCTTGGAC CTGTGCGCTG 1800
 65 TGGAACCCCG TGAGCGCCCG AGCCGGGCCC GCCTGGAGCT GCGTTTCGG GCGGCGGCGG 1860
 CCGCAGCCCC GGAGGGCGGC TGGGAGCTGA GCGTGGCGCA AGCGGGCCAG GCGGCGGGCG 1920
 CGGACCCCGG GCGGCTGCTG CTCGCGCAGT TGGTGCCCGC CTGGGGCCCG CCAGTGGCGG 1980
 CGGAGCTGCT GGGCGCGCTT TGGGCTCGCA ACGCTCATG GCGCGCAGC CTCGCGCTGG 2040
 CGCTGGCGCT ACGCCCCCGG GCCCTGCGCG CCTGCGCGGG CCTGGCCGAG GCCTCGCTGC 2100
 70 TGCTGGTGAC CCTCGACCGG CGCCTGTGCG ACCCCCTGGC CCGGCGGCGG CCGGAGCGCG 2160
 AACCGGTGTT GGGCGGCGGC CCGGGGGGCG CTTGTGCGCG GCGGCGGCTG TACGTGAGCT 2220
 TCGCGGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCGCGG CGGCTTCTCT GCCAACTACT 2280
 GCCAGGCTCA GTGCGCGCTG CCGCTGCGCG TGTGCGGGTC CCGGGGGCGG CCGGCGCTCA 2340
 ACCAGCTGCT GCTGCGCGCG CTGATGCAGC CCGCGGCCCG GGGAGCGCGC GACCTGCCCT 2400
 75 GCTGCGTGCG CCGCGCGCTG TCGCCCATCT CCGTGTCTTT CTTTGACAA AGCGACAAAG 2460
 TGGTGTGCG CGAGTATGAG GACATGGTGG TGAACGAGTG CGGCTGCGCG TAACCCGGGG

80 Seq ID NO: 246 Protein sequence
 Protein Accession #: NP_067090.1

1 11 21 31 41 51
 MAAAGPAAGP TGPEPMPHYA QLVQRGWGSA LAAARGCTDC GWGLARRGLA EHAHLAPPEL 60
 LLLALGALGW TALRSAATAR LFRPLAKRCC LQPRDAARKP ESANKFLPYL GWSYSAYLL 120
 FGTDPYFFHD PPSVPYDWTG GMVAFPRDIAA AYLLQGSFYG HSIYATLYMD TWRKDSVVML 180

LHHVVTLLILI VSSYAFRIYHN VGILVFLFHD ISDVQLEFTK LNIYFKSRGG SYHRLHALAA 240
 DLGCLSPFGS WFWRLYWF LKVLATSHC SLRTVPDIPF YFFFNALLLL LTLMLNYWFL 300
 YIVAFPAKVL TGQVHELKDL REYDTAAQS LKPSKAERPL RNLGVKDKRF

5

Seq ID NO: 247 DNA sequence
 Nucleic Acid Accession #: NM_002081.1
 Coding sequence: 222..1898

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 CGGACCTTG GCTCTGCCCT TCGCGCGCGC GAACTGCGCA GGACCGCGCC AGGATCCGAG 180
 AGAGGCGCGG GCGGGTGGCC GGGGCGCGCG CCGGCCCCCG CATGGAGCTC CGGCGCGCGG 240
 15 GCTGGTGGCG CCGTATGTGC GCGCGAGCGC TGGTGGCGTG CGCGCGCGCG GACCGCGCCA 300
 GCAAGAGCGG GAGCTGGCGC GAGGTCCGCG AGATCTACGG AGCCAGGGGC TTCAGCCTGA 360
 GCGACGTGGC CCAGGCGGAG ATCTCGGGTG AGCACTGCG GATCTGTCC CAGGGCTACA 420
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 20 TOGATGACCA CTTCAGCAC CTGCTGAACG ACTCGGAGCG GACGCTGCAG GCCACCTTCC 600
 CCGGCGCTTT CCGAGAGCTG TACAGCAGA ACGCGAGGGC CTTCGGGAC CTGTACTCAG 660
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 GGGCCCGCCT GCTCGAGCGC CTCCTCAAGC AGCTGCACCC CCAGCTGCTG CTGCTGATG 780
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 25 GAGAGTGGCT CCGTGGCGCG ACCCGTGCCT TCGTGGCTGC TCGCTCTTT GTGCGGGGCC 900
 TGGGCGTGGC CAGCGAGTGT GTCCGGAAAG TGGCTCAGGT CCGCTTGGGC CCGGAGTGTCT 960
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 CCTGCCCTGA CTATTGCGCA AATGTGCTCA AGGGCTGCTT TGCCAACCAAG GCGGACCTGG 1080
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 30 CTGCGGTGT GAGAGTGTCT ATCGGAGCGG TGCAACAOTG GCTGGCGGAG GCCATCAACG 1200
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 GCGAGCTCCA GGACTTCTGG ATCAGCCTCC CAGGGACACT GTGAGTGAAG AAGATGGCCC 1440
 35 TGAGCACTGC CAGTGATGAC CGCTGCTGGA ACGGATGGC CAGAGGCGCG TACCTCCCCG 1500
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 CCAAGCCGGA CATGACCATC CGGAGCAGGA TCATGCACTT GAAGATCATG ACCAACCGGC 1620
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 40 GCTCGGGCAG CCGTGATGGC TGTCTGATGT ACCTCTGGCG CCGGAAGGTC AGCAGGAAGA 1740
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 TCCTGGCCCT TACAGTAGCC AGGCCCCGCT GCGGTAATC GCGCCAGGC CCCAGGGACA 1920
 GAGGCGAAGG ACTGACTTTG CCAAAAATAC AACACAGAGC ATATTTAAT CACCTCAGCC 1980
 45 TGGAGAGGCC TGGGTGGGA CAGGGAGGGC CCGCGGCTCT GAGCAGGGGC AGGCGCAGAG 2040
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 50 CTACAGAGGA AGCTTCAAG CAACCGCTG GAGCCACAG CGAGCCTGTG CCTTCTCTCC 2280
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 55 GGAGTCTGAG GACTGTCTCT CCACAGACCC TGCACTGAGG GCGCTCCAT GCGCAGATGA 2580
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 60 CCGGCACTG CACACGGGAA TGCTTAGGTC CCTTCCGAC CCAGCCAGCT GCACTGCAGG 2940
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 TGTCTTGTG CATGGAGAGC TGTTOGCTCC TCCAGATGS CTTCGAGGC CCGCAGGGCC 3060
 CACCTTGGAC CCGTGTGACC TCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC 3120
 CTGAGCGGCG CCTCTTCCC TCTGTGCCG CAGCTGCCAG GTGGCCTGTG GGAGGGTGG 3180
 65 TGTGGTGTG GGAAGGGGTC CTGAGGGGG AGGAGGACTT GAGGCTCTG GGGGCGAGCT 3240
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 OGCACAGTGG ACGGAGGTCC CCGGTGCTG GTCAGGTCCC CATGGCTTGT TCTCTGGAAC 3360
 CTGACTTTAG ATGTTTGGG ATCAGGAGCC CCAACACAG GCAAGTCCAC CCTAATAA 3420
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 70 CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGGCT CAGACCCAC CCTAGCTCA 3540
 TCTCTGGAAG GGGCAGCCCT GAGTGGTCA TGGTCAAGGC AGTGGCCAG CTGTCTGTG 3600
 CCTTCTCCA CAAGGTCCCC CCACCGCTCA GTGTCAAGCG GTGAGTGTG TCTTTTGG 3660
 TCCTGTATG AATAAAGGC TGGAAACCTA AA

75

Seq ID NO: 248 Protein sequence
 Protein Accession #: NP_002072.1

1 11 21 31 41 51
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 MELRARGWVL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGPSLSVDP QAEISGEHLR 60
 80 ICPQGYTCCT SEMEENLANR SHABLETALR DSRVLQAML ATQLRSFDDH FOHLNDSE 120
 TLQATPPGAF GELTYQARA FRDLYSELRL YVRGANLHLE ETLAEPWALR LERLLFKQLHP 180
 QLLLPDDYLD CLGKQABALR PFGRAPREL RLRATRAVAA RSPVQGLGVA SDVVRKVAQV 240
 PLGPECSRVA MKLVYCAHCL GVPGARPCPD YCRNVLKGL ANQADLDAEW RNLLDSMVL 300
 TDKFWGTSGV ESVGSVHTW LAEAINALQD NRDTLTAKVI QGQNEKVP QGPGPEEKRR 360

RGKLAPRPR PSQTLEKLV SBAQAQLRDVQ DFWSLPGTL CSEKHALSTA SDDRCWNGMA 420
 RGRYLPEVMG DGLANQINNP EVEVDITKPD MTRQQIMQL KIMTNRLRSA YNGNDVDFPD 480
 ASDDGS GSGS

5

Seq ID NO: 249 DNA sequence
 Nucleic Acid Accession #: NM_001492.3
 Coding sequence: 8..1864

10 1 11 21 31 41 51
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 CATTTTCCCT CCCACAGACAC GGCCCGCTGG CGTCTTCGAG CTGCAGATCC ACTCTTTCGG 120
 GCGGGGTCCA GGCCCTGGGG CCGCGCGGTC CCGCTGCAGC GCCCGGCTCC CCTGCGCCCT 180
 15 CTCTCTCAGA GTCTGCCCTGA AGCCTGGGCT CTCAGAGGAG GCCCGCCAGT CCCCGTGGC 240
 CCGGGGCGCT GCGCTGAGTG CGCGCGGACC GGTCTACACC GAGCAGCCCG GAGCGCCCGC 300
 GCCTGATCTC CCACTGCCCG ACGGGCTCTT GCAGGTGCCC TTCGGGAGC CCTGGCCTGG 360
 CACCTTCTCT TTCACTATCG AAACCTGGAG AGAGGAGTTA GGAGACCAGA TTGGAGGGCC 420
 CGCTGGAGC CTGCTGGGCG GCGTGGCTGG CAGGCGGCGC TTGGCAGCCG GAGGCCCGTG 480
 20 GGCCCGGGAC ATTACAGCGG CAGGCGGCTG GGAGCTGGCG TTCTCGTACC GCGCGCGCTG 540
 CGAGCGCGCT GCGCTCGGGA CGCGTGCAC GCGCTCTGCG CGTCGCGCA GCGCCCGCTC 600
 GCGGTGCGGT CCGGACTGCG GCCCTGGCGC ACGCTCGAG GACGAATGTG AGGCGCGCTG 660
 GGTGTGCCGA CAGGCTGCA GCCCTGAGCA TGGCTTCTGT GAACAGCCCG GTGAATGCG 720
 ATGCTAGAG GCGTGGAGTG GACCCCTCTG CACGCTCCCT GTCTCCACCA GCAGCTGCC 780
 CAGCCCCAGG GCGCGTCCCT CTGCTACCAC CGGATGCCTT GTCCCTGGGC CTGGGCCCTG 840
 25 TGACCGGAAAC CGCTGTGCCA ATGGAGGCAG CTGTAGTGAG ACACCCAGGT CCTTTGAATG 900
 CACCTGCCCG CGTGGGTCTT ACGGGCTGCG GTGTGAGGTG AGCGGGGTGA CATGTGCAGA 960
 TGGACCTGCG TTCAACGGCG GCTTGTGTGT CGGGGGTGCA GACCTGACT CTGCTACAT 1020
 CTGCCACTGC CCACTGGTGT TCCAAGGCTC CAACTGTGAG AAGAGGGTGG ACCGGTGCAG 1080
 CCGTGCAGCA TGCCGCAATG GCGGACTCTG CCTGGACCTG GGCCACGCCG TGCGCTGCCG 1140
 30 CTGCGCGGCC GCGCTCGCGG GTCTCGCTG CGAGCACGAC CTGGAAGACT GCGCGGGCGC 1200
 CGCTCGCGCT AACGGCGGCA CGTGTGTGGA GGGCGGGCGC GCGCACCGCT GCTCTGCGC 1260
 GCTGGGCTTC GCGCGCGCGC ACTGCGCGCA GCGCGCGGAC CCGTGGCGCG CCGGCCCTG 1320
 TGCTCACGGC GCGCGCTGCT ACGCCCACTT CTCGCGCCTC GTCTGCGCTT GCGCTCCCG 1380
 35 CTACATGGGA GCGCGGTGTG AGTTCCCACT GCACCCCGAC GCGCAAGCG CCTTGCCCGC 1440
 GGCCCGCGCG GCGCTCAGCG CCGGGGACCC TCAGCGCTAC CTTTTCCTC CGGCTCTGG 1500
 ACTGCTCGTG GCGCGGGCGG TGCGCGCGC TGCGCTCTTG CTGCTCCAGG TGCGCGCGC 1560
 TGCCCACTCC CAGGATGCTG GTCTCGCTT GCTGGCTGGG ACCCGGAGC CGTCAGTCCA 1620
 CGCACTCCCG GATGCACTCA ACAACCTAAG GAOCGAGGAG GGTTCGGGG ATGGTCCGAG 1680
 40 CTGCTCCGTA GATTGAATC GCCCTGAAGA TGTAGACCT CAAGGGATTT ATGTATATC 1740
 TGCTCCTTCC ATCTACGCTC GGGAGGTAGC GACGCCCTT TCCCGCCGC TACACACTGG 1800
 GCGCGCTGG CAGAGGCAGC ACCTGCTTTT TCCCTACCTT TCCTGATTC TGTCCGTGAA 1860
 ATGAATTGGG TAGAGTCTCT GGAAGGTTT AAGCCATTT TCAGTTCTAA CTTACTTTCA

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Seq ID NO: 250 Protein sequence
 Protein Accession #: NP_058637.1

1 11 21 31 41 51
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 50 MVSPRMSGLL SQTIVILALIF LPQTRPAGVF ELQIHSFGPG PGPGAPRSPC SARLPCLRF 60
 RVCLKPGLSE EAAESPICALG AALSARGPVY TEQPGAPAPD LPLPDGLLQV PFRDAWPGTF 120
 SFIIETWREE LGDQIGGPAPW SLLARVAGRR RLAAGGPPAR DIQRAGAWEL RFSYRARCPE 180
 PAVGTACTRL CRPSAPSRIC GPGLRPAAPL EDECEAPLVC RAGCSPEHGF CEQPGECRCL 240
 EGWTGPLECTV PVSTSSCLSP RGPSSATTGC LVPGEPPCDG NPCANGGSCS ETPRSFECTC 300
 55 PRGFYGLRCE VSGVTADGPF CFNGGLCVGG ADEPDSAYICH CPFGPGGNSNC EKRVRDCSLQ 360
 PCRNGGLCLD LGHALRCRCR AGFAGPRCEH DLDDCAGRAC ANGGTCVEGG GAHRCSCALG 420
 FGGRDCRERA DPCAARPCAH GGRCYAHFSG LVACAPGPMY GARCEFPVHP DGASALPAAP 480
 PGLRPGDPQR YLLPPALGLL VAAGVAGAAL LLVHVRRRGH SQDAGSRLLA GTPEPSVHAL 540
 60 PDALNNLRQ EGSGDGFSSS VDWNRPEVDV PQGIYVISAP SIYAREVATP LFPPLHTGRA 600
 GQRQHLLFPY PSSILSVK

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Seq ID NO: 251 DNA sequence
 Nucleic Acid Accession #: CAT cluster

65 1 11 21 31 41 51
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 GAAATATAAC CATTGCAATT AGAAAATATC CAAAATAGCC TGTATCTTC CACTGGCCT 60
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 GCTCAATTC CTTATATGAC TTCAGACTGG AGAAGCCTGT TAAACCACTG TTAGTTTCAG 180
 70 TTAGAAAGTC TGAGAGACTT TATACATAAA TTCTCAATTT GGCTGCTGTA CAGTGCCAG 240
 AGTTTACTA CTGAGTGCAG CGTTGAGAAG ACCCTTGTTT ATTACATTT GAAGCACTGT 300
 TTGTGCAAAAC AACCTTTTCT TGTAAAGTGC CTGTATTCCT TTCAATTACT TCATGTCAG 360
 GGGTGCTATT TACCTAGAAC CATTGTCTAC TACAATTAAC ATTACATTA CAAAGTGTGT 420
 GGTTTTCTTT TTCAAGGAGG TTCAATTAAG GCAATAAGAT GTTTGCTGGA GAAACCTATT 480
 75 GTTACTGAA AGCACTCAAT GAAGTCAAT TACTGAAGCT TTTGCTACA TCTTGTCTT 540
 TTATGTAAT ATGTTAATA TAACATCTAA GGAAAATAAA CAATATTATA ATTATGTGT 600
 TGCCATTGTC ATATCAACT TGCTTTGTAT CATACTAATG TTACATACT TATCGATCAA 660
 TAAAAATACA TTTCAATGTT AAAAAAAAAA AAAAAAAA

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Seq ID NO: 252 DNA sequence
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
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 AGGTACTGCC AGAAAGGATC AGGACCTGGA GTCTGGCAAG AGGAAGACAG AGGCCTGTGT 60

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GGGAAGCGAG TTGTTATCTT TGGTTATCTA GCTGTATGAG TGTATTGGTC TTCATAAAGC 120
TAGATAAACC AGAAGTAAAA CTCTCTCAAG ATCGCGGGG AGCGTGTGAG AATGAAAGAC 180
TACAGCCGAG AGACAGATAA AACCCAGAAAG GTCCAGGAATA CTTATTGAAT CTAACCTTTGT 240
TTTTGTTTGT TTTTCTTCTT TATGATTAAA GGTGGGATGA GAGAAAATTA AATGACACAC 300
ACATGCTAAA ATATCAAGGT TCCAGATATG TCTTGAGAGG GGTGTGTGCA GCTGCAAAAG 360
AGAAGTGTAT AGTGATAATG AGTAAAGATG CATGTGCAGT TTGTTCTATT TTAAGGCCAA 420
AGTTATATCA GGGATTCTTT TCTTAGAAAG GTGTGCGAGA GATGTCTGGT ACCTAGTTTA 480
AAAATGATTC CATATATATG AGACTTGGGC AGTTCCTTTG GGAGGCACCT CCCTCTCAAA 540
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TCTATTCAAA ATACAAGGAC AGATGCTTCT CTGTTCCAAG AGGGTTTCTT TGAGGAAGCT 780
ACTGAAGCAG AAAGACATGA TGGAGACGAG ATCGCTCCCT CTCTGTGCAA AGTGTAAAAA 840
AAATGTTCTG TCTTACTCTG CGCCTAGCAT TGGAAATGAA AGTGACATTT AOGCCACAAC 900
CCACGTGTGC GCCTCCTCTC TTTTGTTTTA AGGATGATCA GGTCTATCCA GGAAACAGCT 960
CTGGCATCCC AAATGAAAT AATTAGGACG TATATAGACC TGACAAAAAT GGAAAGGGGG 1020
TGGGGAATCT GAGGGTCTGT CTGCTTAAT TGATTCGCT AAACGGAATG CAGGAGATGT 1080
GAACGGCAGG AGCTCCGAT TCCCACGCTC GGGGGCAAGT GATAAAGCGG GGCCGGGCAG 1140
CCTATGACAG ACAGCCCTGT TGGGGGGTGG GGGTATGAAA AAAACATCAA GTGCACACAC 1200
CATACTATC TCATCGCTT AAGAAAGTAA AGGCATTTC CACCCACAGC CATCTGCAGC 1260
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TTAACCATG TTTAATCTGG CCATAATTAA GTTGGCTTT CTTCGTTGTT TGAGATTITC 1380
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AATGTCAAAA TCTCAGTCCA TGAGATTATG GCCTTGTGAC CACATTTTGT CTTTGTGTTT 1500
GGGTGGGCAA ATGCTGTATG AGATAAAATA CATATCTCTA TATAACAGTC GTTATTATAA 1560
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AACAAATATG TAAAAAGTTT GTTTTGGAAAT AGTCTCAGCT AGATGGGTCT AAATAGCCAT 1740
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CATTGTGCGC TTTTCTATAA AGTCCCTAAG TTTTCCATAT GTCACCAAGC AAACATTGTT 1860
ATAGGCATT TACACAGAAAT ATAACCATG CAATTAGAAA ATATCCAAAA TAGCCTGTTA 1920
TCTTCCAGT GGCCTAGATT ATTGACAATC CCAATATATC AATTTTCTT TAAAGTAGT 1980
ACAATTTCTT TTGTAGCTTC AATTCTTAT ATGACTTCAG ACTGGAGAAG CCTGTTAAAC 2040
CACTGTAGT TCCAGTATGA AAGTCTGAGA GACTTTATAC ATAAATCTC AATTGGCTG 2100
CTGTACACT GCACAGATT TACTACTGTA GTGACCGTTG AGAAGACCTT TGTATTATTA 2160
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TTACTTCATG TCCAGGGGTG CTATTTACCT AGAACCATG TCTACTACAA TTAACATTTA 2280
CATTACAAG TGTTGTGTTT TCTTTTCAA GGAGGTTCAA TTAAGGCAAT AAGATGTTG 2340
CTGGAGAAAC CTATTGTTTA CTGAAAGCAC TCAATGAAGT CAAATTACTG AAGCTTTTGC 2400
CTACACTTG GTCTTTTATG TAAATATGTT AAATATAACA TCTAAGGAAA ATAAACAATA 2460
TTATAATTAT GTGTTTGCCA TTGTCATATC AAACCTGCTT TGTATCATAC TAATGTTACA 2520
TAACCTATCG ATCAATAAAA ATACATTTC AATGTT

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45 Seq ID NO: 253 DNA sequence
Nucleic Acid Accession #: NM_001650.2
Coding sequence: 40.1011

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AGGCGGTGGG GTAAGTGTGG ACCTTTGTGT ACCAGAGAGA ACATCATGGT GGCTTTCAAA 120
GGGCTCTGGA CTCAGCTTTT CTGGAAAGCA GTCCAGCGG AATTCTCTGC CATGCTTATT 180
TTTGTCTCC TCAGCCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG 240
GTGACATGG TTCTCATCTC CCTTGTCTT GGACTCAGCA TTGCAACCAT GGTGCACTGC 300
TTTGGCCATA TCAGCGGTGG CCACATCAAC CTGTCAGTGA CTGTGGCCAT GGTGTGCACC 360
AGGAAGATCA GTCTGTCGCA GTCTGTCTTC TACATGCGAG CCCAGTGCCT GGGGGCCATC 420
ATTGGAGCAG GAATCCTCTA TCTGTGCACA CCTCCAGTG TGGTGGGAGG CCTGGGAGTC 480
ACCATGTTTC ATGGAATCT TACCGCTGGT CATGCTCTCC TGGTTGAGTT GATAATCACA 540
TTTCAATTGG TGTATTATAT CTTTGCCAGC TGTGATTCCA AACGGACTGA TGTCACTGGC 600
TCAATAGCTT TAGCAATTGG ATTTTCTGTT GCAATTGGAC ATTTATTGTC AATCAATTAT 660
ACTGGTGCCA GCATGAATCC CGCCCGATCC TTTGGACCTG CAGTTATCAT GGGAAATTGG 720
GAAAACCATT GGAATATATG GGTGGGGCCC ATCATAGGAG CTGTCTCTGC TGGTGGCCTT 780
TATGAGTATG TCTTCTGTCC AGATGTTGAA TTCAACGTC GTTTTAAAGA AGCCTTCAGC 840
AAAGCTGCCC AGCAACAAAG AGGAAGCTAC ATGGAGGTGG AGGACAACAG GAGTCAGGTA 900
GAGACGGATG ACCTGATTCT AAAACCTGGA GTGGTGCAATG TGATTGACGT TGACCGGGGA 960
GAGGAGAAGA AGGGGAAAGA CCAATCTGGA GAGGTATTGT CTTCAATATG ACTAGAAGAT 1020
CGCACTGAAA GCAGACAGA CTCCTTAGAA CTGTCTCAG ATTTCTCTCC ACCCATTAAG 1080
GAAACAGATT TGTATATAAT TAGAAATGTG CAGGTTTGT GTTTCATGTC ATATTACTCA 1140
GTCTAAACAA TAAATATTTC ATAATTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT 1200
TCCAAATCTA AAAAAAGAAA TATTTTAAAG ATGTTCTTAA GCAAAATATAT ACCTATTTTA 1260
TCTAGTTACC TTTCAATTAAC AACCAATTTT AACOGTGTGT CAAGATTGTT TTAAGTCTTG 1320
CCTGACAGAA CTCAAAGACA CGTCTATCAG CTTATTCTCT CTCTACTGGA ATATTGTTAT 1380
AGTCAATTCT TATTGGAATA TTTATTCTAT TAAACTGAGT TTAACAAATG C

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75 Seq ID NO: 254 Protein sequence
Protein Accession #: NP_001641.1

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1 11 21 31 41 51
| | | | |
MSDRPTARRW GKCGPLCTRE NIMVAFKGVW TQAFWKAVTA EPLAMLIPVL LSLGSTINWG 60
GTEKPLPVDV VLIISLCFGLS IATMVQCFGE ISGGHINPAV TVAMVCTRKI SIAKSVFYIA 120
AQCLGAIIGA GILYLVTPPS VVGGLGVTMV HGNLTAGHGL LVELIITFQL VFTIFASCD 180
KRTDVTGSIA LAIGFSVAIG HLPFAINYGA SMNPARSPGP AVINGNWEKH WIYVVGPIIG 240
AVLAGGLLEY VPCPDVEPIR RFKEAFSKAA QOTKGSYMEV EDNRSQVETD DLILKPGVVH 300

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VIDVDRGEEK KGKQDSGEVL SSV

Seq ID NO: 255 DNA sequence

Nucleic Acid Accession #: U26742.1

Coding sequence: 325..1449

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1	11	21	31	41	51	
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GGCAGCGGAC	CCGGCACTTC	CAACATTATT	AAATAATAAG	AAAGCGGCTC	CTACTCCAGG	120
CTCAACACCTC	CCTGCAGACC	AATGGACACC	TTCTAAGAGT	TTGGCGAGTC	AGTGACTGAA	180
GGGCCCCGTC	ATTCCAAGAT	AAATAGGATT	TACCAATCCT	TGGATGAAGT	GCTTGGGAAG	240
TCITTTAAGTG	CCATAATCAA	CTGCCATTTC	AAAGAATATA	GATGGTTTTC	AAAAGTTCAT	300
GCTGTCCCTT	CATTGAATTT	TAGAATGATT	GAAGATAGTG	GGAAAAGAGG	AAATACCATG	360
GCAGAAAGAA	GATCGCTGTT	TGCAGAGATG	AGGGCTCAAG	ATCTGGATCG	CATCOGACTC	420
TCCACCTACA	GAACAGCATG	CAAGCTTAGG	TTTGTTTACA	AGAAATGCAA	TTTGCACTCG	480
GTGGACATAT	GGAATGTGAT	AGAAGCATTC	CGGGAATAAT	CTCTGAACAA	CCTGGACCCA	540
AACACTGAAC	TCAACGTGTC	COGCTTAGAG	GCTGTGCTCT	CCACTATTTT	TTACCAGCTC	600
AACAAACGGA	TGCCAACACC	TCACCAAAATC	CATGTGGAGC	AGTCCATCAG	CCTCCTCCTT	660
AACCTTCTCG	TTGCAGCGTT	TGATCCGGA	GGCCATGGTA	AAATTTCACT	ATTTGCTGTC	720
AAATATGGCTT	TAGCCACATT	GTGTGGAGGG	AAGATCATGG	ACAAATTAAG	ATATATTTTC	780
TCAATGATTT	TGACTCCAG	TGGGGTGATG	GTTTATGGAC	GATATGACCA	ATTCCTTCGG	840
GAAGTCTCA	AACATACCCAC	GGCAGTTTTT	GAAGGTCCCT	CATTGTGGTA	CACAGAACAG	900
TCAGCCAGAT	CCTGTTTCTC	CCACAGAGAA	AAAGTCACGT	TAAATGGTTT	CTTGACACCG	960
CTTATGTCAG	ATCCTCCCCC	GCACTGTCTG	GTCTGGTTGC	CTCTCTGCA	TCGACTAGCA	1020
AATGTGGA	ATGCTCTCCA	TCCGGTTGAG	TGTTCTCTACT	GCCACAGTGA	GAGTATGATG	1080
GGATTTTCCT	ACCGATGCCA	ACAGTGTGAC	AATTACCCAGC	TCTGTCAGGA	CTGCTTCCTG	1140
AGGGGACATG	CCGGTGGTTT	TCATAGCAAC	CAGCACCAAA	TGAAAGAGTA	CAOGTCATGG	1200
AAATCACCTG	CTAAGAACCT	GACTAATGCA	TTAAGCAAGT	CCCTGAGCTG	TGCTTCCAGC	1260
CGTGAACCTT	TGCACCCCAT	GTTCCAGAT	CAGCCTGAGA	AGCCACTCAA	CTTGGCTCAC	1320
ATGTTTGATA	CTTGGCCTCC	CAGACCTGTA	ACCAGCATGA	ACGACACCTT	GTTCTCCAC	1380
TCGTGTTCCCT	CCTCAGGAAG	TCCTTTTATT	ACCAGGAGCT	CGGACGGTGC	TTTGGTGGGA	1440
TGCGTCTAGA	TGGATAACAT	GACTTCTTCT	ACCTTAAAT	ATTCTATATA	TACTTTGAGC	1500
TGTTCTGGTT	CCTCCAGGGT	GCAATGTAACC	CATTAAACCA	AAATATGATT	ATTTCCCTTT	1560
TTTCCCATTT	TCAGTCAATT	TGGAATGTTT	TCTGTGAACC	ACAGTTGGGT	TGTTTAAAGC	1620
TCACATTTCT	TTCTGTCAAC	ACAGAGATTG	GCCTACGGTT	TCTGTTTGA	GGGTGCTGTT	1680
CAATAAGCT	GTGTACACTA	AATGTCC				

Seq ID NO: 256 Protein sequence

Protein Accession #: AAC50424.1

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1	11	21	31	41	51	
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ALRENALNNL	DPNELNVSR	LEAVLSTIFY	QLNKRMPPTH	QIHVEQSISL	LINFLAAFD	120
PEGHGKISVF	AVKMLATLC	GGKIMDKLRY	IFSMISDSSG	VMVYGRYDQF	LRVLEKLFTA	180
VFEQPSFGYT	EQSARSCFSQ	QKVTLLNGFL	DTLMSDPFPQ	CLVWLPPLHR	LANVENVFHP	240
VECSYCHSES	MMGFYRRCQ	CHNYQLQDCD	FWRGHAGGSH	SNQHQMKBYT	SNKSPAKILT	300
NALSKSLSCA	SSREPLHPMF	PDQPEKPLNL	AHIVDTWPPR	PVTSMNDTLF	SHSVPSGSP	360
FITRSSDGA	GGCV					

Seq ID NO: 257 DNA sequence

Nucleic Acid Accession #: NM_004172.1

Coding sequence: 179..1807

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1	11	21	31	41	51	
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TGTGGGTGAT	TCCAGACAC	TGAAGTGCAA	AGAAGAGACC	CTCCTAGAAA	AGTAAATAT	180
GACTAAAAGC	AATGGAGAAG	AGCCCAAGAT	GGGGGCGAGG	ATGGAGAGAT	TCCAGCAGGG	240
AGTCCGTAA	CGCACACTTT	TGGCCAAGAA	GAAAGTGACG	AACATTACAA	AGGAGGATGT	300
TAAAGTTAC	CTGTTTGGGA	ATGCTTTTGT	GCTGCTCACA	GTCAACGCTG	TCAATGTGGG	360
TACAATCCTT	GGATTTACCC	TCCGACCATA	CAGAATGAGC	TACCGGGAAG	TCAAGTACTT	420
CTCCTTTCCT	GGGGAACCTC	TGATGAGGAT	GTTACAGATG	CTGGTCTTAC	CACCTATCAT	480
CTCCAGTCTT	GTCAACAGAA	TGGCGGCGCT	AGATAGTAAG	GCATCAGGGA	AGATGGGAAT	540
GCGAGCTGTA	GTCTATTATA	TGACTACCA	CATCATTGCT	GTGGTGATG	GCATATCAT	600
TGTCATCATC	ATCCATCCTG	GGAAGGCGAC	AAAGGAAAAC	ATGCACAGAG	AAGGCAAAAT	660
TGTACGATG	ACAGCTGCAG	ATGCCCTTCT	GGACTTGATC	AGGAACATGT	TCCCTCCAAA	720
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GCCCATCCAG	GCCACGAGAA	CGCTTGTGGG	TGCTGTGATA	AACAATGTGT	CTGAGGCCAT	840
GGAGACTCTT	ACCCGAATCA	CAGAGGAGCT	GGTCCAGTTC	CCAGGATCTG	TGAATGGAGT	900
CAATGCCCTG	GCTGTAGTTG	TCTTCTCCAT	GTGCTTCGGT	TTTGTGATTG	GAAACATGAA	960
GGAAACAGGG	CAGGCCCTGA	GAGAGTCTTT	TGATTCTCTT	AACGAAGCCA	TCATGAGACT	1020
GGTAGCAGTA	ATAATGTGGT	ATGCCCCCGT	GGGTATTCTC	TTCTGATTG	CTGGGAAGAT	1080
TGTGGAGATG	GAGACATG	GTGTGATTGG	GGGGCAGCTT	GCCATGTACA	CGTGACTGTT	1140
CATTGTTGGC	TTACTCATTC	ACGCAGTCAT	CGTCTTGCCA	CTCCTCTACT	TCITGGTAAC	1200
ACGGAAAAAC	CCTTGGGTTT	TTATTGGAGG	GTTGTGCA	GCACCTCATCA	COGCTCTGGG	1260
GACCTCTTCA	AGTTCTGCCA	CCCTACCCAT	CACCTTCAAG	TGCTTGGGAG	AGAACATGAG	1320
CGTGGACAAG	CGGCTACCCA	GATTCTGTCT	CCCGTAGGGA	GCCACCATTA	ACATGGATGG	1380
GACTGCGCTC	TATGAGGCTT	TGGCTGCCAT	TTTCATTGCT	CAAGTTAACA	ACTTTGAATC	1440
GAACCTCGGA	CAAATTATTA	CAATCAGCAT	CACAGCCACA	GCTGCCAGTA	TTGGGGCAGC	1500
TGGAATTCCT	CAGGGGGGCC	TGGTCACTAT	GCTCATTTGT	CTGACATCTG	TGGGCTGCC	1560
CACAGACGAC	ATCAAGCTCA	TCATCGCGGT	GGACTGGTTC	CTGGATGCC	TCCGACCA	1620

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CACCAACGTA CTGGGAGACT CCCTGGGAGC TGGGATTGTG GAGCACTTGT CACGACATGA 1680
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 TTCTGACTGG TATACCTATT TCATTAGTAG CTAGGTGCAC ATATACATCT AGCAGAGCTG 2340
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 ATTACAAACA AAGGATTGTA AAACACCAAG AGTACAGGTC TTCTTAAAGG AAGAATAAAA 2940
 AAGAAGAGGT TCAATTTTCT GGCCTTTTCT TTCACTGAA ACACCTTTTC TOGAGTCCAA 3000
 AATCATTTCC CCCGTGAAGT CTGCTTACCA AAACATAAGA CGACTTATAT AITTTGAAAGA 3060
 AGTCAAAATGA ATGAGCTCTC TAATAGAAGT CCATGAGTTG AGTGGGTATT TCTTATTGTA 3120
 AAGTGTTTTT CTTTAATCAA AAGTCTTAG AATGAGGGAA ACAAAATATT TATTGTGTTT 3180
 GGAATCCCAT TTATCAATC ATTCAAAATC TTCAGCTGGA GTGGGGTTTG CTTTGTGTTT 3240
 GTTTGTGTC ATTAAGAGAAA TGGTAGAAGA TGAATCAGTA TGAAGACACT GTCAATGAGG 3300
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 TTAATTTTAA CCCCTAAGG AATATCCAGT CAAAGACGCT GAGTGGGAGC TGTCAAGGAG 3420
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 GAGGCTCTAT TTCGGAATA CACTACAAAT GTTAAAGTAC GTGGCTGTCC TCTTAAAGCA 3660
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 ATATACTAAC CATTTCTTAT GGAAAGGTCC TGTGGGAGC CCATCTCTC GCCAAGCCAT 3780
 CACAGGCTCT GCATACACAT GCACCTAGTG TGGACTGGGA AGCATTACTT TGTAGATGTA 3840
 TTTTCAATAA AGAAAAAAAT AGTTTTACAT T

Seq ID NO: 258 Protein sequence
 Protein Accession #: NP_004163.1

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 MRAYVYVMTT TIIAVVIGII IVIIHPGKG TKENMHREGK IVRVTAADAF LDLIRNMFPP 180
 NLVEACRQF KTNYEKRSEK VPIQANETLV GAVINNVSEA METLTRITEE LVPVPGSVNG 240
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 IVEMEDMGVI GGQLAMYTVT VIVGLLIHAF IVLPLLYFLV TRKNPWFVIG GLLQALITAL 360
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Seq ID NO: 259 DNA sequence
 Nucleic Acid Accession #: NM_021948.1
 Coding sequence: 48..2783

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	GAGAGTCAGA	AGCTTCCAGG	CCTCCAAGGG	TCCATGGACC	ACCTACTGAG	ACTCTGCCCA	1680
	CTCCCAGGGA	GAGGAACCTA	GCATCCCCAT	CACCTTCCAC	TCTGGTTGAG	GCAAGAGAGG	1740
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15	CAOGAAGGAG	CTGGGAGGAG	GCAGAGACCC	AGTGCCGGAT	GTACGGCGCG	CATCTGGCCA	2220
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	TCCGACTCAA	CGACAGGACC	ATCGAAGGCG	ACTTCTTGTG	GTCCGATGGC	GTCCCCCTCG	2340
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	GGGAAGGACT	GGCCAGCGC	AATCTGCGCG	TGATCOGATG	CCAAGAGAAC	GGTCGTTGGG	2640
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25	CCAGCCCCAT	GCCAGGTCCC	TAGGGGCAA	GGCCTTGAAC	ACTGCGGGCC	ACAGCACTGC	2820
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Seq ID NO: 260 Protein sequence
Protein Accession #: NP_068767.1

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35	SLALSELREN	DSGIYRCEVQ	HGIDSSDAV	EVKVKGVVFL	YREGSARYAF	SFSGAQEACA	180
	RIGAHIAIPE	QLYAAYLGYY	EQCDAGWLS	QTVRYPIQTP	REACYGMDG	FPVGRNYGVV	240
	DPDDLVDVYC	YASDLNGLF	LGDPPEKLT	BEARAYCQER	GABIAITGQL	YAAWDGGLDH	300
	CSPGWLADGS	VRYPITVPSQ	RCGGGLPGVK	TLFLFPNQTG	FPNKHRSFNV	YCFRDSAQFS	360
	AIPEASNPAS	NPASDGLBAI	VTVTETLEEL	QLPQBATESE	SRGAIYSIPI	MEDGGGSSST	420
40	PEDPABAPRT	LLEFETQSMV	PPTGFSSEEG	KALEEEKERYE	DEBEKEBEE	EEVEDEALN	480
	AWPSLSSPG	PEASLPTPEA	AQEBLSQAP	ARAVLQPGAS	PLPDGSEAS	RPFVRVHGPT	540
	ETLPTPRERN	LASPSSTLV	EAREVGEATG	GPGLSGVPRG	ESEETGSEEG	APSLLPATRA	600
	SEGTRELEAP	SEDNSTRTAP	AGTSVQAQPV	LPTDSASRGG	VAVVPASGDC	VSPCHNGGT	660
	CLEEBEGVRC	LCLPGYGGDL	CDVGLRFCNP	GNDAPQAGCY	KHFSTRRSWE	EAEQTCRMYG	720
45	AHLASISTPE	BQDFINNRYY	EYQWIGLND	TIEGDFLWSD	GVPLLYENWN	PQGPDSYFLS	780
	GENCVVMVWH	DQQWSDVPC	NYHLSYTKM	GLVSCGPPPE	LPLAQVFGPR	RLRYEVDTVL	840
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Seq ID NO: 261 DNA sequence
Nucleic Acid Accession #: NM_004386.1
Coding sequence: 2..3967

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	CCCCACGTCA	CAACATGGAG	ACCTAGAGAC	CCCATCCTCT	GGGGATGAGG	GGGAGATTCT	1140
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 Protein Accession #: NP_004377.1

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Seq ID NO: 264 Protein sequence
Protein Accession #: Bos sequence

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SSVKSEVKES KDFIKPKLVT VIRSGVKPRK AVRILLNKKT AHSFEQVLTD ITEAIKXASG 240
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YKIGKVIGDG NFAVVKECID RSTGKEFALK IIDKAKCCGK EHLENEVSI LRRVKHPNII 420
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Seq ID NO: 265 DNA sequence
Nucleic Acid Accession #: AB020684.1
Coding sequence: 1..1744

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CATATATGGC ACATATTAA GTGGCAGCCG ATTAGGAGGC CTGGTTACAG TGTGTGCTTT 300
CTTTTCAAT CATGGAGAGT GTACCCGTGT AATGTGGACA CCACCTCTCC GTGAAAGCTT 360
CTCATATCCA TTCTTGTTTC TTCAGATGTT GCTAGTGACT CATATTCTCA GGGCTACAAA 420
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5 CGGTGGACAC TTGAGGCTGA GGATGGGAGT TGACATGAGC AGGGAGAGGG AGGTGCGCGC 3660
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 15 GAAAGTATGT ATCAGGAATA AAGTGATATT GCATAGGAGT ATGTATTTT TATGAATTTT 4380
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Seq ID NO: 266 Protein sequence

Protein Accession #: BAA74900.1

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 SYPFLVLQML LVTHILRATK LVRGSLIAJC ISNVFMLPW QPAQFVLLTQ IASLFAVVVV 180
 25 GYIDICKLRK IYIHMISLA LCFVLMFNS MLLTSYASS LVIINGILAM KPHFLKINVS 240
 ELSLWVIQGC FALPGTVILK YLTSKIFGIA DDAHIGNLLT SKFPSYKDFD TLLYTCAAEF 300
 DPMKEKTEPLR YTKLFLPVV LVVFAIVRK IISDMWGLA KQQTIVRKHQ FDHGLVYHA 360
 LQLLAYTALG ILIMRLKPL TPHCMVASL ICSRQLFGWL FCKVHPGATV FAILAAMSIQ 420
 GSNALQTNW IVGBFSNLPQ EELIEWIKYS TKPDVAFAGA MPTMASVKLS ALRPIVNHPP 480
 30 YEDAGLRART KIVYSMSRK AAEVKRELI KLKVNYYILE ESWCVRSSKP GCSMPEIMDV 540
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Seq ID NO: 267 DNA sequence

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Coding sequence: 59..1600

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Seq ID NO: 268 Protein sequence

Protein Accession #: AAC50426.1

1 11 21 31 41 51
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 PEGHGKISVF AVKMALATLC GKKIMDKLRY IFSMISDSSG VMVYGRYDQF LREVLKLPTE 180
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 5 VECSYCHSES MMGFYRYCQQ CHNYQLQDQC FWRGHAGGSH SNQHQMKEYT SWKSPAKKLT 300
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Seq ID NO: 269 DNA sequence

Nucleic Acid Accession #: NM_001276.1

Coding sequence: 127..1278

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Seq ID NO: 270 Protein sequence

Protein Accession #: NP_001267.1

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 KSVPPFLRTH GFDGLDLAWL YPGRDKQHF TTLIKEMKAE FIKEAQPGKK QLLLSAALSA 180
 60 GKVTIDSSDY IAKISQHLDF ISIMTYDFHG AWRGTTGHS PLFRQEDAS PDRFSNTDYA 240
 VGYMLRLGAP ASKLVMGIPT FGRSPTLASS ETGVGAPISG PGIPGRFTKE AGTLAYYEIC 300
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Seq ID NO: 271 DNA sequence

Nucleic Acid Accession #: NM_006474.1

Coding sequence: 181..669

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 GCCTCAAAAG TGGCCACAG TCACTCCAGC GAGAAAGTGG ATGGAGACAC ACAGACAACA 540
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 TCTGACTCT GTGGCCCTGT CCTGAGCTC GTGGGAGAGG GATGACCTG GGAACATTG 780
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Seq ID NO: 272 Protein sequence
 Protein Accession #: NP_006465.1

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 | | | | |
 MWKVSALLFV LGSASLWVLA EGASTGQPED DTBTGLLEGG VAMPGAEDDV VTPGTSEDRY 60
 KSLGLTLVAT SVNSVTGIRI EDLPT9ESTV HAQEQSPSAT ASNVATSHST EKVGDGTQTT 120
 10
 VEKDLSTVT LVGIIVGVLL AIGFIGGIIV VVMKMSGRY SP

Seq ID NO: 273 DNA sequence
 Nucleic Acid Accession #: CAT cluster

15
 1 11 21 31 41 51
 | | | | |
 GCGGCGGCCA GCTTGCAAG CCGAAGTCTG GCCGGCTCT TCGACTCGCT GCGCCACGTC 60
 CCGGGGGGTG CCGAGCCGGC GGGGGGTGAG GTGGCTGGGC CGGCGGCCGG GCTAGGAGGT 120
 GCGGGCACTG GGGGCGGGGG AGGGGACGTG GCAGGCCCGG CGGGGGCCAC GCGGATCCCA 180
 20
 GGGGCCAGGA AGGTCCCGCT GCGGGCAAGC AATCTGCCTC GTCCTTCTT CACGAGAGCG 240
 TCCCGGGCAG GCGGCGGGGG GTGTGGCCGG TCGGGGCGGG ACGTGAGCTT GGGCGACCTG 300
 GAGAAGGGCG CGGAGGCCGT GGAGTTCTTT GAGCTGCTGG GGCCGACTA CGGCGCCGGC 360
 ACGGAGGGCG CAGTCTTGCT TGCCCGCCGAG CCTCTGAGCG TGTTCGCCGC CGGAGCCTCC 420
 25
 GTACTGCGGG GACCCCGGGA GCTGGAGCCC GGCTCTTTG AGCCGCCGCC GGCAGTGGTG 480
 GGAAGACTAC TGTACCCCGA GCGCTGGAGC GTCCCGGGCT GCTCCCGGAC CAAAAGAGC 540
 CCTTGAAGTG CCTCCCGGG CGGGTTGACC TTGAACGAGC CCTTGAGCCC CCTGTACCCC 600
 GCCGCTGCGA ATTTCTCCCG GCGGGGAGGA CGGGCCGGGC CATTGGGCTT CTTTCGCCCC 660
 CTTCTTCCA GACTGCGCTT TGC

30
 Seq ID NO: 274 DNA sequence
 Nucleic Acid Accession #: Eos sequence

35
 1 11 21 31 41 51
 | | | | |
 CAAAGAGGCC GGGCTCCAGC TCCGGGGGTC CCGCAGTAC GGAGGCTCCG GCGGGGAACA 60
 CGTCGAGAGG CTGCGCGGCA AGCAAGACTG CGGCTCCGTT GCGCGGCGCG TAGTCGGGCC 120
 CCAGCAGCTC AAAGAAGTCC AGCGCTCCG CGGCTTCTC CAGGTGCGCC AAGCTCACGT 180
 40
 CCGGCCCGCA CGGGCCACAC CCGCGCGGCG CTGCCCGGGA CGGCTCGGTG AAGAAGGAGC 240
 GAGGCAGATT GCGTGCCCGC AGCGGGAGCT TCCTGGCCCC TGGGATCGCC GTGGCCCCCG 300
 CGGGGCGCTG CAGTCCCGCT CCGCGGCCCG CAGTGCCGCG ACCTCCTAGC CGGCGCGCGC 360
 GCGCAGCCAC CTCACCCCCC GCCGCTCCGG CACCCCGGGG GACGTGGCGC AGCGAGTCGA 420
 AGAGCGGGCG CAGACTTCGG CTTTGCAAGC TGGCGGCGCG

45
 Seq ID NO: 275 DNA sequence
 Nucleic Acid Accession #: NM_001118.1
 Coding sequence: 74..1651

50
 1 11 21 31 41 51
 | | | | |
 AGCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGTG 60
 GCCAAGAGT GTCATGGCTG GTGTGCTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCGTG 120
 TCCGTGGGGC CCGGGCAGAC TCCGCAAGAG ACGCGCAGCC TGCAAGTCCG CGGCCAGAG 180
 ACACATTGGG GCTGACCTGC CGCTGCTGTC AGTGGGAGGC CAGTGGTGTG GGCCAAGAG 240
 55
 TGTCTAGGCT GGTGTGCTGC ACGTTTCCCT GGCTGCTCTC CTCTGCTGTC CTATGGCCCC 300
 TGCCATGCAT TCTGACTGCA TCTTCAAGAA GGAGCAAGCC ATGTGCTCTG AGAAGATCCA 360
 GAGGGCCAAAT GAGCTGATGG GCTTCAATGA TTCTCTTCCA GGCTGTCTG GATGTGGGA 420
 CACATCAAGC TGTTGGAAGC CCGCCCATGT GGGTGAGATG GTCTGTGTCA GCTGCCCTGA 480
 GCTCTTCCGA ATCTTCAACC CAGACCAAGT CTGGGAGACC GAAACCAATG GAGAGTCTGA 540
 60
 TTTTGGTGAC AGTAATCTCT TAGATCTCTC AGACATGGGA GTGGTGAGCC GGAAGTGCAC 600
 GGAGGATGGC TGCTCGGAAC CCTTCCCTCA TTACTTTGAT GCCTGTGGGT TTGATGAATA 660
 TGAATCTGAG ACTGGGGACC AGGATTATTA CTACCTGTCA GTGAAGGCC TCTACAAGGT 720
 TGGCTACAGC ACATCCCTCG TCACCTTCAC CACTGCCATG GTCATCTTTT GTGCTTCCG 780
 GAAGCTGCAC TGCACACGCA ACTTCATCCA CATGAACCTG TTTGTGTGT TCAITGCTGAG 840
 65
 GCGATCTCC GTCTTCATCA AAGACTGGAT TCTGTATGCG GAGCAGGACA GCAACCACTG 900
 CTTTACTTCC ACTGTGGAAT GTAAGGCCGT CATGGTTTTC TTCCACTACT GTGTTGTGTC 960
 CAACTACTTC TGGCTGTTCA TCGAGGGCCT GTACCTCTTC ACTCTGCTGG TGGAGACTTT 1020
 CTTCCCTGAA AGGAGATACT TCTACTGGTA CACCATCATT GGTGGGGGGA CCCCACATGT 1080
 GTGTGTGACA GTGTGGGCTA CGCTGAGACT CTACTTTGAT GACACAGGCT GCTGGGATAT 1140
 70
 GAATGACAGC ACAGCTCTGT GGTGGGTGAT CAAAGGCCCT GTGGTTGGCT CTATCATGTT 1200
 TAATCTTTTG CTTTATTATG GCATTATOGT CATCTTGTG CAGAAACTTC AGTCTCCAGA 1260
 CATGGGAGGC AATGAGTCCA GCATCTACTT GCGACTGGCC CGGTCCACCC TGCTGCTCAT 1320
 CCCACTATTG GGAATCCACT ACACAGTATT TGCCCTTCCG CCAGAGAATG TCAGCAAAAG 1380
 75
 GGAAGAGCTC GTGTTTGAGC TGGGGCTGGG CTCCTTCCAG GGCTTTGTGG TGGCTGTCTT 1440
 CTACTGTTTT CTGAATGGTG AGGTACAAGC GGAGATCAAG CGAAAATGGC GAAGCTGGAA 1500
 GGTGAACCGT TACTTCGCTG TGGACTTCAA GCAACGACAC CGTCTCTGCG CCAGCAGTGG 1560
 GGTGAATGGG GGCACCCAGC TCTCCATCCT GAGCAAGAGC AGCTOCCAAA TCCGATGTC 1620
 TGGCTTCCCT GCTGACAATC TGGCCACCTG AGCCATGCTC CCT

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 Seq ID NO: 276 Protein sequence
 Protein Accession #: NP_001109.1

1 11 21 31 41 51
 | | | | |
 MAGVVHVSIA AHGACPNWR GRLRKGRAAC KSAAQRHIGA DLPLLSVGQ WCNPRSVMAG 60

VVHVSLAALL LLEPMAPMHS DCIFPKKEQAM CLEKIQORANE LMGFNDSPPG CPGMMDNITC 120
 WKPAHVGEV LVSCPELPRI FNPQVNETE TIGESDFGDS NSLDLSDMGV VSRNCTEDGW 180
 SEPPPHYFDA OGFDEYESET GDQDYFYSV KALYTVGYST SLVLITAMV ILCRPRKLC 240
 TRNFHMLP VSFMLRAISV FIKDWILYAE QDSNHCFTST VECRAVMVFP HYCVVSNYFW 300
 LFIEGLYLFT LLVETFFPER RYFYWTIIG WGTPTVCVTV WATLRLYFDD TGCHMDNDST 360
 ALWWVIRKPV VGSIMVNFVL FIGIIVILVQ KLQSPDMGNN ESSYLRRLAR STLLLIPLFG 420
 IHYTVFAPSP ENVSKRERLV FELGLGSFQG FVVAVLYCPL NGEVQAEIKR KWSWKVWRY 480
 FAVDFKRRHP SLASSGVNGG TQLSILSKSS SQIRMSGLPA DNLAT

Seq ID NO: 277 DNA sequence
 Nucleic Acid Accession #: NM_004000.1
 Coding sequence: 36..1193

1 11 21 31 41 51
 AGAAGAAGCT GGCCAAGGAT ATGGGAGCAA CCACCATGGA CCAGAAGTCT CTCTGGGCAG 60
 GTGTAGTGGT TTGCTGCTT CTCCAGGAG GATCTGCCTA CAAACTGGTT TGCTACTTTA 120
 CCAACTGTGC CCAGGACCGG CAGGAACGAG GAAAATTCAC CCCTGAGAAT ATTGACCCCT 180
 TCCTATGCTC TCATCTCATC TATTCATTCG CCAGCATCGA AAACAACAAG GTTATCATCA 240
 AGGACAAGAG TGAAGTGATG CTCTACCAGA CCATCAACAG TCTCAAAACC AAGAATCCCA 300
 AACTGAAAT TCCTTGCTCC ATTGAGAGGT ACCTGTTTGG TTCCAAAGGG TTCCACCCCTA 360
 TGGTGATTC TTCTACATCA CGCTTGGAAAT TCATTAATC CATAATCCTG TTTCTGAGGA 420
 ACCATAACTT TGATGGACGT GATGTAAGCT GGATCTACCC AGATCAGAAA GAAACACTC 480
 ATTTCACTGT GCTGATTCAT GAGTTAGCAG AAGCCTTTCA GAAGGACTTC ACAAATCCA 540
 CCAAGGAAAG GCTTCTCTTG ACTGCGGGCG TATCTGCAG GAGGCAATG ATTGATAACA 600
 GCTATCAAGT TGAGAACTG GCAAAAGATC TGGATTTTCA CAACCTCCTG TCCTTTGACT 660
 TCATGGGTCT TTGGGAAAG CCCCTTATCA CTGGCCACAA CAGCCCTCTG AGCAAGGGGT 720
 GGCAGGACAG AGGGCCACAG TCCTACTACA ATGTGGAATA TGCTGTGGGG TACTGGATAC 780
 ATAAGGAAAT GGCATCAGAG AAGGTGGTCA TGGGCATCCC CACATATGGG CACTCCTTCA 840
 CACTGGCCTC TGCAGAAACC ACCGTGGGGG CCCCTGCTC TGGCCCTGGA GCTGCTGGAC 900
 CCATCAGAGA GTCTTCAGGC TTCCTGGCCT ATTATGAGAT CTGCCAGTTC CTGAAAGGAG 960
 CCAAGATCAC GCGCCTCCAG GATCAGCAGG TTCCTACGC AGTCAAGGGG AACCAAGTGG 1020
 TGGGCTATGA TGATGTGAAG AGTATGGAGA CCAAGGTTCA GTTCTTAAAG AATTAAACC 1080
 TGGAGGAGC CATGATCTGG TCTATTGACA TGGATGACTT CACTGGCAAA TCCTGCAACC 1140
 AGGGCCCTTA CCTCTTTGTC CAAGCAGTCA AGAGAAGCCT TGGCTCCTTG TGAAGGATTA 1200
 ACTTACAGAG AAGCAGGCAA GATGACCTTG CTGCTGGGG CCTGCTCTCT CCCAGGAATT 1260
 CTCATGTGGG ATTCCCTTGG CCAGGCTGGC CTTTGGATCT CTCCTTCAAG CCTTCTCTGA 1320
 CTCCTCTTTA GATCATAGAT TGGACCTGGT TTTGTTTCC TGCAGCTGTT GACTTGTGTC 1380
 CCTGAAGTAC AATAAAAAA ATTCATTTTG CTCAGTA

Seq ID NO: 278 Protein sequence
 Protein Accession #: NP_003991.1

1 11 21 31 41 51
 MDQKSLWAGV VVLLLLQGGG AYKLVCYFTN WSQDRQEPGK FTPENIDPFL CSHLIYSFAS 60
 IENNKVILKD KSEVMYQTI NSLKTNPKL KILLSIGGYL FGSKGPHPMV DSSTRLEFI 120
 NSIILPLRNH NFDGLDVSWI YPDQKENTHF TVLIHELAE FQKDFTKSTK ERLLLTAGVS 180
 AGRQIMDSNY QVSKLAKLDL FINLLSDFDH GSWKEPLITG HNSPLSKGWQ DRGPSYINV 240
 EYAVGWVHK GMPSEKVMVG IPTYGHSPFL ASAETTGVAG ASGPAAAGPI TESSGFLAYY 300
 EICQFLKGAQ ITRLDQQVQ YAVKGNQWVQ YDDVKSMETK VQFLKNLNLG GAMINSDMD 360
 DFTGKSCNQG PYPLVQAVKR SLGSL

Seq ID NO: 279 DNA sequence
 Nucleic Acid Accession #: NM_015166.1
 Coding sequence: 116..1249

1 11 21 31 41 51
 TGCTGGAAGT CCTCAACCA GAGACCAAGT CTCCCAACGG CAGAGCAGCG GGGGAGATAA 60
 AGAAGTGGTG ACAGCTGGCT GTACATTCAG CACAGCTGTG GTGTCCCAA GTGCCATGAC 120
 CCAGGAGCCA TTCAGAGAGG AGCTGACCTA TGACCGGATG CCCACGCTGG AGCGGGGCGG 180
 GCAAGACCCC CCAGCTATG CCCCAGACGC GAAGCCGAGC GACCTGCAGC TGTGGAAGAG 240
 ACTGCCCCCC TGCTTCAGCC ACAAGACGTG GGTCTTCTCT GTGCTGATGG GGAGCTGCCT 300
 CTGGGTGACC TGGGGGTTTT GCTGTACCT GGGGAACGTG TTCCCGGCTG AGATGGAITA 360
 CTGCGCTGT GCTCAGGCT CTTCATCCC CTCCGCAATT GTGAGCTTCA CGTCTCCAG 420
 GAGGAACGCC AATGTGATTC CCAACTTTC AATATTGTTT GTTCCACGT TTGCTGTGAC 480
 CACTAGTGT TTAATTGGT TTGGATGCAA ACTAGTCTG AACCCATCAG CAATAAACAT 540
 CAACTTCAAC CTATCTCTGC TGCTCTGCT GAGAGTCTC ATGGGCGCCA CGGTGATCAT 600
 CGCTGCACGG TCCAGCGAGG AGGACTGCAA GAAAAGAAAG GGCTCCATGT CTGACAGGCG 660
 CAACATTCTG GACGAAGTGC CATTTCTGCT TCGGTCCTG AAATCTTACT CAGTGTGGA 720
 GGTAAATCGCA GGCATCTCTG CGTCTCTGG GGGGACTATT GCGCTGAAGC TGGATGACTC 780
 AGTTTCAGGC CCACACTCT CAGTGAAGTT CTTTGGATC CTAGTGGCCT CTTTCCAAG 840
 TGCCATTGCC AGTCAATGG CAGCAGAGTG TCCAGCAGG TGTCTGTGG AGTCTCTGAT 900
 TGCCATAAGC AGCCTCAGT CTCGCTGCT GTTCACAGC TCTGGATATC TGTCTATCAG 960
 CATCATGAGA ATCTGTGAGA TGTTTAAGGA TTACCGCCA GCCATAAAC CATCTACGA 1020
 TGTGCTGCTG CTGCTGCTGC TGCTAGTCT CCTGCTCAG GCGGCGCTCA ACACGGGCAC 1080
 CGCCATCCAG TCGCTGCTGC TCAAGGTCAG TGCAAGGCTG CAGGGTGATC CCTGGGACAC 1140
 CCAGAACGGC CCGCAGGAGC GCCTGGCTGG GAGGCTGGCC AGGAGCCCC TGAAGGAGTT 1200
 CGACAAGGAG AAAGCCTGGA GAGCGTCTG GTTGCAATG GCCAGTGAC CCCAGAGCGC 1260
 GGAACCGGG TGGCAGGCGC CAGCCTGGCC CCAAGCATGG AAACGCACAA CCCTAATCG 1320
 CCCTGAGCTA CTGCTCTAA CACTCTTTT CCCTTGTGT AGGGCAAAAC AGGCTGCAGG 1380
 TGGGGTTTTT ACTTCTTAGG GTAGTTTAA TTAAAAATAG GCCAATGTTG GCTAGTCTGT 1440
 GCCTCAGTGA GATCAGTCA CTCCAGTGG CTCGCTGTC GTAACAGCAG GAGCATGGCC 1500

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GCAACTTCCC AGGCCGAGGA AGGGCCCCCG GCTGGGCTTC TTGAGAGCCC CACCCCTGAA 1560
 CTGGCCCCAG CTCTCTTCCC TGCTCTCTCT ATGGCTTGGG CTGGAGTGGG CTCTCTGGAC 1620
 CTGACACAGC TGTGGGTCCC TGCGTCTCCT GCCCACTCTG ACCGGGCTTC CTCCCTCCAC 1680
 GCTTAGGGTC TGTCCCGGGT ACTCAGTCAG CCCAGTGGGA TCTTACCCAC TTCCCTGCAA 1740
 GGTGCACTCT CCCCAGGCTC AGGCTGCCCC GCGGCTCTTC CTGGACAGTG AGAGCAGGGC 1800
 TTGGCGCCTC TGTCTGGGCC CGGGAGCCGC AGGGGCCCTC CCTCCAGAGC CTGGGCGCAA 1860
 GCGACACAGG CTGCGCTGTC TCTCCAGGT GAAATCCACA CCAGTCCACG CCGGGTCGCC 1920
 TGCCCTGTCT CCTACTTAG ACCCAGTCAT TCTAGAGGGA TCCACGCCCA CACTGGCCGG 1980
 CCCACGTCTT GGTGCTGTCT ATGCCAGCT TGGAGTGCCA CGTGGCCGCT GCCACGTCC 2040
 CCGGCACGTG CATGCCACGC TTGGAGTGCC ACATGGCCGC TGCCACGCTC CCGGCACTG 2100
 TCATGCCAGC CTGGAGTGC CAGTGGCCG CTGCTGTGAC AGGCAGTGT CTGGGGGTG 2160
 GGGCTGCATC CAAGGCTTTG TAAACCGGCT GGAACACGTC TCCCTGGCCC CAGTGACCGG 2220
 GGGAGCTGA GCCCTCCCTC CTGTGTGTTG CTCCATTAC TCAAAATGCA GGACAGATCA 2280
 GGTGAGAGCC CAGGAATTCT CACAGGTTCA CCCAGCGCCC TCTACCTCTC AGCAAGTACT 2340
 TTGTCTTGAT CCTCACTGAG AAGGCCCCAG GGCAGCGGTC TTCTCCATCT CGCTGTGTTT 2400
 GGGGTCTTAG GGTACAGCCC AGGCGGTAC TGCCCACTG OCAGGCTGCA GGGACAGTTG 2460
 GGTGTGAGAA TAAACCTGGC TTTGGGTAGT GCCATGGCCA GGAGTGGGTT TCCTGTGCTC 2520
 TCCTGTCTCC GAGGGGCGCT GGTCTCTCCC AGCTGACGGC AGTAAATCCA CAGTGAGTTG 2580
 GGGGACGTG GAAACTGGAA TGCTGTACT TTGATAATTA CTTTCCAGCA GGTGTTTTCC 2640
 TTCACATGGT TTTGTGTTCT TTCTTCTGA TCTGAGAAGA CATGAACGTT TTCTCTTAC 2700
 CGCCGTGGGG TGTATTGACT GGTCCCCAT GGGCTGTGCG AAAGGCCCGG AGATGCATCT 2760
 GTGGCTCGGG GCCATCAAGC TCAAAGAAC AGGAGGCGTG GGAGATGCAG CTGGATGGGG 2820
 CGGCTGCGAG ACCTGCCAG GGGGTTGAG GACCTCCCA GGTTCCTCAC TGCGAACAG 2880
 GAGTGACTCT GGCTGCCAG ATACCTTCAT GGTGTTCATG ACAAGTGGAA TCATTATTTT 2940
 CAACCATGGA AGGGGGATGC AGGCAAGACA CCTTCCCAGC TGCTCTAGA GGGGACAGC 3000
 CAGGCCCTCT CTGCACTCTC CGGCAGCTCC GGAAGGACAC AGTCAGGGGC CGGGCAACA 3060
 CTTTGGCCAC AGCCCAAAAC AAGCGCCACC GTGGGAGAGG AGAGGCTGCT GTCACTGGTA 3120
 CGGATGCGAG ACCCCACCTC GTCTGCAGGC CACCCCCACC TCCCTGCAGC TTTGAGGCTG 3180
 CGGGGCTCTG CTCTCTGGGA TGGGGTGGGA GCCACAGGGA CGACCCGGGG CGGGCTGATG 3240
 TCTTCTTGGG GGCAGACCGA AGAGCTCAAG TTTGAGATC AGAATTAGGC ACTTGGAAAC 3300
 TTTTGTCTGG CTTCGACTTT CTTATTTTCT TATTTTAGAG CGCTTAAAAA ATCCGGAATA 3360
 ATGGGGTTTA AAGAACTGT CTCCTTTCAG CTACATTTTT GTTTAATAAC CTGAGCAAT 3420
 AAACGCTGAC TTGACAGCT G

Seq ID NO: 280 Protein sequence
 Protein Accession #: NP_055981.1

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1 11 21 31 41 51
 MTQEPFREEL AYDRMPTLER GRQDPASYAP DAKPSDLQLS KRLPPCFSHK TWVFSVLMGS 60
 CLLVTSGPSL YLGNVFPDEM DYLRCAAGSC IPSAIVSFTV SRRNANVIFN PQILPVSTFA 120
 VTTTCLIFWG CKLVLPNSAI NINFNILILL LLELLMAATV IIAARSSSED CKKKKGSMSD 180
 SANILDEVFP PARVLKSYV VEVIAIGISAV LGGIIALNVD DSVSGPHLSV TFPFIIIVACF 240
 PSALASHVAA ECPSCKLIVV LIAISSLTSP LLFTASGYLS FSIIRIVEMF KDYPPIAIPKS 300
 YDVLILLILL VLLQLAGLNT GTAIQCVRFK VSARIQAGASV DTQNGPQERL AGEVARSPK 360
 EPDKKEAWRA VVVQMAQ

Seq ID NO: 281 DNA sequence
 Nucleic Acid Accession #: NM_004518.1
 Coding sequence: 43..2577

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60
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1 11 21 31 41 51
 GCTGAGCCTG AGCCCGACCC GGGGCGCCTC CGCCAGGCA CCATGGTGGC GAAGTCGCGC 60
 AACGGCGGGG TATACCCCGG CCGAGCGGGG GAGAAGAAGC TGAAGGTGGG CTTCGTGGGG 120
 CTGACCCCGG CGCGGCCCGA CTCCACCCCG GACGGGGCGC TGCTGATGCG CGGCTCCGAG 180
 GCCCCCAAGC GCGGCAGCAT CCTCAGCAAA CCTCGCGCGG GCGCGCGGGG CGCCGGGAAG 240
 CCCCCAAGC GCAACGCTTT CTACCGCAAG CTGAGAAATT TCCTCTACAA CGTGCTGGAG 300
 CGGCGCGCGG GCTGGGCGTT CATCTACAC GCCTAGCTGT TCCTCTGCTT TTTCTCTGTC 360
 CTGCTGCTGT CTGTGTTTTC CACCATCAAG GAGTATGAGA AGAGCTCGGA GGGGGCCCTC 420
 TACATCCTGG AAATCGTGAC TATCGTGGTG TTTGGCGTGG AGTACTTGGT GCGGATCTGG 480
 GCCGACGGCT GCTGCTCGCG GTACCGTGGC TGGAGGGGGC GGCTCAAGTT TGCCCGGAAA 540
 CCGTCTGTG TGATTGACAT CATGGTGCTC ATCGCTCCA TTGGGTGCTT GGCOCGCGGC 600
 TCCAGGGGCA ACCTCTTTCG CACATCTGCG CTCGGAGGCC TGCGCTTCTT GCAGATTCTG 660
 CGGATGATCC GCATGACCGG GCGGGGAGGC ACCTGGAAGC TGCTGGGCTC TGTGGTCTAT 720
 GCCCAGAGC AGGAGCTGGT CACTGCCTGG TACATCGGCT TCCTTTGTCT CATCCTGGCC 780
 TGGTCTCTGG TGTACTTGGC AGAGAAGGGG GAGAAGCACC ACTTTGACAC CTACGCGGAT 840
 GCACTCTGGT GGGGCTGAT CAGGCTGACC ACCATTGGCT ACGGGGACAA GTACCCCCAG 900
 ACCTGGAACG CGAGGCTCCT TGCGCAACC TTCACCTCA TCGTGTCTCT CTTCCTCGCG 960
 CTGCGCTGAG GCATCTTGGG GTCTGGGTTT GCCCTGAAGG TTCAGGAGCA GCACAGGCAG 1020
 AAGCACTTTG AGAAGAGCGG GAACCCGCGA GCAGGCTGTA TCCAGTGGC CTGGAGATTCT 1080
 TACGCCACCA ACCTCTCGCG CACAGACCTG CACTCCACGT GGCAGTACTA CGAGCGAAGC 1140
 GTCAACGTGC CCATGTACAG ACTTATCCCC CGCTGAACC AGCTGGAGCT GCTGAGGAAC 1200
 CTCAGAGTA AATCTGGACT CGCTTTCAGG AAGGACCCCG CGCCGGAGCC GTCTCCAGAC 1260
 CAGAAGGTA GTTTGAAGA TGTGTCTTTC TCCAGCCCGG GAGGCGTGGC TGCCAAAGGG 1320
 AAGGGTCCC AGGAGGCCCA GACTGTGAGG CGGTCAACCA GCGCGACCA GAGCCTCGAG 1380
 GACAGCCCCA GCAAGGTGCC CAAGAGCTGG AGCTTGGGG ACCCGAGCCG GGCACGCCAG 1440
 GCTTTCTGCT TCAAGGGTGC CGGTCAAGG CAGAACTCAG AAGAAGCAAG CCTCCCGGA 1500
 GAGGACATTG TGGATGACAA GAGCTGCCCG TGCGAGTTTG TGACCGAGGA CCTGACCCCG 1560
 GGCCTCAAGG TCAGCATCAG AGCCGTGTGT GTCATGCGGT TCCTGTGTCT CAAGCGGAAG 1620
 TTAAGAGAGA CCGTGGCGCC CTACGACGTG ATGGAAGTCA TOGAGCAGTA CTCAGCGCGC 1680
 CACCTGGACA TGCTGTCCCG AATTAGAGC CTGAGTCCA GAGTGGACCA GATCGTGGGG 1740
 CGGGGCCACG CGATCACGGA CAAGGACCGC ACCAAGGGCC CGCCGAGGC GGAGCTGGCC 1800
 GAGGACCCCA GCATGATGGG ACGGCTCGGG AAGGTGGAGA AGCAGTCTCT GTCCATGGAG 1860

	AAGAAGCTGG	ACTTCTGGT	GAATATCTAC	ATGCAGCGGA	TGGGCATCCC	CCCGACAGAG	1920
	ACCGAGGCT	ACTTTGGGG	CAAGAGCCG	GAGCCGGGG	CGCGTACCA	CAGCCCGGAA	1980
	GACAGCCGG	AGCATGTGA	CAGGCACGG	TGCATTGTCA	AGATCGTGG	CTCCAGCAGC	2040
5	TCCACGGGG	AGAAGAACTT	CTCGGCGCCC	CCGCGCGCG	CCCTGTGCA	GTGTCCGGC	2100
	TCCACTCTCT	GGCAGCCACA	GAGCCACCG	CGCCAGGGC	ACGGCACCTC	CCCGTGGGG	2160
	GACCAAGGCT	CCCTGGTGG	CATCCCGCG	CGCCTGCCC	ACGAGCGGTC	GCTGTCCGG	2220
	TACGGGGGG	GCAACCGCG	CAGCATGGAG	TTCCTGGGG	AGGAGGACAC	CCCGGGCTGC	2280
	AGGCCCCCG	AGGGGACCT	GCGGACAGC	GACACGTCCA	TCTCCATCCC	GTCCGTGGAC	2340
10	CACAGGAGC	TGGAGCGTTC	CTTCAGCGG	TTCAGCATCT	CCAGTCCAA	GGAGAACCTG	2400
	GATGCTCTCA	ACAGCTGTGA	CGCGGCGTG	GCGCTTGTG	CCAAAGTCAG	GCCCTACATT	2460
	GCGGAGGAG	AGTCAGACAC	CGACTCCGAC	CTCTGTACCC	CGTGGCGGCC	CCCGCCACGC	2520
	TCCGCCACCG	GCGAGGGTCC	CTTTGGTGAC	GTGGGCTGG	CCGGGCCAG	GAAGTGAGGC	2580
	GGCGCTGGG	CAGTGAGACC	GCCCGGGCC	CTCTCAGCA	CGGTGCTCC	GAGGTTTGA	2640
	GGCGGGAACC	CTCTGGGGCC	CTTTCTTAC	AGTAACTGAG	TGTGGCGGGA	AGGGTGGGCC	2700
15	CTGGAGGTTT	CACGGCGGTG	TGAAGGATGG	GGGCTCCTGG	CAGTGACCTT	TTACAAAAGT	2760
	TATTTTCCAA	CAGGGCACTC	CCAGGCCCTG	TGCCATTGA	GGTGCTCCG	CTGGGCTGTC	2820
	TCCCTACCCC	TCCCTGTGCT	GGAGCCTGTC	CCAAAAGGT	GCCAACTGGG	AGGCCTCGGA	2880
	AGCCACTGTC	CAGGCTCCCA	CTGCCGTGCT	GCTCTGTTCC	CAAAAGCAGC	GTGTGTGGCC	2940
20	TCCGGCCCTG	CGGTGGCATG	AAGCATCCCT	TCTGGTGTGG	GCATCGCTAC	GTGTTTGTGG	3000
	GGCAGGTTT	CACGGCGGTG	CCCTTGCTGT	CTCCCTGGG	CTGGCTCGAG	CCTGGGGTCC	3060
	ATGTCCCTTT	GCGTCCCGT	CATGGGGCAG	GGAATCCATA	GCGGGGCCCA	CAGGCAGGGG	3120
	TATGAGTGG	TCCACCCCAA	CGCAGCACCA	GCCCAGGCCA	CGCTCCCGG	TGTCCCCAGT	3180
	TCCGTCTCAG	CTACTCGGAC	TCCAGGACCC	TGGAGAAGGG	AGACCTGGCA	GTGGAGGGAG	3240
25	GCTGTGCTGT	GTGTCCCGCT	CGAGGTGTGA	CCCGCCCTGC	TCTTCCCTCC	CCCGCCAGGT	3300
	GTGGCCCGCT	CTGCTCTTTC	CTCCCCAAC	AGTATGGCCC	CACCTGCTCT	TTCCCTTCCC	3360
	CCCAAGGTGT	GGCCCCACCT	GTTCTTTTCT	CCCTGCGCGA	GGTGTGACCC	CACCTGCTCT	3420
	TTCTCCCTTC	CCAGTATGGC	CCCACTGCT	CTTCTCTCC	CCGAGGTGAG	GCCCCGCTG	3480
	CTCTTCTCTC	CATGGGAGAG	CGCTGAGGCG	TGCGCACCTG	GGCAGAGTT	GGGGCTCTGC	3540
30	AGGATGAGGA	AGACAGGCCA	ATCCCTTCCC	TCCAGAGAGC	TGGCCGCCCA	GCAGGAGGGA	3600
	CTGAGGCCAG	ACTCATGTTC	AGCAAGGAAC	GTGTGGTGTG	TCCCTGGGA	AGTCTCTGGG	3660
	CCCTGGGAAG	AGGGAAGGTG	CACGTCCTGG	GATGGTTGCG	GGGCCCTGTT	TTGGGAGACA	3720
	AAGGGGTAGA	GGGTCTGTCT	TGNGCCCCCC	CAGACTCTAG	CCCGAGCAGT	GCAGCCACCT	3780
	ACTGCCCCAC	GTGAGAGAG	TGCAGCGGGA	AGGAGGCTGG	AGGTGGTGGC	GCGCTGCTTC	3840
	GGGTGTCTGC	GTGAATGAGC	GTGGCCAAAG	ACCAGTGCCA	CCTCATGGCA	AAGAGCTCCC	3900
35	GCAGTGTTTG	TTAGAGTGCA	CATCCTAGCT	GCCCCTGGC	ACACACAGCT	GCTCAGATAC	3960
	ANGTCNGNGT	ACAGGNGTAC	ACATGCANGC	TTGCACACAT	GCACACAGAC	CACATAGCAC	4020
	ACATGTGCAC	TGACACACAC	TGTATAGACC	ATGCACAGTA	CACATAGCTG	CATACACATG	4080
	CCTGCATACA	GGCATACACA	TGCAGGCTTA	CATGTACAGC	TGCACAGATC	ACACACATGC	4140
40	ACACACGTGT	AGCTCACAACA	CAGTATACAC	ATACACAGT	GCACAGACCA	CACACAGCAC	4200
	TAACACATGC	ACACACAAAG	TGCATAGGCC	ACACAGCACA	TGCACACAGG	TGCACAGACC	4260
	ACACAGCACCA	CACAAGTGCA	CAGAGCACAQ	TGCACACATG	CACACACACA	CGCGTGCATG	4320
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45	GTGATGCTGG	AATGTCAAGC	GCGTGTGTGG	GGTATCGAC	TGTCCGGGCT	CCTGGTCCGC	4500
	AGTGGCAGAG	CGCCAGGCG	AGCCAACTAG	GGTCTGTGTC	TGCCCTTCCC	CCCCACAGCC	4560
	TGGCAGCCAT	CCAGAGGAGG	GGCTCTACCA	GATGCCAAGG	TGCCCGGCTG	TCTGTATGGG	4620
	TGTCCGGTGT	GGTCTGTGTC	TTGGTCTGCE	CTGGAGGTGG	CTGGGCCCTC	CTGGGATGGG	4680
	TGGCTCAGCC	TGCAATCCCA	GGCCCCAGCC	CAGGCAGGTG	CTGCTGCCGT	TTGTGGTTTC	4740
50	CTGGCCAGC	TTCTCTTCT	CCCTCTGCAT	AAAAATCAG	TCCGTGAGTC	TTCCAGCTGC	4800
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	GAGCAGGGCA	GGTGCCCAACA	CCCCCCACCG	GAGACAGGCT	GCCCCCTCAG	GATGCCCTTA	4920
	CCCTTTGGGG	GGCTCTGTCT	CAAGCCCCCC	CTTGGAGGCT	GAAATCACCC	CAGGCACCTG	4980
	GAGGGCTTCT	CCAGGGGAGC	ACCCTTTGAG	CTGTGGGTCT	GATCACCCCA	AGTCCCGCAC	5040
55	ACGGAGGAGA	GGCAGAGCCA	GGGCGTGTGG	TTTAAATGTT	GCCCCCTCGG	GGCTGGAGGT	5100
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	AGGAGGATC	CGGTGGGCTG	CGGTCCCGCA	CAGTCAGGGA	CCCCCAATAA	GGACACCCCC	5220
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	CAGAAGGAGC	TGTGAGAGCT	TTGCAGAAAC	GCCCTTGTCC	CGCCCTCTCT	GAGCTATGAA	5340
60	TGCGGTACAG	AGCAGAGGCT	GGGGCATTGG	CAAGATCACA	GGTGTAGTCT	GCACAGCCCC	5400
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70	CCCATGACAG	ACTCCAGGTG	CACATGCAAG	TATGTCCAGG	GCACTGGGGT	GGCGTGAAGA	6000
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	CTGTGCCGGG	CAGCCATCTT	GCAATGCCAC	CCAGCGCGCA	GTCTCACCT	CGGCCCCAGC	6120
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75	ACCCAGGAGC	CTTCCATGAC	CGGGGAGCAT	GAGTGAATGG	GGGGTTCCAG	TTTGTCTGAA	6300
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	GGGAGGTTGT	GGGCAACGCT	GGAGGAGGAG	AGACGGGAGG	GGACCAATTG	GGATGGAGGG	6420
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	CACCTGCGGT	GGTGGCCCTG	GCTGGCCGAG	GAGACTGGCT	CTGGCCAGGG	CCCGGCTCTG	6540
80	AGAGGTCTCT	AGCGTCTGAC	TCTGGGCCAG	GCGCCAGCAA	GGAGGGGCGG	GTCCCCGGGG	6600
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Seq ID NO: 282 Protein sequence

Protein Accession #: NP_004509.1

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AVLAAGSQGN VFATSAIRSL RFLQILRMIR MDRRGGTWKL LGSVVYAHSK ELVTANYIGF 240
LCILILASFLV YLAEGKENDH FDTYADALMW GLITLTITIGY GDKYPQTWNG RLLAATPTLI 300
GVSPFPALPAG ILGSGFALKV QEQHRQKHEP KRENPAAGLI QSAWRFYATN LSRTDLHSTW 360
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GVAAKGKSP QAOVTVRSPS ADQSLEDSPS KVPKSWSPGD RSRARQAFRI KGAAARQNSE 480
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BOYSAGHLM LSRKSLQSR VDQIVGRGPA ITDKDRTGK ABAELFEDFS MMGRLGKVEK 600
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Seq ID NO: 2838 DNA sequence

Nucleic Acid Accession #: AF152496.1

Coding sequence: 1..2391

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Seq ID NO: 284 Protein sequence

Protein Accession #: AAD43757.1

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 Coding sequence: 15..2765

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Seq ID NO: 286 Protein sequence
 Protein Accession #: NP_001785.2

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GTGAGCGGCA CCGGAGCCCT GTCCAGAGAG TACCAGTACG AGGTGTGTCT GACTGGAGGC 2280
TCGGGAGCAA ATGAGTTCAA GTTCTGAAG CCAATTATCC CCAACTTGGT TGCTCAGGGT 2340
GCAGAGAGGG TTAGCGAGGC AAATCCAGT TTCAGGAAGA GCTTTGAATT CACTTAA
  
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Seq ID NO: 288 Protein sequence
 Protein Accession #: AAD43756.1

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1 11 21 31 41 51
MEAGEGKERV PKQRQVLIFP VLLGIAQASC QPRHYSVAEE TESGSFVANL LKDLGLEIGE 60
LAVRGARVVS KGKMKHLQPD RQTGDLLENE KLDREBELGP TPCVLPPQV LLENPLQPFQ 120
AELRIRDVND HSPVFLDKEI LLKIPESITP GTTFLIERAQ DLDVGTNSLQ NYTISPNIHF 180
HLNLQDSLDC IILPQLVLNR ALDREEQPEI RLTLTALDGG SPFRSGTALV RIEVVDINDN 240
VPBPALKLYE VQIPEDSFVG SQVAIVSARD LDIGTNGEIS YAFSQASEDI RKTFRLSAKS 300
GELLRLRQKL FESIQTITVN IQATDGGGLS GTCVVFVQVM DLMNDPPELT MSTLINQIPE 360
NLQDTLIAVF SVSDPDSGDN GRMVCISQDD LPPFLKPSVE NFYTIVISTA LDRETRSEYN 420
ITITVIDFGT PRLTKEHNIT VLVSDVNDNA PAPTQTSYTL FVRENNSPAL HIGSVSATDR 480
DSGTNAQVTV SLLPQDPHPL PLASLVSINA DNGHLFALQS LDYEALQAFE FRVGAADRGS 540
PALSSALIVR VLVLDDANDS PFVLYPLQNG SAPCTELVPR AABPGVLVTK VVAVDGDGSG 600
NAMLISYQLLK ATEPGLFGVW AHNGEVRTAR LLRERDAAEQ RLVLVLKQNG EPPRSATATL 660
HVLVLDGFSQ PYLLLPBAAP AQAQADLLTV YLVVALASVS SLFLFVSLIF VAVRLCRRSR 720
AASVGRCSVP EGPFPGQMDV VSGTGTLSQS YQYEVCLTGG SGTNEFKFLK PIIPNFVAQG 780
AERVSEANPS FRKSFEPT
  
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Seq ID NO: 289 DNA sequence
 Nucleic Acid Accession #: NM_018674.1
 Coding sequence: 390..2009

1 11 21 31 41 51

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CGGAGCACAT GCTGAGCGGA GGGGCTGGGG CTGGGCGGCG TGGGAGAGCA GGGCTGCTC 60
CCTCGCTCAC TGGCTGCTC GCAGGGACAC ACGCAGGGGC TGACAGCTGT GCTGGTGTCTG 120
ATAAGGGAAG CCACAAGGAG ACGATCGAGG AGAGAGACAA GCGGAGCAGG AGGCAGCAGC 180
GGCAGAGGCA GCACCAGGGC TGGGAGCTGT CTGGAGTGGG GAGTGACTCC CCACCTCGG 240
GCCCCCAACC TGTCCCTGTC CTCTTCCCCTG TGGCCCTGAG TTTAGAAGAG CAGCCGCTGC 300
CACCAGTGCC ACTCGGGAGG GCACCAGGGC TGCTGGCTAG GAGGGGACAG GGCAGGGAGG 360
CTCTGGCCAG TCCAGCAGGC CGGGACAGA TGCCGATCGA GATTGTGTGC AAAATCAAT 420
TTGCTGAGGA GGATGCGAAA CCCAAGGAGA AGGAGGCAGG GGATGAGCAG AGCCTCCTCG 480
GGGCTGTTGC CCCTGGAGCA GCCCCCGAG ACCTGGCCAC CTTTGGCAGC ACCAGCACCC 540
TGCAATGACT GGGCCGGGCC TGTGGCCAG GCCCCACGG ACTGGCAGA ACCCTGTGGG 600
CACTGGCCCT ACTCACTCG CTGGCTGCTT TCCTGTACCA GCGGCTGCG CTGGCCCGGG 660
GCTACTGTGAC CGGCTCTCAC CTGGTGGCAA TGGACCCGCG TGCCCGAGCC CAGTGGCGGG 720
GCTTCCCGGC GTCAACCTTC TGCAATATCA ACGCTTCCG GCATTGCGCA CTCAGGATG 780
CGACATCTTT CCACCTGGCC AATCTGACAG GGCTGCCCCC CAAAGACCGG GATGGGCACC 840
GTGCGGGTGC CTGCGCTAC CCAGAGCCTG ACATGGTAGA CATCTCAAC GCACTGGCC 900
ACGAGCTCGC CGACATCTCT AAGAGCTGCA ACTTCAGTGG GCATCACTGC TCCGCCAGCA 960
ACTTCTCTGT CAGCTATATC CGCTATGGGA AGTGTACAC CTTCAACGG GACCCGCGGA 1020
GCTCGCTGCC CAGCGGGCA GGGGGCATGG GCACTGGCCT GAGATCATG CTGACATCC 1080
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TTGCGGTGCA GATCGCTAC CAGGAGGAGC CGCCTACAT CCACAGCTG GGGTGGGG 1200
TGTCCCGAGG CTTCAGACC TTTGTGCTCT GCGAGGAACA GCGGCTGACC TACCTGCCCC 1260
AGCCCTGGGG CACTGCGGC GCAGAGAGTG AGCTCAGGGA GCTGAGCTT CAGGGCTACT 1320
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GCCACTGCGG GATGTGTCAC ATGCCAGGCA ATGAGACCAT CTGCCACCA AATATCTACA 1440
TGAGTGTGCG AGACCAACA CTGGACTCCC TGGGTGGGG CCTGAGGGC CGGTCTTCT 1500
GCCCCACCCC CTGCAACCTG ACACGCTATG GAAAGAGAT CTCCATGGTC AGGATCCCCA 1560
ACAGGGGCTC AGCCGGTAC CTGGCGAGGA AGTACAACCG CAACAGAGCC TACATAGGG 1620
AGAACTTCTT GGTCTAGAT GTCTTCTTTG AGGCCCTGAC CTCTGAAGCC ATGGAGCAGC 1680
GAGCAGCTTA TGGCTGTGCA GCGCTGCTGG GAGACCTCGG GGGACAGATG GGCCTGTTCA 1740
TTGGGGCCAG TCTCTCACG TTGCTGAGA TCCTGAGTA CATCTATGAG GTGTCTGGG 1800
ATCGACTGAA GGGGATATGG AGGCGTCCCA AGACCCCTC GCGGACCTCC ACTGGGGGCA 1860
TCTCCACTTT GGGCTTCAG GAGCTGAAG AACAGAGTCC CTGCGGAGC CTGGGCGAG 1920
CGAGGGTGGG GGGGCTCAG AGTCTGCTCC CCAATCACCA CCACCCCAC GGTCCCCAG 1980
GAGGTCTCTT TGAAGATTTT GCTTGTAGG ACGTGTCTGT GACTGAAAG ACCCAGGAGT 2040
CTGGGACCCC TCTGGGATC CCGAGCACAT TCTCTGCTC CTGGGAGAGG CCGGGGGG 2100
GTGCTCACTG GAGGGCCAG GACTCAGTTC CTGCTCTCAT CTTCCCTGC CTTGATGTA 2160
GCTGCTTGGC ACAAAGTCC TTCTTGTCCA CACCCCTTAT CCCCAGGCTG GTGCCCGGG 2220
AGGCTGAGAG ACCAGGCCAT GGGCCCTCAC GGAGAGGAAG GGAAGGAAG AGAGGGAGGG 2280
GAGGATAGA GCCCATCCCA GCGGGGAGG GGGAGCCCTC TGTACTTTG TAAATATTA 2340
GGGAAAGCCG GGTGGGGGGA GGGGATACAG ATGTAGAAAG TGGGTAGGGC TACAGGGGTG 2400
GGTGATTTAG GACAGCCAG GGTCCAGCC CCAATGTGAG CAGGATAGGG AGAGCCOCAG 2460
GACTCAGGAG TGCTGGGCTG GTCTACTTTC CTGCCCCCTC CCAGGCCAG CTCCCTCTCT 2520
GGCAGGGGGA GATGATGGCC CAGCAGGCTT GGGCCAGCTC CCACTTCCCC CTGCACAGC 2580
CCACCCCTTA GATCCCTTC TATAGGGAG GGGCAGGAGA CCTTCCAGAC TTGGCTGAG 2640
CTTGAGGGT GGAAGGGAG CCTTCTCAGT CTTCTCTCCC TCCAGTCTGA TTTTATAAG 2700
TGCTGACGAG
  
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Seq ID NO: 290 Protein sequence
Protein Accession #: NP_061144.1

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1 11 21 31 41 51
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MPLEIVCKIK FAEEDAKPKE KEAGDEQSLI GAVAPGAAPR DLATPASTST LHGLGRACGP 60
GPHGLRRLTW ALALLTSLAA FLYQAAGLAR GYLTRPHLVA MDPAAPAFVA GPPAVTLNLI 120
NRRFHSALSD ADIFHLANIT GLPPKDRDGH RAAGLRYPBP DMVDILNRTG HQLADMLKSC 180
NFGSHHCASG NFSVVYTRYG KCYTFNADPR SSLPSRAGGM GSGLEIMLDI QQEYLPPIWR 240
BTNETSFPEAG IRVQIHSQEE PPYIHLQGFQ VSPGFQTFVS CQEQLRTYLP QFWGNCRAS 300
ELREPELQYV SAYSVSACRL RCEKEAVLQR CHCRMVEMPG NETICPNFIY IECADHTLDS 360
LGGGPEGPFC CPTPCNLTRY GKEISMVRIP NRGSAARYLAR KYNRNETYIR ENFLVLDVFP 420
EALTSAMEQV RAAYGLSALL GDLGGQMLGF IGASILTLLB ILDYIYEVSW DRLKRVWRPP 480
KTPLRSTGG I STLGLQELK EQSPCPSLGR AEGGGVSSLL PNHHPHGPFP GGLFEDFAC
  
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Seq ID NO: 291 DNA sequence
Nucleic Acid Accession #: Bos sequence
Coding sequence: 62..895

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1 11 21 31 41 51
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CACTGCTCTG AGAATTGTG AGCAGCCCTT AACAGGCTGT TACTTCACTA CAACTGACGA 60
TATGATCATC TTAATTACT TATTTCTCTT GCTATGGGAA GACACTCAG GATGGGGATT 120
CAAGGATGGA ATTTTTCATA ACTCCATATG GCTTGAACGA GCAGCCGGTG TGTACCACAG 180
AGAAGCAGCG TCTGGCAAT ACAAGCTCAC CTAAGCAGAA GCTAAGGCGG TGTGTGAATT 240
TGAAGCGCGC CATCTGSCAA CTTACAAGCA GCTAGAGGCA GCCAGAAAA TTTGATTTC 300
TGCTCTGTCT GCTGGATGGA TGGCTAAGGG CAGAGTTGGA TACCCCATTG TGAAGCCAGG 360
GCCCACTGT GGAATTGGAA AAAGTGGCAT TATTGATTAT GGAATCCGTC TCAATAGGAG 420
TGAAAGATAG GATGCTATT GCTACAACCC ACACGCAAG GAGTGTGGTG GGTCTTTAC 480
AGATCCAAAG CAAATTTTAA AATCTCCAGG CTTCCCAAT GAGTACGAAG ATAAACCAAT 540
CTGCTACTGG CACATTAGAC TCAAGTATG TCAGGTATT CACCTGAGTT TTTTAGATT 600
TGACCTTGAA GATGACCCAG GTTGTCTGGC TGATTATGTT GAAATATATG ACAGTTACGA 660
TGATGTCCAT GGTCTTGTGG GAAGATACTG TGGAGATGAG CTTCAGATG ACATCATCAG 720
TACAGGAATAT GCATGACCT TGAAGTTTCT AAGTGATGCT TCAGTGACAG CTGGAGGTTT 780
CCAAATCAAA TATGTTGCAA TGGATCTCTT ATCCAAATCC AGTCAAGGAA AAAATACAA 840
TACTACTTCT ACTGGAATA AAAACTTTTT AGCTGGAAGA TTTAGCCACT TATAAAAAA 900
AAAAAAGGA TGATCAAAAC ACACAGTGT TATGTTGAAA TCTTTTGGAA CTCCTTTGAT 960
  
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CTCACTGTGA TTATTAACAT TTTTATTAT TTTTCTAAA TGTGAAAGCA ATACATAATT 1020
 TAGGGAAAT TGGAAATAT AGGAACTTT AAAAGAGAAA ATGAAACCTC TCATAATCCC 1080
 ACTGCATAGA AATAACAAGC GTTAACATT TCATATTTT TCTTTTCAGT CATTTTTCTA 1140
 TTTGTGGTAT ATGTATATAT GTACCTATAT GTATTTCAT TTGAAATTTT GGAATCCTGC 1200
 TCTATGTACA GTTTGTATT ATACTTTTAA AATCTTGAAC TTTATAAACA TTTTCTGAAA 1260
 TCATTGATTA TTTACAAAA ACATGATTTT AAACAGCTGT AAAATATTCT ATGATATGAA 1320
 TGTTTTATGC ATTATTTAAG CTTGTCTCTA TTGTTGGAAT TTCAGGTCAT TTTCTATAAT 1380
 ATTGTTGCAA TAAATATCTT TGAACACACA AAAAAAAAAA AA

Seq ID NO: 292 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 MIILYLFL LLWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
 EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCQFGRGTGI IDYGIRLNRS 120
 ERNDAYCYNP HAKECCGVFT DPKQIFKSPG PFNEYEDNQI CYWHIRLKYG QRIHLSPLDF 180
 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF 240
 QIKYVAMDPV SKSSQGNKTS TTSTGNKNFL AGRFSLH

Seq ID NO: 293 DNA sequence
 Nucleic Acid Accession #: NM_007115.1
 Coding sequence: 69..902

1 11 21 31 41 51
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 GGGGATCTAA GGATGGAATT TTTCTAACT CCATATGGCT TGAACGAGCA GCCGGTGTGT 180
 ACCACAGAGA AGCACGGTCT GGCATAATACA AGCTCACCTA CGCAGAAGCT AAGCGGGTGT 240
 GTGAATTGGA AGGCGGCCAT CTCGCAACTT ACAAGCAGCT AGAGGACGCC AGAAAAATTG 300
 GATTTCATGT CTGTGCTGCT GGATGGATGG CTAAGGGCAG AGTTGGATAC CCCATTGTGA 360
 AGCCAGGGCC CACTGATGA TTTGGAAAA CTGGCATTAT TGATTATGGA ATCCGTCTCA 420
 ATAGGAGTGA AAGATGGGAT GCCTATTGCT ACAACCCACA CGCAAGAGAG TGTGGTGGCG 480
 TCTTTACAGA TCCAAAGCGA ATTTTAAAT CTCCAGGCTT CCCAATGAG TACGAAGATA 540
 ACCAAATCTG CTACTGGCAC ATTAGACTCA AGTATGGTCA GCGTATTCAC CTGAGTTTIT 600
 TAGATTTTGA CCTTGAAGAT GACCCAGGTT GCTTGGCTGA TTATGTTGAA ATATATGACA 660
 GTTACGATGA TGTCCATGGC TTTGTGGGAA GATACTGTGG AGATGAGCTT CCAGATGACA 720
 TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTTCTAAG TGATGCTTCA GTGACAGCTG 780
 GAGGTTTCCA ATCAAAATAT GTTGCAATGG ATCCTGTATC CAAATCCAGT CAAGGAAAAA 840
 ATACAAGTAC TACTTCTACT GGAATAAATA ACTTTTATAG TGGAAAGATT AGCCACTTAT 900
 AAAAAAATAA AAGGATGATC AAAACACACA GTGTTTATGT TGGAACTCTT TGGAACTCCT 960
 TTGATCTCAC TGTATTATTA AACATTATTT TATTATTTTT CTAAATGTGA AAGAAATACA 1020
 TAATTTAGGG AAAATTGGAA AATATAGGAA ACTTTAAACG AGAAATGAA ACCTCTCATA 1080
 ATCCCACTGC ATAGAAATAA CAAGCGTAA CATTTTCATA TTTTTCCTT TCAGTCAATT 1140
 TTGTAATTTG GTATATATGA TATATGTACC TATATGTATT TGCAATTGAA ATTTTGGAA 1200
 CCTGCTCTAT GTACAGTTT GTATTATACT TTTTAAATCT TGAACCTTAT GAACATTTC 1260
 TGAATCTCAT GATTATCTTA CAATAACATG ATTTTAAACA GCTGTAAAT ATTCTATGAT 1320
 ATGAATGTTT TATGCAATTAT TTAAGCCTGT CTCTATTGTT GGAATTTCAG GTCATTTCAT 1380
 TAAATATTGT TGCAATAAAT ATCCTTCGGA ATTC

Seq ID NO: 294 Protein sequence
 Protein Accession #: NP_009046.1

1 11 21 31 41 51
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 MIILYLFL LLWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
 EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCQFGRGTGI IDYGIRLNRS 120
 ERNDAYCYNP HAKECCGVFT DPKRIFKSPG PFNEYEDNQI CYWHIRLKYG QRIHLSPLDF 180
 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF 240
 QIKYVAMDPV SKSSQGNKTS TTSTGNKNFL AGRFSLH

Seq ID NO: 295 DNA sequence
 Nucleic Acid Accession #: NM_001218.2
 Coding sequence: 116..1180

1 11 21 31 41 51
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 CCGGCGCAGC CTGCACGCGG CGGCGGTGCT CCTGCTGGTG ATCTTAAAGG AACAGCCTTC 180
 CAGCCCCGCC CCAGTGAACG GTTCCAAGTG GACTTATTTT GGTCTGTATG GGGAGAATAG 240
 CTGGTCCAAG AAGTACCCGT CGTGTGGGGG CCTGCTGCAG TCCCCATAG ACCTGCACAG 300
 TGACATCTCT CAGTATGACG CCAGCCTCAC GCCCCTCGAG TTCCAAGGCT ACAATCTGTC 360
 TGCCAACAAG CAGTTTCTCC TGACCAACAA TGGCAATTCA GTGAAGCTGA ACCTGCCCTC 420
 GGACATGCAC ATCCAGGGCC TCCAGTCTCG CTACAGTGCC ACGCAGCTGC ACCTGCACTG 480
 GGGGAACCGG AATGACCCGC ACGGCTCTGA GCACACGCTC AGCGGACAGC ACTTGGCCGC 540
 CGAGCTGCAC ATTTGTCATT ATAACTCAGA CCTTATCTCT GACGCCAGCA CTGCCAGCAA 600
 CAAGTCAGAA GGCTCGCTGT TCCTGGCTGT TCTCATTTAG ATGGGCTCCT TCAATCCGTC 660
 CTATGACAAG ATCTTCAGTC ACCITCAACA TGTAAGATAC AAGGSCCAGG AAGCATTCGT 720
 CCGGGGATTC AACATTGAAG AGCTGCTTCC GGAGAGGACC GCTGAATATT ACCGCTACCG 780
 GGGGTCCCTG ACCACACCCC CTTCGAACCC CACTGTGCTC TGGACAGTTT TCCGAAACCC 840
 CGTGCAAAAT TCCAGGAGAC AGCTGCTGGC TTTGGAGACA GCCCTGTACT GCACACACAT 900

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GGACGACCCCT TC0CCCAGAG AAATGATCAA CAACTTCCGG CAGGTCCAGA AGTTCCGATGA 960
GAGGCTGGTA TACACCTCTCT TCTCCCAAGT GCAAGTCTGT ACTGCGGCAG GACTGAGTCT 1020
GGGCATCATC CTCTCACTGG CCCTGGCTGG CATTCTTGGC ATCTGTATTG TGGTGGTGGT 1080
GTCCATTGGG CTTTTCAGAA GGAAGAGTAT CAAAAAAGGT GATAACAAGG GAGTCATTTA 1140
CAAGCCAGCC ACCAAGATGG AGACTGAGGC CCACGCTTGA GGTCCCGGGA GCTCCCGGGC 1200
ACATCCAGGA AGGACCTTGC TTTGGACCCCT ACACACTTGG GCTCTCTGGA CACTTGGGAC 1260
ACCTCAAGGT GTTCTCTGTA GCTCAATCTG CAAACATGCC AGGCTCAGG GATCCTCTGC 1320
TGGGTGCCTC CTTCCTTGGG GACCATGGCC ACCCCAGAGC CATCCGATCG ATGGATGGGA 1380
TGCACTCTCA GACCAAGCAG CAGGAATTCA AAGCTGCTTG CTGTAAGTGT GTGAGATTGT 1440
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AAAAACATTT CATCCGGGGC TTTGCCAGAG CGTGCTTTCA AGTGTCTGGG AAAGTCTGCT 1560
GCTTCTCCAA GCTTTCAGAC AAGAATGTGC ACTCTCTGCT TAGGTTTTCG TTGGGAAACT 1620
CAACTTCTTT CCTCTGGAGA CGGGGCATCT CCTCTGATT TCCTTCTGCT ATGACAAAAC 1680
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CCTCTGGATC ACAGACACTG CACAGACCTT AGGGAATGGC AGGTTCAAGT TCCACTTCTT 1860
GGTGGGGATG AGAAGGGAGA GAGAGCTAGA GGGACAAAGA GAATGAGAAG ACATGGATGA 1920
TCTGGGAGAG TCTCACTTGG GAATCAGAAT TGGAAATCACA TTCTGTTTAT CAAGCCATAA 1980
TGTAAGGACA GAATAATACA ATATTAAAGT CAAATCCAAAC CTCTGTCAG TGGAGCAGTT 2040
ATGTTTATA CTCTACAGAT TTTACAAATA ATGAGGCTGT TCCTTGAAGA TGTGTTGTTG 2100
CTGTGCTCTG GAGGAGACAT GAGTTCGAG ATGACCCAAT CTGCTTTGA ATCTGGAGGA 2160
AATAGGCAGA AACAAAATGA CTGTAGAACT TATTCTCTGT AGGCCAAATT TCATTTCAGC 2220
CACTTCTGCA GGTCCCTAC TGCCAACTG GAATGGAGAC TTTTATCTAC TTCTCTCTCT 2280
CTGAAGATGT CAAATCGTGG TTTAGATCAA ATATATTTC AGCTATAAAA GCAGGAGGTT 2340
ATCTGTGAG GGGCTGGCA TCAATGATTT AGGGCAAGT AATAATGGAA TGCTACTAAG 2400
ATACTCCATA TTCTTCCCGG AATCACACAG ACAGTTTCTG ACAGGCGCAA CTCCTCCATT 2460
TTCTTCCCGG AGGTGAGAAC CCTGTGGAGA TGAGTCAGTG CCATGACTGA GAAGGAACCG 2520
ACCCCTAGTT GAGAGCACTT TGCAGTTCCG CGAGAAGTTT CTGATTCACA GTCTCATTTT 2580
GACAGCATGA AATGCTCTCT TGAAGCATAG CTTTTTAAAT ATCTTTTCC TTCTACTCCT 2640
CCCTCTGACT CTAAGAATTC TCTCTCTGG AATCGCTTGA ACCAGGAGG CGGAGGTTGC 2700
AGTAAGCCAA GGTCAATGCC CTGCACCTA GCCTGGGTGA CAGAGCGAGA CTCCATCTCA 2760
AAAAA AAAA
  
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Seq ID NO: 296 Protein sequence
Protein Accession #: NP_001209.1

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MPRRSLHAAA VLLLVLKBEQ PSSPAPVNGS KWTYFGPDGE NSWSKYPSC GGLLQSPIDL 60
HSDILQYDAS LTPLEFQGYN LSANKQFLIT NNGHSVKLML PSDMHIQGLQ SRYSATQLHL 120
HWGNPNDFHG SEHTVSGQHF AAEHLIVHYN SDLYPDASTA SNKSEGLAVL AVLIEMGSPN 180
PSYDKIFSHL QHVKYKGQEA FVFPFNIBEL LPERTAERYR YRGLSTPPC NPTVLWTVFR 240
NEVQISQFAL LALETALVCT HMDDPSPREM INNFRQVQKF DERLVYTSFS QVQVCTAAGL 300
SLGIILSLAL AGILGICIVV VVSIWLPFRK SIKKGONKGV IYKPKMET EABA
  
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Seq ID NO: 297 DNA sequence
Nucleic Acid Accession #: NM_006632.1
Coding sequence: 377..1582

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ACGCGTCCGC CCAACGCTCC GCCACGCGT CCGTCCGGG CCAGAGCGCA GGTGTACCTG 60
GCGGCGGTGC TGGAGCACCT GACCGCGAG ATCCTGGAGC TGGCTGGCAA CCGGCGCCGC 120
GACAAGAAGA CCGCATCAT CTGCGCCAC CTGTAGCTGG CCATTGCAA CGCGAGGAG 180
CTTAACAAGC TGCTGGGCGA AGTCAACATC GCGCAGGCGG GTGTCTTGGC CAACATTCAG 240
GGCGTCTTTC TGCCCGAGAA GACCAAGAGC CACCACAAGG CCAAGGGTGA AAACCATTC 300
CTAGAGAGAG AGAAACACAA TGGCCACCAA GACAGAGTTG AGTCCACAG CAAGGGAGAG 360
CAAGAACGCA CAAGATATGC AAGTGGATGA GACACTGATC CCCAGGAAG GTCCAAGTTT 420
ATGTTCTGCT CGCATATGAA TAGCCCTGCT CTACATTTC TGCAATTTCA CAACGATAGC 480
ACAAAATGTC ATCATGAACA TCACCATGGT AGCCATGGTC AACAGCACA GCCCTCAATC 540
CCAGCTCAAT GATTCTCTG AGGTGCTGCC TGTGACTCA TTTGGTGGCC TAAGTAAAGC 600
CCCAAGAGAT CTCTCTGCAA AGTCTCAAT ACTTGGGGGT CAGTTTGCAA TTTGGGAAA 660
GTGGGGCCCT CCACAAGAAC GAAGCAGACT CTGCAGCATT GCTTTATCAG GAATGTTACT 720
GGGATGCTTT ACTGCCATCC TCATAGGTGG CTTCATTAGT GAAACCTTG GGTGGCCCTT 780
TGTCCTCTAT ATCTTTGGAG GTGTGGCTG TGTCTGTGCT CTCTCTGCT TGTGTGTGAT 840
TTATGATGAC CCTTTCTCT ATCCATGGAT AAGCACCTCA GAAAAAGAAT ACATCATATC 900
CTCCTTGAAA CAACAGGTGC GGTCTTCTAA GCAGCCTCTT CCCATCAAG CTATGCTCAG 960
ATCTCTACCC ATTTGGTCCA TATGTTTAGG CTGTTTCAGC CATCAATGGT TAGTTAGCAC 1020
AATGGTGTGA TACATACCAA CTTACATCAG CTCTGTGTAC CATGTTAACA TCAGAGACAA 1080
TGGACITCTA TCTGCCCTTC CTTTATTGTT TGCCCTGGGTC ATAGGCAATG TGGAGGGCTA 1140
TCTGGCAGAT TTCTTCTTAA CCAAAAAGTT TAGACTCATC ACTGTGAGGA AAATTGCCAC 1200
AATTTTAGGA AGTCTCCOCT CTTGAGCACT CATTGTGTCT CTGCCCTACC TCAATTCGG 1260
CTATATCACA GCAACTGCCT TGCTGAGCCT CTCTTGGGGA TTAAGCACAT TGTGTCACTC 1320
AGGAATTTAT ATCAATGCTC TAGATATTGC TCCAAGGTAT TCCAGTTTTC TCATGGGAGC 1380
ATCAAGAGGA TTTTCGAGCA TAGCACTGT CATTGTACCC ACTGTACGCG GATTTCCTCT 1440
TAGTCAGGAC CCTGAGTTTG GGTGGAGGAA TGTCTTCTC TTGCTGTTG CGSTAAACCT 1500
GTTAGGACTA CTCTTCTACC TCATATTGAG AGAAGCAGAT GTCCAAGAA GGGCTAAAGA 1560
GAGAAAACCT ACTCGTTTAT GAAGTATACC CACCTTGGAT GGAAGAATCA TTAGGCACCG 1620
TATTGCATAA AATAGAAGGC TTCCGTGATG AAAATACCAG TGAAGAATTT TTTTTCCT 1680
GTGGCTCTTT TCAATTATGA GATCAGTTCA TTATTTTATT CAGACTTTT TTTGAGAGAA 1740
ATGTAAGATG AATAAAAAAT CAAATAAAAT GATAACTAAG AAAAAA AAAA
  
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Seq ID NO: 298 Protein sequence
Protein Accession #: NP_006623.1

1 11 21 31 41 51
5 MQVDETLIPR KGPSLCSARY GIALVLHFCN FTIAQNVIM NITMVMVNS TSPOSQNLDS 60
SEVLVDSFG GLSKAPKSLP AKSSILGGQF AIWEKNWPPQ ERSRLCSIAL SGMLLGCTFA 120
ILIGGFISET LGWPFVFIYF GGVGCVCCLL WFWVIYDDPF SYPWISTSEK EYIISLKKQ 180
VGSSKQPLPI KAMLRSLPIW SICLGCFSHQ WLVTMVVYI PTYISSVYHV NIRDNGLLSA 240
LPFIVAVWIG MVGGYLAFL LTKKFLITV RKIATILGSL PSSALIVSLP YLNSGYITAT 300
10 ALLTLSCGLS TLQSGIYIN VLDIAPRYSS PLMGASRGFS SIAPVIVPTV SGFLLSQDPE 360
FGWRNVFLL FAVNLLGLLF YLIFGEADVQ EWAKERKLTR L

Seq ID NO: 299 DNA sequence
Nucleic Acid Accession #: NM_003058.1
Coding sequence: 145..1812

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20 TCGGGCCCTC CTGCCTGCAG GATCATGCC ACCACCGTGG ACGATGTCTT GGAGCATGGA 180
GGGGAGTTTC ACTTTTCCA GAAGCAAATG TTTTCTCTT TGGCTCTGCT CTGGCTTACC 240
TTGCGGCCCA TCTACGTGGG CATCGTCTTC CTGGGCTTCA CCCCTGACCA CCGCTGCGGG 300
AGCCCGCGAG TGGCGAGCT GAGTCTGCGC TGGGCTTGA GTCTCTGACA GGAAGTGAAC 360
25 TACAGCGTGC CGSGCCAGG ACCTGCGGGC GAAGCCTCCC CAAGACAGTG TAGGCGCTAC 420
GAGGTGGACT GGAACACAGG CACCTTTGAC TGGTGGGACC CCTGGGCCAG CCGGACACCC 480
AACAGGAGCC GCTCGCCACT GGGCCCTGCG CGGACCGGCT GGGTGTACGA GACGCTTGGC 540
TCGTCCATCG TCACCGAGTT TAACCTGGTA TGTGCCAATC CTTGGATGTT GGACCTATTC 600
CAGTCATCAG TGAATGTAGG ATTCTTTATT GGCTCTATGA GTATCGGCTA CATAGCAGAC 660
AGGTTTGGCC GTAAGCTCTG CCTCTAACT ACAGTCTCA TAAATGCTGC AGCTGGAGTT 720
30 CTATGGGCA TTCCCCCAAC CTATACGTGG ATGTTAATTT TTGCTTAAT CCAAGGACTG 780
GTCAGCAAG CAGGCTGGTT AATAGGCTAC ATCTGTATTA CAGAATTGT TGGGCGGAGA 840
TATCGGAGAA CAGTGGGAT TTTTACCAA GTTGCCATA CAGTGGGCT CCTGGTGCTA 900
GCTGGGGTGG CTACGCACT TCCTCACTGG AGGTGGTTCG AGTTCACAGT TGCCTGCCC 960
AACTTCTCT TCTGTCTCTA TTACTGGTGC ATACCTGAGT CTCCCGAGTG GCTGATCTCC 1020
35 CAGAATAAGA AGCTGAAGC CATGAGAATC ATTAAGCACA TCGCAAGAA AAAATGGAAA 1080
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40 GGTGACATA TCACTCTGGA TTCTTCTAC TCTGCCCTGG TTGAATTTCC AGCTGCCTTC 1320
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GTGCGAGGG CAGCCTGTCT GGCTCAGT TTTATACCTG GTGATCTACA ATGCTAATA 1440
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GTCAATGCTG AGCTGTACCC CACATTCAAT AGGAATCTTG CGGTCCACAT CTGTTCTCTA 1560
45 ATGTGTGACA TTGGTGGCAT CATCAGGCA TTCTGTGCTT ACCGGCTCAC TAACATCTGG 1620
CTGAGCTCC CGCTGATGGT TTTGGGCGTA CTGGGCTTGG TTGCTGGAGG TCTGGTGCTG 1680
TTGCTTCCAG AAATAAAGG GAAAGCTTTC CCTGAGACCA TCGAGGAAGC CGAAATATG 1740
CAAAGACCAA GAAAAATAA AGAAAGATG ATTTACCTCC AAGTTCAGAA ACTAGACATT 1800
CCATTGAATC AAGAAGAGAG ACCGTTGCTG CTGTCATGAC CTAGCTTTGA TGGCAGCAAG 1860
50 ACCAAAGTA GAAATCCCTG CACTCATCAC AAAGCCCAT CAACTCAACC AAACCTACCC 1920
CTGAGCCCTA TCAACCTAGG TCTACAGCCA GTGGAGTCTA TTGTACACTG TGAATAATA 1980
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CATGGACAT TGGTTTCTG GAGGTTTCTT TTTCOGATCT TTGTATTTT TTAATTTGA 2100
70 TTTCTTTCTT TGAATGTCTA GCAACAGAA TACATAGGGG AACTGTGGGC TAGGCAANA 2160
AAATAGAAA AGTGTGAAA ACAGTAAAGT TGGGAGAGGA GCATCTATTT TCTTAAAGAA 2220
ATAAACACC NAAACAAAA AAAAAA AAAAAA

Seq ID NO: 300 Protein sequence
Protein Accession #: NP_003049.1

1 11 21 31 41 51
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65 PCRDWVYET PGSSIVTEFN LVCANSWMLD LFQSSVNVGF FIGSMSIGYI ADRFGRKLCL 180
LTVLINAAA GVMAISPTY TWMLIFRLIQ GLVSKAGWLI GYLITTEFVG RRYRRTVGIF 240
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RIIKHIAKIN GKSLPASLQR LRLEERTGKK LNPFFLDLVR TPQIRKHTMI LMYNFTSSV 360
LYQGLIMBMG LAGDNIYLD FYSALVEFPA AFMIILTIDR IGRYPWAAS NMVAGAACLA 420
70 SVFIPGDLQW LKIIISCLGR MGIWAVEIV CLVNAELYPT FIRNLGVHIC SSMCDIGGII 480
TPFLVYRLTN IWLELPLMVF GVLGLVAGGL VLLLPETGKG ALPETIEEAS NMQRPRKNKE 540
KMIYLVQVQL DIPLN

Seq ID NO: 301 DNA sequence
Nucleic Acid Accession #: NM_012206.1
Coding sequence: 52..1131

1 11 21 31 41 51
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80 GTTGGTGGAG AGGCAGGTCC ATCTGTACAC CTACCGTCC ACTACAGTGG AGCTGTACAC 180
TCAATGTGCT GGAATAGAGG CTATGTCTCT CTATTCACAT GCCAAATAGG CATTTGTCTGG 240
ACCAATGGAA CCAACGTAC CTATCGGAAG GACACACGCT ATAAGCTATT GGGGACCTT 300
TCAAGAGGG ATGTCTCTTT GACCATAGAA AATACAGCTG TGTCTGACAG TGGCGTATAT 360

5 TGTGCGCGT TTGAGCACCG TGGGTGGTTC AATGACATGA AAATCACOGT ATCATTGGAG 420
 ATTGTGCCAC CCAAGGTCCAC GACTACTCCA ATTGTACAA CTGTTCCAC CGTCACGACT 480
 GTTGCAGCA GCACCACTGT TCCAACGACA ACGACTGTT CAAAGACAAC TGTTCACACA 540
 ACAATGAGCA TTCCAACGAC AACGACTGTT CCGACGACAA TGACTGTTT CACGACAAACG 600
 AGCGTTCCAA CGACAACGAG CATTCACAACA ACAACAAGTG TTCCAGTGAC AACAAOGGTC 660
 TCTACCTTTG TTCTCCAAT GCCTTTGGCC AGGCAGAAC ATGAACCACT AGCCACTTCA 720
 CCATCTTCAC CTCAGCCAGC AGAAACCCAC CCTACGACAC TGCAGGGAGC AATAAGGAGA 780
 GAACCCACCA GCTCACCATT GTACTCTTAC ACAACAGATG GGAATGACAC CGTGACAGAG 840
 TCTTCAGATG GCCTTTGGAA TAACAATCAA ACTCACTGT TCCTAGAAC TAGTCTACTG 900
 10 ACGGCCAATA CCACTAAAGG AATCTATGCT GGAGTCTGTA TTTCTGCTT GGTGCTTCTT 960
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 AGTGTTCAT TTAGCAGCCT TCAAAATAAA GCTTTGCAAA ATGCAGTTGA AAAGGAAGTC 1080
 CAAGCAGAG ACAATATCTA CATTGAGAA AGTCTTTATG CCAOGGACTA AGACCCAGTG 1140
 15 GTGCTCTTTG AGAGTTTACG CCCATGACTG CAGAAGACTG AACAGGTATC AGCACATCAG 1200
 ATGTCTTTTA GACTCCAAGA CAATTTTCT GTTTCAGTTT CATCTGGCAT TCCACATGT 1260
 CAGTGATCT GGGTAGAGTA ACTCTCCAC TCCAACTGT GTATAGTCAA CCTCATCATT 1320
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 TCTCTCAAC ATGAACACTT TAGAATGTGA TGTCTCTTT AGACCCATA AATCTGTAT

Seq ID NO: 302 Protein sequence
 Protein Accession #: NP_036338.1

25 1 11 21 31 41 51
 MHPQVILSL ILHLADSVAG SVKVGGEAGP SVTLPCHYSG AVTSMCNWRG SCSLFTQNG 60
 IVWNGTHVT YRKOTRYKLL GDLRRDVS L TIENTAVSDS GUYCCRVHR GWFNMDKITV 120
 SLEIVPPKVT TPIVITVPTT VTTVRTSTV PTTTIVPTT VPTTMSIPTT TTVPTMTVS 180
 TTTSVPTTTS TPTTSTVPVT TTVSTFVPPM PLFRQNHFPV ATSPSSPQPA ETHPTTLQGA 240
 30 IRRPTSSPL YSYTTDNDT VTSSDGLWN NNQTQLFLEH SLLTANTTKG IYAGVCISVL 300
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Seq ID NO: 303 DNA sequence
 Nucleic Acid Accession #: NM_001044.1
 Coding sequence: 129..1991

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 CTAAGGAGCC CAATGCCGTG GCGCCGAGG AGGTGAGCT CATCTTGTG AAGGAGCAGA 240
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 AGGATCGGGA GACCTGGGGC AAGAAGATCG ACTTCTCCT GTCCGTGATT GGCTTTGCTG 360
 45 TGGACCTGGC CAACTCTGCG CGGTTCCTCT ACCTGTGCTA CAAAAATGTT GCGGGTGCCT 420
 TCCTGGTCCC CTACCTGCTC TTCTATGCTA TTGCTGGGAT GGCATTTTC TACATGGAGC 480
 TGGCCCTCGG CCAAGTTCAAC AGGGAAGGGG CCGCTGGTGT CTGGAAGATC TGCCCCATAC 540
 TGAAAGGTGT GGGCTTCAAG GTCATCTCTA TCTCACTGTA TGTGCGCTTC TTCTACAAGC 600
 TCATCATCGC CTGGGCGCTG CACTATCTCT TCTCCTCTT CACCAAGGAG CTCCCTGGGA 660
 50 TCCACTGCAA CAACTCTGCG AACAGCCCA ACTGCTCGGA TGCCATCCT GGTGACTCCA 720
 GTGGAGACAG CTCGGGCTTC AACGACACTT TTGGGACCC ACCTGCTGCC GAGTACTTTG 780
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 GGCAGCTCAC AGCCTGCCTG GTGCTGTGTA TCGTGTGCT CTACTTCAGC CTCTGGAAGG 900
 CGGTGAAGAC CTCAGGGAAG GTGGTATGGA TCACAGCCAC CATGCCATAC GTGGTCTCTA 960
 55 CTGCGCTGCT CTGCGTGGG GTCACTCTCC CTGGAGCCAT AGACGGCATC AGAGCATACC 1020
 TGAGCGTTGA CTCTACCGG CTCTCGGAGG CGTCTGTTTG GATTGACGCG GCCACCCAGG 1080
 TGTGCTTCTC CCGTGGCGTG GGGTTGGGG TGCTGATGCG CTCTCCAGC TACAACAAGT 1140
 TCACCAACAA CTGCTACAGG GACGCGATTG TCACCACTCC CATCACTCC CTGACGAGCT 1200
 TCTCTCGCGG CTCTGCTGTC TTCTCTCTCC TGGGGTACAT GGCACAGAAG CACAGTGTGC 1260
 60 CCATCGGGGA CGTGGCCAAG GACGGGCCAG GGTGATCTTT CATCATCTAC CCGGAAGCCA 1320
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 TCCCTGCTCT GTTCTGGTTC ACCAACGGTG GCATCTACGT CTTCAGCTC CTGGACCAAT 1560
 65 TTGAGCGCGG CAGCTCCATC CTCTTTGGAG TGCTCATGGA AGCCATCGGA GTGGCCTGGT 1620
 TCTATGGTGT TGGGCACTTC AGCGACGACA TCCAGCAGAT GACCGGGCAG CGGCCAGCC 1680
 TGTACTGGCG GCTGTCTGCG AAGCTGGTCA GCGCTGCTT TCTCTGTTT GTGGTCTGCG 1740
 TCAGCATGTT GACCTTCAGA CCCCCCACT ACAGGAGCTA CATCTTCCC GACTGGGCCA 1800
 ACGCGCTGGG CTGGGTCTTC GCCACATCTT CCAATGGCAT GGTGCCATC TATGGGCTT 1860
 70 ACAAGTCTTG CAGCTGCTCT GGGTCTTTC GAGAGAACT GGCCTAGGCC ATTGCACCCG 1920
 AGAAGGACCG TGAGCTGGTG GACAGAGGGG AGGTGOGCCA GTTCAAGCTC CGCCACTGGC 1980
 TCAAGTGTGA GAGGGAGCAG AGACGAGAGC CCGAGGAAGT CATCTGCAA TGGGAGAGAC 2040
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 CTCTACTGAA AACACAAACA ACAAGCAGA AGACTCTCTT CTCTGACTG TTTACACTT 2160
 75 TCCGTGCGCG GAGCGCACTC GCGGTGCTCT TGTGTTGCTG TAATAAGGAC GTAGATCTGT 2220
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 CTCACAGTAG CTTCCTAGAC CATTTACTTT GCCCATATTA AAAAGCCAAG TGTCTGTCTT 2460
 80 GGTTTAGCTG TGCAGAGGT GAAATGGAGG AAACCAACAA TTCATGCAAA GTCTCTTCCC 2520
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 GTCTGTTTCA AGCTATGGA GGATGGGGT CTTGGTATGT CTCACAGGA AATTCTGTTT 2640
 ATGTTCTTGC AGCAGAGAGA AATAAACTC CTTGAAACCA GCTCAGGCTA CTGCCACTCA 2700
 GGCAGCTGTT GGTCTCTTGT GGTGTAGGGA ACGGCTGAG AGGAGCGTGT CCTATCCCCG 2760
 GACGATGCA GGGCCCCAC AGGAGCGTGT CCTATCCCCG GACGATGCA GGGCCCCAC 2820

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AGGAGCATGT CCTATCCCTG GACGCATGCA GGGCCCCCAC AGGAGCGTGT ACTACCCACG 2880
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TGGAGCGTGT ACTACCCACG GACGCATGCA GGGCCCCCAC AGGAGCGTGT CCTATCCCTG 3000
GACCGGACGC ATGCAGGGCC CCCACAGGAG CGTGTACTAC CCCAGGACGC ATGCAGGGCC 3060
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CATCAATAAC AACAGTTTTT ATGTTTGCGA ATGGCTTTT AAAATCATAT TTACCTGTGA 3300
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CACACTGCCC TCTGCCACTG ACAGGAAAGT GGATGCCATA GTTTGAATTC ATGCTCAAG 3480
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GCCTGTGAAC TGCCAGGACG CTGCAGTTAG CACAGAGGAT GGCCTCCCA TTGCCTTCTG 3660
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GGGCTTCCC CATGCCCTC TGGGGAGGGA CACAGAGGAC AGTTTCCCCA TCGCTTCTG 3780
TTGTGTTTGA ATGACAGAGA GAGCGGCTTC CCAATCGCCT TCTGGGGAGG GGCCTCGTGT 3840
AGCAACCCAG GTGTGTCCG TGTCTGTGA CCAATCTCTA TTCAGCATCG TGTGGGTCCC 3900
TAAGCAAT AAAAGACATC CACAATGGAA AAAAAAAG GAATTC

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Seq ID NO: 304 Protein sequence
Protein Accession #: NP_001035.1

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1 11 21 31 41 51
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GQFNREGAAG VWKICPILKG VGFTVILISL YVGFYFNVII ANALHYLFSS FTTELPHIHC 180
NNSWNSPNCS DAHPGDSSGD SSGLNDTFTG TPAAEYFERG VLHLHQSHGI DDLGPPRNQL 240
TACLVLVIVL LYFSLWKGVK TSGKVVWITA TMPYVVLTLAL LLRGVTLPGA IDGIRAYLSV 300
DFYRLCEASV WDAATQVCF SLGVGFVULI AFSSYNKFTN NCYRDAIVTT SINSLTSPSS 360
GPFVVSFLGY MAQKHSVPIG DVAKDGPGLI PIYPEAIAT LPLSSAWAVV PFIMLLTLGI 420
DSAMGGMESV ITGLIDEPQL LHRHRELFTL FIVLATPILLS LFCVTNGGIY VFTLLDHPAA 480
GTSILFGLVI EAIGVAPFYG VQGFSDDIQQ MTGQRPSLYW RLCWKLVSFC PLLFVVVVS 540
VTFRPPHYGA YIFPDWANA L GWVIATSSMA MVPIYAAKF CSLPGSFREK LAYALAPEKD 600
RELVDREGEV QFTLRHWLKV

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Seq ID NO: 305 DNA sequence
Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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1 11 21 31 41 51
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CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCACAGAGT TGGCCCGGAT GCAGAGGAT 180
TCCCTCTGG GAGGAGGCTC TTCTGGGGA GATGACCCAC TGGGCGAGGA GGATCTGCCC 240
AGTGAAGAGG ATTACCCAG AGAGGAGGAT CCACCCGAG AGGAGGATCT ACCTGGAGAG 300
GAGGATCTAC CTGAGAGGGA GGATCTACCT GAAGTTAAGC CTAATCAGA AGAAGAGGGC 360
TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCTG GAGATCCTCA AGAACCCAG 420
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CCTGCGAGA TCAAGTGTG TCACCTCAGC ACCGCTTTG CCAGAGTTGA CGAGGCTTTC 840
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ACCAGCGTGC CGTTCCTTGT GCAGATGAGA AGGCAGACA GAAGGGGAAC CAAAGGGGGT 1380
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Seq ID NO: 306 Protein sequence
Protein Accession #: NP_001207.1

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DPQSPQNNAH RDKRGDDQSH WRYGGDPFVP RVSPACAGRF QSPVDIRPQL AAFCPALRPL 180
ELLGPQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGRFY RALQLHLHWG AAGRPGSEHT 240
VEGRFPFAEI HVVELSTAPA RVDEALGRPG GLAVLAAPLE EGPEENSAYE QLSRLLEIA 300
EGSEETQVPG LDISALLPSD PSRYFYEGS LTPPCAQGV IWTVPNQTM LSAQLHLTL 360
DTLMGPGDSR LQLNFRATQP LNRVIEASF PAGVDSPRA AEPVQLNSCL AAGDILALVF 420
GLLFAVTSVA FLVQMRQRH RGTGKGVSYR PAEVAETGA

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	GTGCTGTGCC	TGCAACCACT	GATAGCTGCT	TTTGGGTCA	CCTTCAGTA	TGGGTACAAC	180
10	GTGGCTGTG	TCAACTCCCC	AGCACTGCTC	ATGCAACAT	TTTACAATGA	GACTTACTAT	240
	GGTAGAGCCG	GTGAATTACG	GGAAAGACTC	CCCTTGACGT	TGCTGTGGTC	GTGAACGGTG	300
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	TTTGGCAGAA	AAGGAGGCCCT	GCTGTTCAC	AACATATTTT	CTATGCTGGC	TGGGATCTTA	420
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15	GGAAATGTG	CAGGTGTATC	TTCCAACGTG	TGTCCTAGT	ACTTACGGGA	GCTGGCCCTC	540
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	GTGGCCCAAG	TCITTTGGTCT	TCGGGAATCTC	TCGTCAAAG	TAGATGGCTG	CGCGATCTTG	660
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	GCAGAGAAGG	CCGCGGGCTT	CATCTCCTGT	CTGAAGCTGT	TCCCGATGCG	CTCGCTGGCC	900
	TGGCAGCTGC	TGTCATCATC	CGTCTCATCT	GGGGGCCAGC	AGCTGTGGCG	CGTCAACGCT	960
	ATCTACTACT	ACGCGGACCA	GATCTACCTG	AGGCGCGGCG	TGCGGAGAGA	GCAGCTGCGAG	1020
25	TACGTGACCG	CGCGCAGCG	GGCCGTGAAC	GTGGTCAATG	ACTCTGCGCG	CGGTGTGGTG	1080
	TGAGAGCTCC	TGGGTCCGGG	GCTGTGTCGT	CTCTGGGGCT	TCTCCATCTG	CTCATGACGG	1140
	TGTGCGTGC	TCATCTGCAG	TCTGGCACTC	CAGGACACAG	TGTCTCGGAT	GCCATACATC	1200
	AGCATCTCT	GTGTCATCTC	CTAGCTCATG	CAGATCGCCC	TCGGGGCCAG	TCCCATATCC	1260
	GGCGTGTCTA	CTCATGAGAT	TTCTCTGAG	TCCTCTGCGC	CATCTGCGCT	CATGGTGGCC	1320
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30	GGCCCTGGCC	CGTACAGCTC	ATGTGTCTCC	GGCGTGATCT	GCTCTCTCAC	CACCATCTAC	1440
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	ACCAAGATGA	ATAAGGTGTG	TGAAGTGTAC	CGCGAAAAGG	AGGAAGCTGA	AGGACTTCCA	1560
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35	ACTCTGATGT	GGAAATCAGT	CCTCATCTCC	AGGCTCCCCA	CCCGATGGG	AACTGTGCAA	1740
	AGGCGTGCT	TGCTGTTCTT	GAAAGCTGGC	TGCTCTCTCT	CATGTTGGCC	TGTCAACAGA	1800
	CCCGAGTCAA	TTAAACAGCT	GGTCTCCAC	TTTGCTGGTT	CAGCCTTGTG	GTGACCTCTG	1860
	GTAACGCTGC	TCCAACCTGA	TGGGTCAACC	TTTGTGTGGC	TCTGTGTAAT	ATTAACAACA	1920
	CAGTTACTAT	AGTGGTGAGA	TGGAAGGAAT	CAAAATTTGC	CAGAGAAACT	AACTCGGTGT	1980
40	CCCCAACAGG	TCTTCCGGGG	CCATGGGCAT	TTGTTTAGTA	CCAAATTCAT	GCTCTATCCA	2040
	GATCTCTTTC	CAGAAATATC	TGTCTAGGAA	GGTGTGATGT	CAGAAACCAT	GACATCCAGA	2100
	AAGCTGAGGA	ACAGGTTCTC	GTGGACAGAT	TGAGTCAGAA	TTCTCTATCC	AAATTTATTT	2160
	GTTAGTGGA	AATGGAATGT	CTTCTGTGTA	GTCATATAAA	TGAACCTGAT	CATTTTTC	

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	FMEDPFLTL	WSVTVMFPF	GGFIGSLVVG	PLWNKFGKRG	ALLFNNIFSI	VPALLMGCSR	120
	VATSPELI1	SRLLVGICAG	VSSNVVMYML	GGFAPKNLRG	ALGVVPQLFI	TVGILVAQIF	180
	GLRNLLANVD	GWPILLGLTG	VPAAQLLLLL	PKPPESPRLY	LIQKQDBAAA	KKALQTLRGN	240
	DSVDREVAEI	ROEDAEAKAA	GRISVLKLFER	MSLEWVLLOS	IIVLMGGQQL	SGVNAYIYYA	300
55	DQIYLSAGVP	EEHVQYVTAT	TGAVNVMTF	CAVFPVLLG	RLRLLLLGFS	ICLLACCVLT	360
	AALALQDVTG	WMPYISIVCV	YISVIGHALG	PSPIPALIT	EIFLQSSRPS	APFMVGSVHN	420
	LSNFVYGLFI	PPIQEGGLPY	SFIVFAVICL	LTTIYFPLIV	PETKAKFTIE	INQIFTRMKN	480
	VSEVYPEKER	LKLEPPVTSE	O				

	1	11	21	31	41	51	
65	GGCTGGTCCC	CTGACAGGTT	GAAGCAAGTA	GACGCCCAGG	AGCCCCGGGA	GGGGGCTGCA	60
	GTTTCCTCTC	TTCTCTTCFG	GCAGCGCTCC	GGCCCCCATC	CGCCCCCTCT	GGCGTAGCGC	120
	AGGTGATGCG	CGCGCGCATG	CGCGAGGAGG	GTTCCGGGCT	CTCGGTGCGG	CGACAGCCCT	180
	ATGGGTGCGT	CGTGGCGGCT	GCTTTGTGTCC	CATTGTGTGC	GGGCTTGGTG	ATCTGCTCTC	240
70	TGGTGTGATC	CCAGCGGCTC	CCACAGGCTC	AGCAGCAGCT	CGCGCTCGAG	TCACTTGGGT	300
	TGGCGATAGC	TGAGCTGACG	CTGAATACAC	CAGGACCTCA	CGAGGACCCC	AGCGTATACT	360
	GGCAGCGGGG	CCCAAGCTAG	GGCGCGCTCT	TGCTGCATGG	ACAGAGAGCT	GACAAGGGGC	420
	AGCTACGTAT	CCATCGTGAT	GGCATCTACA	TCGATACAC	CCAGGTGAGC	TCGGCATCTC	480
	GCTCTCTCAC	AGCGGCTCTC	AGGCACATCC	CCACACACCT	GGCGGTGGGA	ATCTGCTCTC	540
75	CGCGCTCCCG	TAGCATCAGC	CTGCTGCGTC	TCAGCTTCCA	CCAGAGTTGT	ACCATTTGCT	600
	CCCAGCGCCT	GACGCCCCCT	GCCCGAGGGG	ACACACTCTG	CACCAACCTC	ACTGGGACAC	660
	TTTTCCTCTC	CCGAACACT	GATGAGACAT	TCCTTTGAGT	CGAGTGGGGT	CGCGCCGTAC	720
	CACCTGCTCT	GATTAGGTTT	TTTAAATTTT	TATTTTATTT	TATTTAAGTT	CACAGAGAAA	780
	AGTGTACACA	CAGGGGCGGC	CGCGGGTTGG	GGTGGGAGTG	TGGTGGGGGG	TAGTGGTGGC	840
80	AGGACAAGAG	AAGGCATTGA	GCTTTTCTCT	CTATTTTCTT	ATTAAAAA		

1071

	1	11	21	31	41	51	
	MPEEGSGCSV	RRRPYGCVLK	AALVPLVAGL	VICLVVICIQ	FAQAQQQLPL	ESLGWDVABL	60
5	QLNHTGPQDD	PLRYWQGGPA	LGRSFLHGPE	LKGQLRIHR	DGIYMHQIV	TLAICSSTTA	120
	SRHHPTTLAV	GLCSPASRSI	SLRLSFLHQT	CTIASQRLTP	LARGDTLCTN	LTGTLPLSRN	180
	TDETPFQVQW	VRP					
	Seq ID NO: 311 DNA sequence						
10	Nucleic Acid Accession #: Eos sequence						
	Coding sequence: 1..3978						
	1	11	21	31	41	51	
15	ATGGTGGGTG	AAGGACCTTA	CCTTATCTCA	GATCTGGACC	AGCGAGGCGG	GCGGAGATCC	60
	TTTGACAGAA	GATATGACCC	CAGCCTGAAG	ACCATGATCC	CAGTGGGACC	CTGTGCAAGG	120
	TTAGACACCA	ACCGGTGGA	TGATGCGGG	CTACTCTCT	TCGCCACATT	TTCTTGGCTC	180
	ACGCCGGTGA	TGCTGAAAGG	CTACCGGCAA	AGGCTGACCG	TAGACACCTT	GCCCCATTG	240
	TCGACATATG	ACTCATCTGA	CACCAATGCG	AAAGATTTC	GAGTCTTTTG	GGATGAAGAG	300
	GTAGCAAGGG	TGGGTCTGTA	GAAGGCTCTG	CTGAGCCACG	TGGTGTGGAA	ATTCAGAGG	360
20	ACACCGCTGT	TGATGGACAT	CGTGGCCAAC	ATCCTGTGCA	TCATCATGGC	AGCCATAGGG	420
	CGACAGTTTC	TCATTACCCA	AATCTCTCCAG	CAGACTGAGA	GGACCTCTGG	GAAAGTCTGG	480
	GTGCGCATTG	GACTGTGCA	AGCCCTTTT	GCCACCGAGT	TTACCAAGT	CTTCTTTGG	540
	GCCCTTGCT	GGCCATCAA	CTACCGCAG	GCCATCGGT	TGAAGGTGGC	GCTCTCCACC	600
	TTGGTTTTTG	AAACCTAGT	GTCTTCAAG	ACATTGACCC	ACATCTCTGT	TGGCGAGGTG	660
25	CTCAATATAC	TGTCAAGTGA	TAGCTATTCT	TTGTTGAAG	CTGCCCTTGT	TTGTCTTTTG	720
	CCAGCCACCA	TCCCGATCCT	AATGCTCTT	TGTGCGCGGT	ACGCCCTTTT	CATTCTGGGG	780
	CCACAGCTTG	TCACTGGGAT	ATCAGTGTAT	GTCAATTCA	TACCCGTCCA	GATGTTTATG	840
	GCCAAGCTCA	ATTGAGCTTT	CCGAAGGTCA	GCAATTTTGG	TGACAGACAA	GCGAGTTCAG	900
30	ACATGAATG	AGTTTCTGAC	CTGCATCAGG	CTGATCAAAA	TGTATGCCTG	GGAGAAATCT	960
	TTTACCAACA	CTATCCAAGA	TATAAGAAGG	AGGGAAGAA	AATTACTGGA	AAAAGCTGGA	1020
	TTTGTCCAAA	GTGGAACCTC	TGCCCTGGCC	CCCATCGTGT	CCACCATAGC	CATCGTGCTG	1080
	ACATTATCT	GCCACATCCT	CTGAGACGC	AAACTCACCG	CACCGTGGC	ATTTAGTTGT	1140
	ATTGCCATGT	TTAATGTAAT	GAAGTTTCC	ATTGCAATCT	TGCCCTTCTC	CATCAAAGCA	1200
35	ATGGCTGAAG	CGAATGTCTC	TCTAAGGAGA	ATGAAGAAA	TTCTCATAGA	TAAAGCCCCC	1260
	CCATCTTACA	TACCCCAACC	AGAAGACCCA	GATACTGTCT	TGCTTTTAGC	AAATGCCACC	1320
	TTGACATGGG	AGCATGAAGC	CAGCAGGAAA	AGTACCCCAA	AGAAATTGCA	GAACCCAGAA	1380
	AGGCATTTAT	GCAAGAAACA	GAGGTCAAG	GCATACAGTG	AGAGGAGTCC	ACCAGCCAG	1440
	GGAGCCACTG	GCCCAGAGGA	GCAAAGTGAC	AGCCTCAAA	CGGTCTTGCA	CAGCATAAGC	1500
40	TTTGTGGTGA	GAAAGTTATG	TCGTTATCCC	GAAGCCGAGC	TCCTGGCTTG	GAGGTGGCCA	1560
	GCAGTGTGTT	TGGGAGAAAT	CATCAGAGGA	TACAGGCTTC	ATGGATTTC	TGCTAAAGAC	1620
	AAGGATGAAT	CTAGAAGGCT	TCTTACTTGG	CCCCAAGAG	TGGATAGGAC	TCAAAGGGCA	1680
	GCCAAATACC	TGGGGAAGAT	CTTGGGAATA	TGTGGGAATG	TGGGAAGTGG	AAAGAGCTCC	1740
	CTCCTTGAG	CTCTCTAGG	ACAGATGCAG	CTGCAGAAAG	GGGTGGTGGC	AGTCAATGGA	1800
45	ACTTTGGCCT	ACGTTTACCA	GCAGGCATGG	ATCTTTCATG	GAAATGTGAG	AGAAAAATA	1860
	CTCTTTGAG	AAAAGTATGA	TCACCAAGG	TATCAGCACA	CAGTCCGCTG	CTGTGGCCTC	1920
	CAGAAGGACC	TGAGCAACCT	CCCCTATGGA	GACCTGACTG	AGATTGGGGA	GCGGGGCTC	1980
	AACCTCTCTG	GGGGGCGAGG	GCAGAGGATT	AGCCTGGCCC	GCGCTGTCTA	CTCCGACCGT	2040
	CAGCTCTACC	TGCTGGACGA	CCCCCTGTGG	GCCGTGGAGC	CCCACGTGGG	GAAGCAAGTC	2100
50	TTTGAAGAGT	GCATTAAAGAA	GACGCTCAGG	GGAAAGACAG	TCGTCCTGGT	GACCCACCGG	2160
	CTACAGTCT	TAGAGTCTTG	TGATGAAGTT	ATTTTATTAG	AAATGGGAGA	GATTGTGAA	2220
	AAGGGAACCC	ACAAAGGAGT	AATGGAGGAG	AGAGGGCGCT	ATGCAAAAT	GATTTCACAAC	2280
	CTGCGAGGAT	TGCAGTTCAA	GGATCTTGAA	CACCTTTACA	ATGCAGCAAT	GGTGGAGGCC	2340
	TTCAAGAGGA	GCCCTGCTGA	GAGAGAGGAA	GATGCTGGA	TAATCGGGTA	CCTCCTTTCT	2400
	CTCTTCACTG	TGTTCTCTTT	CCTCTGATG	ATTGGCAGCG	CTGCCTTCAG	CAACTGGTGG	2460
55	CTGGGTCTCT	GGTTGGACAA	GGGCTCAGG	ATGACCTGTG	GGCCCCAGGG	CAACAGGACC	2520
	ATGTGTGAGG	TCGGCGCGGT	GCTGGCAGAC	ATCGGTCAAG	ATGTGTACCA	GTGGGTGTAC	2580
	ACTGCAAGCA	TGGTGTTCAT	GCTGGTGTG	GGCGTCAACA	AAGGCTTCGT	CTTCAACCAAG	2640
	ACCACACTGA	TGGCATCTCT	CTCTCTGCAT	GACACGGTGT	TTGATAAGAT	CTTAAAGAGC	2700
	CCAATGAGTT	TCTTTGACAC	GACTCCCACT	GGCAGGCTAA	TGAACCGTTT	TTCCAAGGAT	2760
60	ATGGACGAGC	TGATGTGAG	GCTGCCCTTT	CACGCAAGAG	ACTTTCGCA	GCAGTTTTTT	2820
	ATGGTGGTGT	TTATTCTCGT	GATCTTGGCT	GCTGTGTTTC	CTGCTGTCTT	TTTAGTGTGT	2880
	GCCAGCCTTG	CTGTAGGCTT	CTTCATCTTG	TTACGCATTT	TCCACAGAGG	AGTCCAGGAG	2940
	CTCAAGAAGG	TGGAGAATGT	CAGCCGCTCA	CCCTGGTTCA	CCCACATCAC	CTCCTCCATG	3000
65	CAGGGCCTGG	GCATCAATTA	CGCCTATGGC	AAGAAGGAGA	GCTGCATCAC	CTATACTTCA	3060
	TCCAAAGGCC	TGTCATTGTC	ATACATCATC	CAGCTGAGCG	GACTGTCTCA	AGTGTGTGTG	3120
	CGAACCGGAA	CAGAGAGCGA	AGCCAAATTC	ACCTCCGTGG	AGCTGCTCAG	GGAATACATT	3180
	TCGACCTGTG	TTCTTGAATG	CACTCATCCC	CTCAAAGTGG	GGACCTGTCC	CAAGGACTGG	3240
	CCACAGCTGTG	GGGAGATCAC	CTTCAGAGAC	TATCAGATGA	GATACAGAGA	CAACACCCCC	3300
70	CTTGTCTCTG	ACAGCCTGAA	CTTGAACATA	CAAAGTGGGC	AGACAGTCCG	GATTGTTGGA	3360
	AGAACAGGTT	CCGGAAGTCT	ATCGTTAGGA	ATGGCTTTGT	TTGCTCTGGT	GGAGCCAGCC	3420
	AGTGGCACAA	TCTTTATTGA	TGAGGTGGAT	ATCTGCATTC	TCAGCTTGGG	AGACCTCAGA	3480
	ACCAAGCTGA	CTGTGATCCC	ACAGGATCCT	GTCTCTGTTG	TAGGTACAGT	AAGGTACAAC	3540
	TTGGATCCCT	TTGAGAGTCA	CACGATGAG	ATGCTCTGGC	AGGTTCTGGA	GAGAATCTTC	3600
75	ATGAGAGACA	CAATAATGAA	ACTCCAGAAA	AAATTACAGG	CAGAAGTCAC	AGAAAATGGA	3660
	GAAACCTTCT	CAGTAGGGGA	ACGTGAGCTG	CTTTGTGTGG	CCCGAGCTCT	TCTCCGTAAT	3720
	TCAAAGATTA	TCTCTCTTGA	TGAAGCCACC	GCCTCTATGG	ACTCCAAGAG	TGACACCCCTG	3780
	GTTCAAGACA	CCATCAAAAG	TGCCCTCAAG	GGCTGCACTG	TGCTGACCAT	CGCCCAACCG	3840
	CTCAACACAG	TCTCAACTG	CGATCAAGTC	CTGGTTATGG	AAAATGGGAA	GGTGATTGAG	3900
80	TTTGACAAGC	CTGAAGTCTT	TGCAGAGAAG	CCAGATTCTG	CATTTCGAT	GTTACTAGCA	3960
	GCAGAAGTCA	GATTGTAG					

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Protein Accession #: Eos sequence

1 11 21 31 41 51
 5 MVBGGPYLIS DLDQRRRRS FAERYDPSLK TMIPVRPCAR LAPNFVDDAG LLSFATPSWL 60
 TPVMVKGFRQ RLTVDTLPL STYDSSDTNA KRFRVLWDEE VARVGPEKAS LSHVVWKFOR 120
 TRVLMDIVAN ILCIIMAAIG PTVLIHQILQ QTERTSGKVM VGIGLCIALF ATEFTKVFFW 180
 ALAWAINYRT AIRLKVVALST LVFENLVSPK TLTHISVGEV LNILSSDSYS LPEAALFCPL 240
 PATIPILMVF CAQYAFFILG PTALIGISVY VIFIPVQMF AKLNSAFRRS AILVTDKRVQ 300
 TMNEFLT CIR LKMYAWEKS FTNTIQDIRR RERKLEKAG FVQSGNSALA PIVSTIAIVL 360
 10 TILSCHILLRR KLTAPVAFVS IAMPNVMKFS IAILPFSIKA MAEANVSLRR MKKILIDKSP 420
 PSYITQPEDP DTVLLLANAT LTWEHEASRK STPKKLQNK RHLCKQRSE AYSERSPPAK 480
 GATGPEEQSD SLKSVLHSIS FVVRKLCRYP EAQLLAWRWP AVFVGRIIRG YRPHGFSAKD 540
 KDESRRLLTW PQEVDRTQRA AKYLGIKILGI CGNVGSGKSS LLAALLGQMQLQKGVVAVNG 600
 TLAYVSQQA W IPHGNVRENI LPGEKYDHQR YQHTVRVCG L QKDLNLFPYG DLTEIGERGL 660
 15 NLSSGQQRRI SLARAVYSR QLYLLDDPLS AVDAHVGKHV FEBCIKKTLR GKTVVVLVTHQ 720
 LQFLESCDEV ILLEDGEICE KGTHELMEE RGRYAKLIHN LRGLQPKDPE HLYNAAMVEA 780
 FKESPAEREE DAGIIGYLLS LFTVFLFLIM IGSAAFSNNW LGLWLDKGSR MTCGPQGNRT 840
 MCEVGAVLAD IQGHVYQWVY TASMVFMVLF GVTKGPFVTK TILMASSSLH DTVFDKILKS 900
 PMSFEDTTP T GRIMNRFSD MDELVDRLPF HAENFLQQFF MVVPIVLILA AVFPAVLV 960
 20 ASLAVGFIL LRIHFHRQVE LKKVENVSRS FWFTHITSSM QGLGIIHAYG KKESCITYTS 1020
 SKGLSLSYII QLSGLLQVCV RTGTETQAKF TSVELLREYI STCVPECTHP LKVGTCPKDW 1080
 PSGEITFRD YQMYRDNTP LVLDLSNLNI QSGQTVGIVG RTGSGKSSLG MALFRLVEPA 1140
 SGTIFIDEVD ICILSLEDLR TKLTVIPQDP VLFVGTVRYN LDPFESHTDE MLWQLERTF 1200
 MRDTIMKLPE KQAEVTENG ENFSVGERQL LCVARALLRN SKIILLDEAT ASMDSKTDTL 1260
 25 VQNTIKDAFK GCTVLTIAHR LNTVLNCDHV LVMENKGVIE FDKPEVLAEK PDSAFAMLLA 1320
 AEVRL

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 Coding sequence: 1-966

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 35 AGCCCGGAGC GCGTCAAGCG GCCCATGAAT GCCTTCATGG TGTGTCGCC CGGGCAGCGG 180
 CGCAAGATGG CCCAGGAGAA CCCCAAGATG CACAACCTGG AGATCAGCAA GCGCTCGGC 240
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 40 AAGACGCTCA TGAAGAAGGA TAAATACAG CTGCCCGGCG GGCTGCTGGC CCGCGCGGCG 420
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 45 ATGAACGGCT CGCCCACTA CAGCATGTCC TACTGCGAG AGGGACCCCC TGGCATGGCT 720
 CTTGGCTCCA TGGGTTGGT GGTCAAGTCC GAGGCCAGT CCAGCCCCC TGTGTTACC 780
 TCTTCTTCCC ACTCCAGGGC GCGCTGCCAG GCGGCGGACC TCGGGACAT GATCAGCATG 840
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 50 ATGTAGGGGC CGGACAGCGA ACTGGAGGGG GGAGAAATTT TCAAGAAAA ACAGGGGAAA 1020
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 AAAAA

Seq ID NO: 314 Protein sequence
 Protein Accession #: CAA83435

1 11 21 31 41 51
 55 HSARMYNMME TELKPPGPQQ TSGGGGNGST AAAAGGNQKN SPDRVIRPMN AFMVWSRGQR 60
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 60 KTLMKDKYT LPGGLLAPGG NSMASGVGVG AGLGAGVNR MDSYAHMNGW SNGSYSMQD 180
 QLGYPHFPL NAHGAQMMP MERYDVSAQ YNSMTSSQTY MNGSPTYSMS YSQQGTGMA 240
 LSGMSGVVK SASSSPVVT SSSHSRAPCQ AGDLRDMISM YLPGAEPVPEP AAPSRLEMSQ 300
 HYQSGFVPGT AINGTLPLSH M

Seq ID NO: 315 DNA sequence
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 Coding sequence: 29..541

1 11 21 31 41 51
 70 CGGACTTGGC TTGTTAGAAG GCTGAAAGAT GATGGCAGGA ATGAAATCC AGCTTGATG 60
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 AGCATTAGAA CGAGATTCTT TGACCAATAT GCATACATCA AAGATTAGTA AAGCACATGT 180
 75 TCCTCTTGG AAGATGACTC TGCTAAATGT TTGCAGTCT GTAAATAATT TGAAACAGCCC 240
 AGCTGAGGAA ACAGGAGAGG TTCAATGAAG GGAGCTTGT GCAAGAAGGA AACTTCTTAC 300
 TGCTTAGAT GCCTTAGCT TGGAAGCAAT GTTGACAATA TACCAGCTCC ACAAATCTG 360
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 80 GCTGTATGAG AATAAACCCA GAAGACCTTA CATACTCAA AGAGATTCTT ACTATTACTG 540
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Seq ID NO: 316 Protein sequence
Protein Accession #: AAB50564

5 1 11 21 31 41 51
MMAGMKIQLV QMLLLAPSSW SLCSDSSEEM KALEADPLTN MHTSKISKAH VPSWKMTLLN 60
VCSLVNMLNS PAETGEVHE EELVARRKLP TALDGPFSLEA MLTIYQLHKI CHSRAFPQHWE 120
LIQEDILDTG NDNKGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSYYY

10 Seq ID NO: 317 DNA sequence
Nucleic Acid Accession #: NM_006536.2
Coding sequence: 109..2940

15 1 11 21 31 41 51
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AGCAITGCAG GTCTTATTGG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA 180
GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
20 ATTGCAATTA ATCCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAAACAT TAAGSAAATG 300
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25 TTCTACTGA ATGATACTT AACAGCTGGC TACGGATCAC GAGGCGAGT GTTGTCCAT 600
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35 ATTCATACCT TCGTGGGCAT TGCCAGTTTC GACAGCAAAG GAGAGATCAG AGCCGAGCTA 1200
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40 TTCTTGGCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCA CTCCATTGCC 1440
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45 ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCTGAGA TTATATTATT TGATCTGAT 1740
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50 TATGCCAATG TGAACAGGGG ATTTTATCCC ATCTTAAATG CCACGTGCAC TGCCACAGTT 2040
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55 GCTCCAGGAA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340
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60 AAGCGAAGTC GTGCAATGAG TGGCATCAGG GAGATATTTA CGTCTCACC CCAGATTTC 2640
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65 CATACTTTAA CGAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATA 2940
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CCTTACACTT TGGCTATGAA CAATAATATA AAATTATTCT TTAAAGTAAT GTCTTTAAAG 3180
70 GCAAAGGGAA GGGTAAAGTC GACCCAGTGT CAAGGAAAGT TTGTTTATT GAGGTGGA 3240
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TCATTAGTT ACTTTGATTA ATTTTCTTTT TCTCCTTATC TGTGCACTAC AGGTGCTTG 3360
TTTACATGAA GATCATGCTA TATTTATAT ATGTAGCCCC TAATGCAAGG CTCTTTACCT 3420
CTTGTCTATT TGTATATAT ATTTACAGAT ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480
75 TTTCACCTGA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT 3540
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TACCTAGGAA A

80 Seq ID NO: 318 Protein sequence
Protein Accession #: NP_006527.1

1 11 21 31 41 51
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 GDDPYTLQYR GCGKEKYIH FTFNPLNDN LTAGYGSRRG VFWHEWAHLR WGVFDEYNND 180
 KPPYINGQNK IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKBGCTFIY NSTQMATASI 240
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 10 AVFPATVEAF VERDSLHFPF VMIIYANVQK GFYPIILNATV TATVEPETGD PVTLLRLDDG 660
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Seq ID NO: 319 DNA sequence
 Nucleic Acid Accession #: NM_000228.1
 Coding sequence: 82..3600

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Seq ID NO: 320 Protein sequence
 Protein Accession #: NP_000219.1

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Seq ID NO: 321 DNA sequence
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Seq ID NO: 322 Protein sequence
Protein Accession #: NP_001935.1

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Seq ID NO: 323 DNA sequence
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Protein Accession #: P39900

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	TACACAGCCA	GGGCTGTGTC	GCTGTCTGAT	AAGAAAAGAT	CATTACCAT	ATGGCTTTCT	360
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10	TCGAAGACAA	GACACACTAG	AGAAACTGTT	CTCAGGCGTG	CCAAGAGGAG	ATGGGCACCT	480
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	GATAAGGATT	TAATTAACAC	TGCCAATTGG	ACAGTCAATT	TTACCATTTT	AAAGGGAAT	1260
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80	GAAGCAGCAG	TTTACAGATG	AGTATCTATG	ATACATATGT	ATAATAAAT	TTGATCGGGT	6120
	ATTAAAGTA	TTAGAAGGTT	GTTATAATTT	CAGAGTATTC	CATGAATAGT	ACACTGACAC	6180
	AGGGGTTTTA	CTTTGAGGAC	CAGTGTAGTC	AAGGGAAAAC	ATGAGTTAAA	AAGAAAAGCA	6240
	GGCAATATTG	CAGTCTTGAT	TCTGCCACTT	ACAGGATAGA	TAAATGCTGA	ACTTTAATGA	6300
	CAAGATGATC	CAACCATAAA	GGTGCTCTGT	GCTTCACAGT	GAATCTTTTC	CCCATGCAGG	6360

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AGTGTGCTCC CCTACAAACG TTAAGACTGA TCATTTCAAA AATCTATTAG CTATATCAAA 6420
 AGCCTTACAT TTAAATATAG GTTGAACCAA AATTTCAAAT CCAGTAACTT CTATTGTAAC 6480
 CATTATTTTT GTGATGTGCT TCAAGAAATG TCATTGGATT TTTGTTTGTA ATAGTAAAT 6540
 ACCGATACA TTTCACGTGT CTTTCAATAT TGATTGGTT GAATATTGGG TCATAATGGT 6600
 TGAGAAGCAT GGACACTAGA GCCAGAATGC TTGGATATGA ATCTCGGATC TGTCACTTAC 6660
 TTCTGTGTGA CCTTTGAAGG GCTACTTATT TCCTCTCTTA GCTTCTCTAT TAAATCAAT 6720
 GAACAATGCC AGCTGCATGG GGTGTGTGAA TGATTAAAT AGTTAATATA CCTAAAGTAC 6780
 ATAGAACT GCCTGCACAT AGTAAAGAA TTATAAGTGT GAGGTAGTTG GTAAATATAT 6840
 GTAGTTGGAT ATACTACGA ACAATATCTA ATCTCTTTT AGGGAATAA AGTTTGTGCA 6900
 TATATATAAT CCGAAACAT G

Seq ID NO: 328 Protein sequence
 Protein Accession #: NP_001932.1

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1 11 21 31 41 51
 MAAGPRRSV RGAVCLHLLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS 60
 ADLIRSSDPD FRVLNDGSVY TARAVALSDK KRSFTIWLSD KRKQTQKEVT VLLEHQKKVS 120
 KTRHRTETVL RRAKRNRWAPI PCSMQENSLG PFPLFLQQVE SDAAGNYTVF YSISGRGVDK 180
 EPLNLFYIER DTGNLFCTRP VDREYDVFD LIAYASTADG YSADLPPLFP IRVEDENDNH 240
 PVTEAIYNF EVLESSRPGT TVGVVCAADR DEPDTHMTRL KYSILQQTFR SPGLFSVHPS 300
 TGVITTVSHY LDREVVDKYS LIMKVQDMQG QFFGLIGTST CIITVDSND NAPTFRQNAV 360
 EAPVEENAFN VEILRIPIED KDLINTANWR VNFTILKGNH NGHPKISTDK ETNEGVLVSV 420
 KPLNVEENRQ VNLEIGVNNE APPARDIPRV TALNRALVTV HVRDLDEGPE CTPAAQYVRI 480
 KENLAVGSKI NGYKAYDPEN RNMNGLRYKK LHPKGMITI DEISGSIITS KILDREVETP 540
 KNLNITVYL AIDKDRSCT GTLAVNIEDV NDNPEILQE YVVICPKMG YTDILAVDPD 600
 EPVHGAPFFY SLFNTSPEIS RLWSLTKVND TAARLSYQKN AGFQYETIPI TVKDRAGQAA 660
 TKLLRVNLCE CTHPTQCRAT SRSTGVILGK WAILAILLGI ALLFVLLTL VCGVFGATKG 720
 KRFPEDLAQ NLIIISNTEAP GDDRVCSANG FMTQTNNSS QGFCGTMGSG MKNGGQETIE 780
 MMKGNGQLE SCRAGHHT LDSCRGGHTE VDNCRYTYSR WHSFTQPLRG EKLHRCNQNE 840
 DRMPSQDYVL TYNVEGRGSP AGSVGCCSEK QBEDGLDFLN NLEPKFITLA EACTKR

Seq ID NO: 329 DNA sequence
 Nucleic Acid Accession #: NM_016583.2
 Coding sequence: 72..842

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1 11 21 31 41 51
 GGAGTGGGGG AGAGAGAGGA GACCAGGACA GCTGCTGAGA CCTCTAAGAA GTCCAGATAC 60
 TAAGAGCAAA GATGTTTCAA ACTGGGGGCC TCATTGTCTT CTACGGGCTG TTAGCCCAGA 120
 CCATGGCCCA GTTTGGAGGC CTGCGCGTGC CCCTGGACCA GACCCTGCC TGAATGTGA 180
 ATCCAGCCCT GCCCTTGAGT CCCACAGGTC TTGCAGGAAG CTTGACAAAT GCCCTCAGCA 240
 ATGGCCTGCT GTCTGGGGGC CTGTTGGGCA TTCTGGAAAA CCTTCGCTC CTGGACATCC 300
 TGAAGCCTGG AGGAGGTACT TCTGGTGCC TCCTTGGGGG ACTGCTTGA AAAGTGAOGT 360
 CAGTGATTC TGGCCTGAAC AACATCATTG ACATAAAGST CACTGACCCC CAGCTGCTGG 420
 AACTTGGCCT TGTGCAGAGC CCTGATGCCC ACCGTCTCTA TGTCAACATC CCTCTCGGCA 480
 TAAAGCTCCA AGTGAATACG CCCTGGTGG GTGCAAGTCT GTTGAAGGCTG GCTGTGAAGC 540
 TGSACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC 600
 TTGGTGAAGT CACCCATTC CCTGGAAGCC TGCAAAATTC TCTGCTTGAT GGACTTGGCC 660
 CCTCCCTCCG TCAAGGTCTT CTGGACAGCC TCACAGGGAT CTTGAATAAA GCTCTGCTGG 720
 AGTTGGTTCA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGGC TTGGACATCA 780
 CCTGGTGCCA TGACATTGTT AACATGCTGA TCCACGGACT ACAGTTTGTC ATCAAGGTCT 840
 AAGCCTTCCA GGAAGGGGCT GGCTCTGCT GAGCTGCTC CCAGTGCTCA CAGATGGCTG 900
 GCCCATGTGC TGAAGATGA CACAGTTGCC TTCTCTCGGA GGAACCTGCC CCTCTCTCTT 960
 TCCACACAGG CGTGTGTAA ATCCATGTG CCTCACCTAA TAAATGGCT CTCTCTCTGC 1020
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 330 Protein sequence
 Protein Accession #: NP_057667.1

65
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1 11 21 31 41 51
 MFQTGLLIVP YGLLAQTMAG FGGLFVPLDQ TLPLAVNPAL FLSPITGLAGS LTNALSNGLL 60
 SGGLLGILEN LPLLDLKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL 120
 VQSPDGHRLY VTPIPLGIKLQ VNTPLVGASL LRLAVKLDIT AEILAVRDKQ ERIHLVLGDC 180
 THSPGSLQIS LLDGLGPLPI QGLDLSLTGI LNKVLPVLVQ GNVCPVNEV LRGLDITLHV 240
 DIYNMLIHGL QFVIKV

Seq ID NO: 331 DNA sequence
 Nucleic Acid Accession #: NM_004363.1
 Coding sequence: 115..2223

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1 11 21 31 41 51
 CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60
 TCCTGGAACT CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120
 TCTCCCTCGG CCCCTCCCCA CAGATGGTGC ATCCCTGGC AGAGGCTCCT GCTCAGACC 180
 TCACCTCTAA CCTTCTGGAA CCGGCCACAC ACTGCCAAGC TCACTATTGA ATCCAGCCG 240
 TTCATGTGCG CAGAGGGGAA GGAGGTGCTT CTACTGTGCC ACAATCTGCC CCAGCATCTT 300
 TTTGGCTACA GCTGGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAT TATAGGATAT 360
 GTAATAGGAA CTCACCAAGC TACCCAGGG CCGCATACA GTGGTCGAGA GATAATATAC 420
 CCCAATGCAT CCTGTCTGAT CCAGAACATC ATCCAGAATG ACACAGGATT CTACACCTTA 480

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CACGTCATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCGG GGTATACCCG 540
 GAGCTGCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT 600
 GTGGGCTTCA CCTGTGAACC TGAGACTCAG GCGCAACCT ACCTGTGGTG GGTAAACAAT 660
 CAGAGCCTCC CGGTCACTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720
 TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAAT 780
 GCCAGGCGCA GTGATTCAGT CATCTGTAAT GTCTCTATG GCCCGGATGC CCCCACCAAT 840
 TCCCTCTTAA ACACATCTTA CAGATCAGGG GAAATCTGA ACCTCTCCTG CCAAGCAGCC 900
 TCTAACCCAC CTGCACAGTA CTCTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960
 GAGCTCTTTA TCCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020
 AACTCAGACA CTGGCTCAA TAGGACCACA GTCACGACGA TCACAGTCTA TGCAGAGCCA 1080
 CCAAAACCCCT TCATCACCAG CAACAACCTC AACCCCGTGG AGGATGAGGA TGCTGTAGCC 1140
 TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200
 CTCCCGTCA GTCCAGGCT GCAGCTGTCC AATGACAACA GGACCTCAC TCTACTCAGT 1260
 GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTGAC 1320
 CACAGCGACC CAGTCATCCT GAATGTCCTC TATGGCCGAG ACGACCCAC CATTTCCCCC 1380
 TCATACACCT ATTACCGTCC AGGGGTGAAC CTCAGCCTCT CCGCCATGC AGCCTCTAAC 1440
 CCACTGCAC AGTATTCTTG GCTGATTGAT GGGAAACATCC AGCAACACAC ACAAGAGCTC 1500
 TTTATCTCCA ACATCACTGA GAAGAACAGC GGAATCTATA CCGCCAGGC CAATAACTCA 1560
 GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCAGAG TCTCTGCGGA GCTGCCCAAG 1620
 CCCTCCATCT CCGCAACAA CTCCAACCC GTGGAGGACA AGGATGCTGT GGCCTTCACC 1680
 TGTGAACCTG AGGCTCAGAA CACAACTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740
 GTCAGTCCCA GGTGTCAGCT GTCCAATGGC AACAGGACCC TCACTCTATT CAATGTACA 1800
 AGAAATGAGC CAAGAGCCTA TGTATGTGGA ATCCAGAATC CAGTGAGTGC AAACCGCAGT 1860
 GACCCAGTCA CCCTGGATGT CCTCTATGGG CCGGACACCC CCATCATTTT CCCCCAGAG 1920
 TCGTCTTACC TTTGGGAGC GAACTCAAC CTCTCTGCC ACTCGGCTC TAACCCATCC 1980
 CCGCAGTATT CTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTATC 2040
 GCCAAATCA CGCCAAATAA TAACGGGACC TATGCTCTT TGTCTCTAA CTGGCTACT 2100
 GGCCGCAATA ATTCCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCTGGT 2160
 CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTGGGGT TGCTCTGATA 2220
 TAGCAGCCCT GGTGTAGTTT CTTCATTTCA GGAAGACTGA CAGTTGTTT GCTTCTCCT 2280
 TAAAGCATTT GCAACAGCTA CAGTCTAAAA TTGCTTCTT ACCAAGGATA TTACAGAAA 2340
 AGACTCTGAC CAGAGATCGA GACCATCCTA GCCAACATCG TGAACCCCA TCTCTACTAA 2400
 AAATCAAAA ATGAGCTGGG CTGGTGGCG OGCACTGTA GTCCAGGITA CTGGGAGGC 2460
 TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCAC 2520
 ACTGCATCC AGTCTGGCAA CAGAGCAAGA CTCATCTCA AAAAGAAAAG AAAAGAAAG 2580
 TCTGACCTGT ACTCTGAAT ACAAGTTTCT GATACCATG CACTGTCTGA GAATTTCCAA 2640
 AACTTTAATG AACTAATCTA CAGCTTCATG AAATGTCCA CCAAGATCAA GCAGAGAAAA 2700
 TAATTAATTT CATGGGACTA AATGAACTAA TGAGGATTGC TGATTCTTTA AATGTCTGT 2760
 TTCCAGATT TCAGGAAACT TTTTCTCTT TAAGCTATCC ACTCTACAG CAATTGATA 2820
 AAATATACTT TGTGAAACAA AAATGAGAC ATTACATTT TCTCCCTATG TGGTCGCTCC 2880
 AGACTTGGGA AACTATTCAT GAATATTTAT ATTGTATGGT AATATAGTTA TTGCACAAGT 2940
 TCAATAAAAA TCTGCTCTT GTATAACAGA AAAA

45 Seq ID NO: 332 Protein sequence
 Protein Accession #: NP_004354.1

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1 11 21 31 41 51
 MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLHVNLPQ 60
 HLFYGSWYKQ ERVDGNRII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY 120
 TLHVKSIDL NBEATGQFRV YPELPKPSIS SNNSKPVEDK DAVAFCTCEPE TQDATYLNWV 180
 NNQSLFVSPR LQLSNGNRTL TLFNVTRNDT ASYKCBTQNP VSARRSDSVI LNVLYGPDAP 240
 TISPLNTSYR SGENLALSCH AASNPPAQYS WFNVTFOQS TOELFIPNIT VNNSGYSYTC 300
 AHNSTGLNR TTVTTITVYA EPPKPPITSN NSNPVEDEDA VALTCRPEIQ NITYLWVWVN 360
 QSLFVSPRLQ LENDNRLTL LSVTRNDVGF YEOGIQNELS VDHSDFVILN VLYGPDPTI 420
 SPSYTYRPG VNLSSLCHAA SNPPAQYSWL IDGNIQQHTQ ELFISNITEK NSGLYTCQAN 480
 NSAGHSRTT VKTITVSAEL KPSPISNNNS KPVEDKDAVA FTCEFEAQNT TYLWVWVQS 540
 LPVSPRLQLS NGNRTLTLEN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDPIISP 600
 PDSSYLSGAN LNLSCSHASN PSPQYSWRIN GIPQHQTVL FIAKITPMNN GTYACFVSNL 660
 ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI

65 Seq ID NO: 333 DNA sequence
 Nucleic Acid Accession #: NM_006952.1
 Coding sequence: 11..793

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1 11 21 31 41 51
 AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCGTGTC TTCCAGGGCC TGCTGATTTT 60
 TGGAAATGTG ATTATTGGTT GTTGGCGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTGT 120
 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
 GGCTGCTCGG ATCGGCATAT TTGTGGCAT CTGCCTCTTC TGCCGTCTCG TTCTAGGCAT 240
 TGTAGGCATC ATGAAGTCCA GCAGGAAAT TCTTCTGGCG TATTTTCATC TGATGTTTAT 300
 AGTATATGCC TTTGAAGTGG CATCTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
 ACCCAACCTC TTCTCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCACAAACA 420
 TGATGACCAAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480
 CAATTGCTGT GCGGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540
 TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
 AGAACCTCTC AACCTGGAGG CTGTGAACT AGGCGTGCTT GGTTTTATC ACAATCAGGG 660
 CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACAACCC TGGGGGGTTG CTTGGTTTGG 720
 ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCCTGGGT ACCATGTTCT ACTGGAGCAG 780
 AATTGAATAT TAAGAA

Seq ID NO: 334 Protein sequence
 Protein Accession #: NP_008883.1

1 11 21 31 41 51
 5 MAKDNSTVRC FQGLLIIFGNV IIGCCGIALT AECIPFVSDQ HSLYPLLEAT DNDDIYGAAW 60
 IGIFVGICLF CLSVLIGVIGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFPTPNL 120
 FLKQMLERYQ NNSPPNDDQ WKNGVTKTW DRLMLQDNCC GVNGPSDNQK YTSAPRTENN 180
 DADYFPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNGQCYE LISGPMNRHA WGVAVFGFAI 240
 LCWTFWVLLG TMFYWSRIEY

10 Seq ID NO: 335 DNA sequence
 Nucleic Acid Accession #: NM_002638.1
 Coding sequence: 120..473

1 11 21 31 41 51
 15 CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CGCCCTCGGA GCCAGGCCAA 60
 GCTGGACGCC ATAAGGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG 180
 AGGCAGCTGT CACGGGAGTT CCTGTTAAGG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
 20 TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300
 CGCAAGAGCC AGTCAAAGGT CCACTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360
 TCOGGTGGCG CATGTTGAAT CCCCTTAACC GCTGCTTGAA AGATACTGAC TGCCAGGAA 420
 TCAAGAAAGTG CTGTGAAGGC TCTTGGCGGA TGGCTGTTT CGTTCCTCCAG TGAAGGGAGC 480
 CGGTCTCTGC TGCACTCTGC CCGTCCCGAG AGCTACAGGC CCATCTGCTT CCTAAGTCCC 540
 25 TGGTGCCTTT CCCCTTCCA CACTGTCCAT TCTTCTCTCC ATTCAAGATG CCCACGGCTG 600
 GAGCTGCCCT TCTCATCCAC TTTCATATAA

Seq ID NO: 336 Protein sequence
 Protein Accession #: NP_002629.1

1 11 21 31 41 51
 30 MRASSFLIVV VFLIAGTLVL EAAVTGVPEVK GQDTVKGRVP FNGQDPVKQ VSVKGQDKVK 60
 35 AQEPVKGVPV TKGSCPIIL IRCAMLNPPN RCLKDTDCPG IKKCEGSGS MACFVFPQ

Seq ID NO: 337 DNA sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71..2560

40 1 11 21 31 41 51
 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CGCCCGTGGC GGCAGCTGCT TCACCCCTCT 60
 CTCTGACGCG ATGGGGCTCC CTGCTGGACC TCTCGCGTCT CTCTCCTTC TCCAGGTTTG 120
 45 CTGGCTCGAG TGCGCGGCGT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
 CTTGGAGGCG GGAGGGCGCG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTATGGG 240
 CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGGGAA 300
 TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
 50 TGAAATATGGC AAGGTCCTT TCCCCAGAG ACTGAATCAG CTCAAGTCTA ATAAAGATAG 480
 AGACACCAAG ATTTTCTACA GCATCACGGG GCGGGGGGCA GACAGCCCC CTGAGGGTGT 540
 CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
 GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTGAGAG AATGGTGCCT CAGTGGAGGA 660
 CCGCATGAAC ATCTCATCA TGTGACCGA CCAGATGAC CACAAGCCCA AGTTTACCCA 720
 55 GGACACCTTC CGAGGAGTG TCTTAGAGGG AGTCCCTACCA GGTACTTCTG TGATGCAGGT 780
 GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAT GGGGTGGTTG CTTACTCCAT 840
 CCATAGCCAA GAACCAAGG ACCCAACGGA CCTCATGTTT ACCATTACCC GGAGCACAGG 900
 CACCATCAGC GTCACTCTCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960
 CATCCAGGCG ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGA 1020
 60 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
 GCGTGAAGAT GCAATGGGCC ATGAGTGACA GAGGCTGACG GTCAGTGATC TGGACGCCCC 1140
 CAATCACCAC GGTGGCGTGG CCACCTACCT TATCATGGGC GGTGAAGACG GGGACCATTT 1200
 TACCATCACC ACCCACTCTG AGAGCAACCA GGGCATCCTG ACAACCAGGA AGGGTTTGA 1260
 TTTTGAGGCC AAAAACCAGC ACACCTGTA CGTTGAAGTG ACCAAGCAGG CCCCTTTTGT 1320
 65 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
 ACCTGTGTTT GTCCACCCCT CCAAGTGTGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
 GCGTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGTACCG 1500
 CATCTGAGGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560
 TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACACATCT ATGAAGTCAT 1620
 70 GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
 ACTGATTGAT GTCAATGACC ATGGCCAGT CCGTGAAGCC CGTCAGATCA CCATCTGCAA 1740
 CCAAGCCCT GTGGCCAGG TGCTGAACAT CAAGGACAAG GACCTGTCTC CCCACCTC 1800
 CCCTTTCCAG GCGGAGCTCA CAGATGACTC AGACATCTAC TGAAGCGCAG AGGTCAACGA 1860
 GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920
 75 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
 GTGCGCACTG CATGGCCATG TCGAAACCTG CCGTGAAGCC TGAAGGGAG GTTTCATCCT 2040
 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGTGCTGCT TTTTGTGGT 2100
 GAGAAGAGAG CGGAAGATCA AGGAGCCCTT CCTACTCCCA GAAGATGACA CCGGTGACAA 2160
 CGTCTTCTAC TATGTGGGAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
 GCTCCACCGA GGTCTGGAGG CCGGGCCGGA GGTGTTCTCT CGCAATGAGC TGGCACCAAC 2280
 80 CATCATCCCG ACACCATATG ACGTCTCTG GCCAGCCAAC CCAGATGAAA TCGCAACTT 2340
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCAAC GCCCGCCCT ACACACCTT 2400
 CTTGGTGTTC GACTATGAGG CGAGCGCGCG TCCCTGAGCT CCTCACCTC 2460
 CTCGCGCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGCTTCAA 2520
 GAAGCTGGCA GACATGTACG GTGGCGGGGA GGAAGACTAG GCGGCTGCC TGCAGGGCTG 2580

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GGGACCAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG 2640
GACTTCGGAG CTGTGCAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
ACGTAGAGT GGTGCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCCTCAG AGGCCAAGTT TCCAGAAGCC 2820
TCTTACCTGC CGTAAATGC TCAACCTGT GTCTGGGCC TGGCCCTGCT GTGACTGACC 2880
TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCTGTGTGA ACTTAATTTT 2940
TTTTTTAAT GCTATCTCA AAACGTTAGA GAAAGTCTT CAAAAGTGCA GCCCAGAGCT 3000
GCTGGGCCCA CTGGCCGTCC TGCATTCTG GTTTCAGAC CCCAATGCC CCCATTCCGA 3060
TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTGGC CCTTATTTT TATTTTCCCT 3120
GTTGCGTTG TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
TAAAGAACT TTTCCAGAA AAAAA

Seq ID NO: 338 Protein sequence
Protein Accession #: NP_001784.2

1 11 21 31 41 51
MGLPRGPLAS LLLLQVCNLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMCPCP 60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
KGFFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLILN KPLDREBIAX 180
YELFGHAYSE NGASVREDPMN ISIIIVTDQND HKPKFTQDTP RGSVLEGVLP GTSVMQVTAT 240
DEDDAIITYN GVVAYSISHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
TMDGDGSGTT TAVAVVEILD ANDNAPMFDK QRYEAHVPEM AVGHEVQRLT VTDLDAPNSP 360
AWRATYILMG GDDGDHFTIT THPESNOGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ ESIPTGEFVC VYTAEDPDKE NQKISYRILR 480
DPAGWLMAMP DSGQVTAUGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLLID 540
VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPTSPFFQ AQLTDDSDIY WTAEVNBEED 600
TVVLSLKKFL LVLLLVLRKK RKIKEPLLLP EDDTRDNVFI YGEEGGGEED QDYDITQLHR 660
GAVLALLFL LVLLLVLRKK RKIKEPLLLP EDDTRDNVFI YGEEGGGEED QDYDITQLHR 720
30 GLEARPEVVL RNDVAPTIP TMYRPRPAN FDEIGNPIIE NLKAANTDPT APPYDTLLVF 780
DYEAGSSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

Seq ID NO: 339 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..672

1 11 21 31 41 51
ATGAGGCTCC AAAGACCCCG ACAGGCCCGG GCGGGTGGGA GCGCGCGGCC CCGGGGCGGG 60
CGGGGCTCCC CCTACCGGCC AGACCCCGGG AGAGGCGCGC GGAGGCTCGG AAGGTTCCAG 120
AAGGGCGGGG AGGGGGCGCC GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGCG 180
CTGCTCGGCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGAGCG CAACCTGACT 240
GCGAGACAAC GAGATCCAGA GGACTCCAG CGAACGGACG AGGGTGACAA TAGAGTGTGG 300
TGTCATGTTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAAAATG 360
ACAGAGCCAT ACTCGGTAT AGCGGCCGTG AAAATATTTC CAGGTTTTTT CATGGTTGCG 420
AAGCAGTGCT CGCTGCTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480
CTCTGGAAG AGCCCATGCC CTTCTTTTAC CTCAGTGTGT GTAAAATTCC CTAAGTCAAT 540
TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAGAAT ATGCTGGGAG CATGGGTGAG 600
AGCTGTGGTG GCGCTGGGCT GGCCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGCGCTC 660
50 AGCCTGTCTT GA

Seq ID NO: 340 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
MRLQRPRQAP AGRRRAPRGG RGSFYRPDPG RGARRLRFRQ KGEGAPRAD PPWAPLGTMA 60
LLALLLVVAL PRVWTDANLT ARQDPEDSQ RTDEGDNRVW CHVCRENTF ECQNPRRCKW 120
TEPYCVIAAV KIFPRFFMVA KQCSAGCAAM ERPKPEEKRF LLEPPMPFFY LKCKKIRYCN 180
60 LBGPPINSSV FKEYAGSMGE SCGGLWLAIL LLLASTAAGL SLS

Seq ID NO: 341 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53..1576

1 11 21 31 41 51
GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
TGCGGGCCCC AAGCGGCGCG CGCTAGCGGC GCGCGCGGCC GAGGAGAAGG AAGAGGCGCG 120
GGAGAAGATG CTGGCGCGCA AGAGCGCGGA CGCTCGCGCG CCGGACAGCG AGGGCGAGGG 180
CGTGACCCCTG CAGCGGAACA TCAAGCTGCT CAACGGCGTG GCCATCATG TGGGGACCAT 240
TATCGGCTCG GGCATCTTGG TGAAGCCAC GGGCGTGCTC AAGGAGGCGG GCTCGCGGGG 300
GCTGCGCTCG TGCGGTGTGG CGCGTGTGGT CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360
CGCGAGCTTC GGCACACCA TCTCCAAATC GGGCGGCGAC TACGCTTACA TGCTGGAGGT 420
CTACGCTCG CTGCGCGCTT TCCTCAAGCT CTGATCGAG CTGCTCATCA TCGGCGCTTC 480
ATCGCAGTAC ATCGTGGGCC TGGTCTTGG CACCTAAGCT CTCAAGCGGC TCTTCCCCAC 540
CTGCGCGGTG CCGGAGGAGG CAGCCAGGCT CGTGGCTGCG CTCTGGTGGT TGCTGCTCAC 600
GGCGGTGAAC TGCTACAGCG TGAAGGCGCG CACCGGGTCC CAGGATGCCT TTGCGCGCGC 660
CAAGCTCTCG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720
75 TGTGTCCAAT CTAGATCCCA ACTTCTCAT TGAAGGCACC AAACCTGGATG TGGGGAACAT 780
TGTGCTGGCA TTATACAGCG GCCTCTTGG CTATGAGGGA TGAATTACT TGAATTGGT 840
CAGAGAGGAA ATGATCAACC CCTACAGAAA CCGTCCCTCG GCCATCATCA TCTCCCTGCC 900
CATCGTAGCG CTGGTGTAGG TGTGACCAA CCGTGGCTAC TTCAACACCC TGTCCACCGA 960
80 GCAGATGCTG TGTGCCGAGG CGTGGCGGTG GACTTCGGG AACTATCAC TGGGCGTCAT 1020

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GTCTGGATC ATCCCGTCT TCGTGGGCTT GTCCTGCTTC GGCTCCGTCA ATGGGTCCCT 1080
GTTACATCC TCAGAGCTCT TCTTGTGGG GTCCCGGAA GGCCACCTGC CCTCCATCCT 1140
CTCATGATC CACCCACAGC TCCTCACCCC CGTGCCTGCC CTGCTGTTC CTGTGTGAT 1200
GACGCTGCTC TAGCCTTCT CCAAGGACAT CTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TGGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
TGAGCTTGAG CGGCCATCA AGGTGAACCT GGCCCTGCCT GTGTCTTCA TCCTGGCCTG 1380
CCTCTTCCCT ATCGCCGCTCT CCTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
CATCATCTC AGCGGGCTGC CGTCTACTT CTTCGGGCTC TGGTGGAAA ACAAGCCCAA 1500
GTGGCTCCTC CAGGCGATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGTGGT 1560
CCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC
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Seq ID NO: 342 Protein sequence
Protein Accession #: XP_035292.2

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1 11 21 31 41 51
MAGAGPKRRA LAAPAAEEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
GTIIGSGIVF TPTGVLEKAG SPGLALVWVA ACGVFSIVGA LCVABLGTTI SKSGGDYAYM 120
LEVYGSLPAP LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCLVL 180
LLTAVNCYSV KAATRVQDAF AAALLLALAL IILLGFVQIG KGDVSNLDPN FSPBGTKLDV 240
GNIVLALYSG LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLFIVTLVYV LTNLAYFTTL 300
STEQMLSSSA VAVDFGNYHL GVMWIIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP 360
SILSMIRPQL LTFVPSLVFT CVMTLLYAPS KDIPSVINFF SFENMLCVAL AIIGMILRHL 420
RKPFLERPIK VNLALPVFFI LACLFIAIVS FWKTPVECGI GPTIILSLGP VYFFGVWWRN 480
KPKWLLQGIF STTVLQQLM QVVPQET
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Seq ID NO: 343 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168..989

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1 11 21 31 41 51
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TCTGGATAG AAATTCAGAC TGCTTGCTGA GTCTTATGCG CGGCTGCTGG GAGCCAGGAG 120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
TCTTTGAGGG ACTCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
TGCTCTGGT CTTCATCTTC CGCGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA 300
GTGATGACCA CAAGGACTTC GACTGCAATA CTGCGCAGCC CGGCTGCTCC AACGCTCTGT 360
TGATGAGTGT CTTCCTGCTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCTCTGTGA 420
CATGCCCTCT ACTGCTCGTG GTCATGCACG TGGCTACCG GGAGGTTTCA GAGAAGAGGC 480
ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGGGG 540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GCGAGCGTG GACATCGCCT 600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCTCTGTG GTCAAGTGCC 660
ACGCAGATCT ATGTCCCAAT ATAGTGGACT GCTTCTATCT CAAGCCCTCA GAGAAGAAAC 720
TTTTCACTCT CTTCATGGTG GCCACAGCTG CCATCTGCAT CCGCTCAAC CTGCTGGAGC 780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCTGGC AGCAAGGAAA GCTCAAGCCA 840
TGTGCACAGG TCATCACCCC CACGCTACCA CCTCTTCTCG CAAACAGAC GACCTCTTT 900
CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCTCC TCTCTTACCA GACCGCCCC 960
GAGACCATGT GAAGAAACC ATCTTGTGAG GGGCTGCTG GACTGGTCTG GCAGGTTGGG 1020
CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGAGGCTC TGGGAGCCAG TTCTAGTCC 1140
TCAACTCCAG CCACTGCCC CAGCTCGACG GCATCTGGCC AGTTCCCTCT CTGCTCTGCA 1200
GCTCGGTTTC CTTTCTAGA ATGAAATAG TGAGGGCCAA TGC
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Seq ID NO: 344 Protein sequence
Protein Accession #: NP_005259.1

60
65

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1 11 21 31 41 51
MNWSIFEGLL SGVNYSTAF GRWLSLVFI FRVLVYLVT A ERVWSDDHKD FDCNTRQPGC 60
SNVCFDEFPF VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRRHRAHG ENSGRLYLNP 120
KKRGRGLWWT YVCSLVFKAS VDLAFLYVPH SFYPKYILPP VVKCHADPCP NIVDCFISKP 180
SEKNIFTLEM VATAAICILL NLVELIYLV S KRCHECLAAR KQAMCTGHH PHGTTSSCKQ 240
DDLSDGLIF LGSDSHPPLL PDRPRDHVKK TIL
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Seq ID NO: 345 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26..457

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1 11 21 31 41 51
CGGGCGAAGC AGCGCGGCGA GCGAGATGCA GCAACGAGGC TTCTCTCTCC TCACCTCCT 60
CGCCCTGCTG GCGCTCACCT CGCGGCTGCG CAAAAGAGAA GATAAGGTGA AGAAGGGCGG 120
CCCGGGGAGC GAGTGCCTCG AGTGGGCTG GGGGCGCTGC ACCCCAGCA GCAAGGATTG 180
CGCGGTGGGT TTCCGCGAGG GCACCTGCGG GGCCAGAAC CAGCGCATCC GGTGCAAGGT 240
GCCTTGCAAC TGGAGAAGG AGTTTGGAGC CGACTGCAAG TACAAGTTTG AGAACTGGGG 300
TGCGTGTGAT GGGGCGACAG GCACCAAGT CCGCCAGGC ACCCTGAAGA AGGCGGCTA 360
CAATGCTCAG TGCCAGSAGA CCATCCGCGT CACCAAGGCC TGCACCCCA AGACCAAGC 420
AAAGGCCAAA GCAAGAGAA GGAAGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA 480
GCCCTGTGTC TCATATGGG CCTGGCCACG CCTCCCTCT CCCAGGCCCG AGATGTGACC 540
CACCAGTGCC TTCTGTCTGC TGGTTAGCTT TAATCAATCA TGCCCTGCTT TGTCCCTCTC 600
ACTCCCAGC CCCACCCCTA AGTGCCCAA GTGGGGAGG ACAAGGGATT CTGGGAAGCT 660
TGAGCCTCCC CCAAGCAAT GTGAGTCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC 720
ATTACTAAGA AACACATCAA ATAAACTGAC TTTTCCCCC CAATAAAGC TCTTCTTTT 780
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TAATAT

Seq ID NO: 346 Protein sequence
Protein Accession #: NP_002382.1

5
10
1 11 21 31 41 51
| | | | |
MQHRGFLLLT LLALLALTSA VAKKDKVKK GPGSECAEN AWGPCTPSSK DGVGFREGT 60
CGAQTQRI RC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLLKA RYNAQCQETI 120
RVTKPCTPKT KAKAKAKKKK GKD

Seq ID NO: 347 DNA sequence
Nucleic Acid Accession #: NM_006783.1
Coding sequence: 1..786

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1 11 21 31 41 51
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ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACTCTC CACCAGCATC 60
GGGAAGGTGT GGATCAGAGT CATCTTTATT TTCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC 180
AAAAATGTGT GCTATGACCA CTTTTCCTCG GTGTCCACCA TCCGGCTGTG GGGCTCCAG 240
CTGATCTTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
ATTAAAAAGC ACAAGGTTTC GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
TTTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCTT TTACRAATGGG 480
TACCACCTGC CCTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCTT TGTGACTGTC 540
TTTATTTCTA GGCCCAACAGA GAAGACCGTG TTTACCATTT TTATGATTTC TGCCTCTGTG 600
ATTTGCATGC TGCTTAACTG GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTITAGG 660
AGATCAAAGA GAGCAGAGAC GCACAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
CAGAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
AGCTAA

Seq ID NO: 348 Protein sequence
Protein Accession #: NP_006774.1

35
40
1 11 21 31 41 51
| | | | |
MDWGLTHPTI GGVNKHSTSI GKVVITVIFI FRVMILVVAQ QEVWGDQED FVNTLQPGC 60
KNVCYDHPFP VSHRLNALQ LIFVSTPALL VAMHVAYYRH ETTRKFRGE KRNDFKDIED 120
IKKKKVRIG SLWWTYTSSI FFRIFEAAR MYVFYFLYNG YHLPWVLKCG IDPCPNLVDC 180
FISRPTEKTV FTIFMISASV ICMILNVAEL CYLLLVKCFR RSKRAQTQKN HPNHALKESK 240
QNEWHELISD SQNAITGFP S

Seq ID NO: 349 DNA sequence
Nucleic Acid Accession #: NM_002571.1
Coding sequence: 99..587

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1 11 21 31 41 51
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CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCCTCTGC 60
TCACCCCTGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
AGGACCTGGA GCTCCCAAGG TTGGCAGGGA CCTGGCCTCT CATGGCCATG GGGACCAACA 180
ACATCTCTCT CATGGGACA CTGAGGGCCC CTCTGAGGGT CCACATCACC TCACTGTITG 240
CCACCCCGGA GGACCAACCTG GAGATCGTTC TGACAGATG GGAGAACCAAC AGCTGTGTGT 300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGGCGAAGCA GGCCACGCTG CTGATACTG ACTACGACAA TTTCTGTITT CTCTGCCTAC 420
AGGACACAC CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCTGTGTGG 480
AGGACATGAT GATCATGAG GGAATTCATCA GGGCTTTTCA GCCCTGCCCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAG CAGATGGAAG AGCGTGCCG TTTCTAGCTC ACCTCCGCTT 600
CCAGGAAGAC CAGACTCCCA CCCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCCCC 660
TTTCAAAGAA TAACCAAGC TCAGAAGAGC ATGAAGTGGT CATCTGTGTC GCCATCCCTT 720
TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAACC CTTGGAGCAT G

Seq ID NO: 350 Protein sequence
Protein Accession #: NP_002562.1

70
1 11 21 31 41 51
| | | | |
MDIPQTKQDL ELPLKAGTWE SMAMATNNIS LMATLKAPLR VHITSLPPT EDNLEIVLHR 60
WENNSCVEKK VLGEKGTGNFK KFKINYTVAN EATLLDLDYD NFLFLCLQDT TTIPIQSMMD 120
YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLKQMBEPC RF

Seq ID NO: 351 DNA sequence
Nucleic Acid Accession #: NM_006500.1
Coding sequence: 27..1967

80
1 11 21 31 41 51
| | | | |
ACTTGGTCT CGCCCTCCGG CCAAGCATGG GGCTTCCAG GCTGGTCTGC GCCTTCTTGC 60
TCGCGGCTG CTGCTGCTGT CCTCGCTGCG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG 120
CGCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180
AGTCCCAAG CAACCTCAGC CATGTGACT GTTTTCTGT CCACAAGGAG AAGCGGAGCG 240
TCATCTTCCG TGTCCGCGAG GCCCAGGGCC AGAGCGAACC TGGGAGTAC GAGCAGCGGC 300

5 TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCTGACTCA AGTCACCCC CAAGACGAGC 360
 GCATCTTCTT GTGCGAGGGC AAGCGCCCTC GGTCCAGGA GTACCGCATC CAGCTCCGCG 420
 TCTACAAAGC TCCGGAGGAG CCAAAACATCC AGGTCAACCC CCTGGGCATC CCTGTGAACA 480
 GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCTCTAAG 540
 TCATCTGGTA CAAGAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCACT 600
 CGTCCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660
 TGGTTAAAGA AGACAAAGAT GCCAGTTTCT ACTGTGAGCT CACTACCCG CTGCCCAGTG 720
 GGAACCATAT GAAGAGATCC AGGGAAGTCA CGTCCCTGT TTTCTACCCG ACAGAAAAAG 780
 10 TGTGGCTGGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT 840
 GTTTGGCTGA TGGCAACCTT CCAACCACTT TCAGCATCAG CAAGCAGAAC CCCAGCACA 900
 GGGAGGCGAG GGAAGAGACA ACCAACGACA ACGGGGTCTT GGTGCTGGAG CCTGCCCGGA 960
 AGGAACACAG AGACCAAGAT GAATGTGAGG CCTGGAACTT GGACACCATG ATATCGCTGC 1020
 TGAGTGAACC ACAGGAACCTA CTGGTGAAGT ATGTGTCTGA CGTCCGAGTG AGTCCGCGAG 1080
 15 CCCCAGAGAG ACAGGAAGGC AGCAGCCTCA CCTGACCTG TGAGGCAGAG AGTAGCCAGG 1140
 ACCTCGAGTT CCAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAGG GGGCCTGTGC 1200
 TTCAGTTGCA TGACCTGAAA CGGGAGGCGAG GAGGCGGCTA TGGTCTGCTG GCGTCTGTGC 1260
 CCAGCATACC CGGCTGTAA CACACACAGC TGGTCAAGCT GGCCATTTT GGCCCCCTT 1320
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 20 GTGAAGCGTC AGGGCACCCC CGGCCACCA TCTCTGGJAA CGTCAACGCG ACGCAAGTG 1440
 AACCAAGACA AGATCCACAG CGAGTCTTGA GCACCTGAA TGTCTGCTG ACCCGGAGC 1500
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 TCTTCTGGA CTGGTCTAAT TTAACCAACC TCACACAGG CTCACACACA ACCACTGGCC 1620
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 25 TGCCGAGGCC GAGAGAGCCG GGGCTGGTCA TCGTGGCTGT GATTGTGTGC ATCTGTGTCC 1740
 TGCCGAGTCT GGGCGCTGTCT CTCTATTTC TCTATAAGAA GGGCAAGCTG CGGTGAGGC 1800
 GCTCAGGAGA GCAGGAGATC ACGCTGCCCC CGTCTCGTAA GACCGAACTT GTAGTTGAAG 1860
 TTAAGTCAAA TAAGCTCCCA GAAGAGATGG GCCTCTGCA GGGCAGCAGC GGTGACAAAG 1920
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 30 CAGCTCCCTT CCCTGCTGG ACCATTCCCA GCTCCCTGCT CACTCTTCTC TCAGCCAAAG 2040
 CCTCCAAAGG GACTGAGAGC AAGCCTCCTG CTCGCCCTAC CTGCAACCCC CTTTTCAGAG 2100
 GGCCACTGGG TTAGGACCTG AGGACCTCAC TTGGCCCTGC AAGCCGCTTT TCAGGGACCA 2160
 GTCCACCACC ATCTCTCCA CGTTGAGTGA AGCTCATCCC AAGCAAGGAG CCCCAGTCTC 2220
 35 CCGAGCGGGT AGGAGAGTTT CTGTCAGAAC GTGTTTTTC TTTACACACA TTATGGCTGT 2280
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 CAAAGAGTTC AGGACAGGAC CCAGGTGCAC CACTGAAGTG AGGACACACC GGAGCCAGGC 2400
 GCTGTCTCAT GTTGAAGTGC GCTGTTTACA CCGCTCCGG AGAGCACCCC AGCGGCATCC 2460
 40 AGAAGCAGCT GCAGTGTTC TCCCACCACC CTCTGCTCG CCTCTTCAA GTCTCTGTG 2520
 ACATTTTTTC TTTGGTCAGA AGCCAGGAAC TGGTGTCTAT CCTTAAAGA TACGTGCCGG 2580
 GGCCAGGTGT GGTGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCGGA GGGGGGGGGA 2640
 TCACAAAGTC AGGACAGAGC CATCTGGCT AACACGGTGA AACCTGTCT CTAATAAAAA 2700
 TACAAAAAAA AATTAGCTAG GCGTAGTGGT TGGCACCTAT AGTCCAGCT ACTCGGAAGG 2760
 CTGAAGCAGG AGAATGATAT GAATCCAGGA GGTGGAGCTT GCAGTGAGCC GAGACCGTGC 2820
 CAGTGACCTC CAGCTGGGCG AACACAGCGA GACTCCGCT CGAGGAAAAA AAAAGAAAAA 2880
 45 ACGCGTACCT GCGGTGAGGA AGCTGGGCGC TGTTTTCCAG TTCAGGTGAA TTAGCCTCAA 2940
 TCCCGTGTCT CACTGTCTCC CATAGCCCTC TTGATGGATC ACSTAAAACT GAAAGGCGAGC 3000
 GGGGAGCAGA CAAAGATGAG GTCTACACTG TCCTTCATGG GGATTAAGG TATGGTTATA 3060
 TTAGACCAA ACTTCTACAA ACCAAGCTCA GGGCCCCAAC CCTAGAAGG CCCAAATGAG 3120
 AGAATGATAC TTAGGATGG AAAACGGGGC CTGGCTAGAG CTTCCGGTGT GTGTGTCTGT 3180
 50 CTGTGTGAT GCATACATAT GTGTGATAT ATGGTTTTGT CAGGTGTGTA AATTGCAAAA 3240
 TTGTTTCTT TATATATGTA TGTATATATA TATATGAAAA TATATATATA TATGAAAAAT 3300
 AAAGCTTAAT TGTCCAGAA AATCATACAT TGCTTTTTTA TTCTACATG GTACCAAGG 3360
 AACCTGGGG CCTGTGAAA TACAACCAA AGGCACACAA AACCGTTCC AGTTGGCAGC 3420
 AGAGATCAGG GGTACCTCT GCTTCTGAGC AAATGGCTCA AGCTCTACCA GAGCAGACAG 3480
 55 CTACCTACT TTTACAGAGC AAAACGTCCC GTATGAAGCA GCACGAAGG CCTGGCAGGC 3540
 TGTAGCAGG AGCTATGTC CTTCCTATCG TTTCCGTCCA CTT

Seq ID NO: 352 Protein sequence
 Protein Accession #: NP_006491.1

60 1 11 21 31 41 51
 GLPRLVCAFL LAACCCCFRV AGVPGEABQP APELVEVEVG STALLKGLS QSQGNLSHVD 60
 WFSVHKEKRT LIFRVRQGG QSEPGYEYQR LSLQDRGATL ALTQVTPQDE RIFLCQGRKP 120
 65 RSQYEYRIQLR VYKAPPEPNI QVNPLGIFVN SKEPEEVATC VGRNGYPIPIQ VIWYKNGRPL 180
 KEKRNVRHIQ SSQTVESSGL YTLQSLKLAQ LVKEDKDAQF YCELNYRLPS GNMKESREV 240
 TVPVFPYPTK VWLEVEPVGM LKEGDRVEIR CLADGNPPPH FSISKQNPST REAEETIND 300
 NGVLVLEPAR KEHSGRYECQ AMNLDIMISL LSEPQELLVN YVSDVRVSPA APERQEGSSL 360
 70 TLTCBAESSQ DLBFQWLREE TDQVLERGPV LQLHDLKREA GGYRCVASV PSIPGLNRTQ 420
 LVKLAIFGPP WMAFKERKVV VKENMVLNLS CEASGHPRT ISMNVNGTAS EQDQDPQRLV 480
 STLNLVLTPE LLETGVECTA SNDLGRNTSI LFLELVNLTI LTPDSNTTGT LSTSTASPH 540
 RANSTSTERK LPPEPESRGVV IVAVIVCILV LAVLGAVLYF LYKKGKLPKR RSGRQEITLP 600
 PSRKTELVEV VKSDKLPPEM GLLQGSSGDK RAPGDQGEKY IDLRH

Seq ID NO: 353 DNA sequence
 Nucleic Acid Accession #: NM_003183.3
 Coding sequence: 165..2639

80 1 11 21 31 41 51
 TCGAGCCTGG CGGTAGAATC TTCCAGTAG GCGGCGGGG AGGAAAAAGA GGATTGAGGG 60
 GCTAGGCCGG GCGGATCCCG TCCTCCCGG ATGTGAGCAG TTTTCGAAA CCCGTCAGG 120
 GSAAGGCTGC CCAGAGAGGT GGAGTCGGTA GCGGGGCGG GAACATGAGG CAGTCTCTCC 180
 TATTCTGAC CAGCGTGGT CCTTCTGTG TGGCGCCGG ACCTCGGAT GACCCGGCT 240
 TCGCCCCCA CCAGAGACTC GAGAAGCTTG ATTCCTTGCT CTCAGACTAC GATATTCTCT 300

CTTTATCTAA TATCCAGCAG CATTCCGGTAA GAAAAAGAGA TCTACAGACT TCAACACATG 360
 TAGAAACACT ACTAATCTTT TCAGCTTTGA AAAGGCATT TAAATTATAC CTGACATCAA 420
 GTACTGAACG TTTTTCACAA AATTTCAAGG TCGTGGTGGT GGATGGTAAA AACGAAAGCG 480
 5 AGTACACTGC AAAATGGCAG GACTTCTTCA CTGGACACGT GGTGGGTGAG CCGTACTCTA 540
 GGGTCTAGC CCACATAAGA GATGATGATG TTATAATCAG AATCAACACA GATGGGGCCG 600
 AATATAACAT AGAGCCACTT TGGAGATTG TTAATGATAC CAAAGACAAA AGAATGTTAG 660
 TTTATAAATG TGAAGATATC AAGAATGTTT CACGTTTGCA GTCTCCAAAA GTGTGTGGTT 720
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 10 AAGAGCTTGT TCATCGAGTG AAAAGAAGAG CTGACCCAGA TCCCATGAAG AACACGTGTA 840
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 CAACTACAAA TTACTTAATA GAGCTAATITG ACAGAGTTGA TGACATCTAT CGGAACACTT 960
 CATGGGATAA TGCAGTTTTT AAAGGCTATG GAATACAGAT AGAGCAGATT CGCATTCTCA 1020
 AGTCTCCACA AGAGGTAAAA CCTGGTGAAG AGCACTACAA CATGGCAAAA AGTTACCCAA 1080
 15 ATGAAGAAAA GGATGCTTGG GATGTGAAGA TGTGCTAGA GCAATTTAGC TTTGATATAG 1140
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 GAACCTCTGG ATTAGCTTAT GTTGGCTCTC CCAGAGCAAA CAGCCATGGA GGTGTTTGTG 1260
 CAAAGGCTTA TTATAGCCCA GTTGGGAAGA AAAATATCTA TTTGAATAGT GGTGTGACGA 1320
 GCACAAGAAA TTATGGTAAA ACCATCCTTA CAAAGGAAGC TGACCTGGTT ACAACTCATG 1380
 20 AATTGGGACA TAATTTTGA GCAAGACATG ATCCGAGTGG TCTAGCAGAA TGTGCCCGA 1440
 ATGAGGACCA GGGAGGGAAA TATGTATGAT ATCCCATAGC TGTGAGTGGC GATCACGAGA 1500
 ACAATAAGAT GTTTTCAAA TGCAGTAAAC AATCAATCTA TAAGACCAAT GAAAGTAAAG 1560
 CCGAGGATGT TTTTCAAGAA CGCAGCAATA AAGTTTGTGG GAACCTGAGG GTGGATGAAG 1620
 GAGAAGAGTG TGATCTCGGC ATCATGTATC TGAACAACGA CACCTGTGTC AACAGCGACT 1680
 25 GCACGTTGAA GGAAGGTGTC CAGTGCAGTG ACAGGAACAG TCCTTGTCTGT AAAAATCTGC 1740
 AGTTTGAAGC TGCCAGAGAG AAGTGCCAGG AGGCGATTAA TGCTACTTGC AAAGGCGTGT 1800
 CCTACTGCAC AGGTAATAGC AGTGAGTGCC CGCCTCCAGG AAATGCTGAA AATGACACTG 1860
 TTTGCTTGGG TCTTGGCAAG TGTAAAGGAT GGAATATGAT CCCTTCTGTC GAGAGGGGAA 1920
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 30 ACCTTTCTGG CCGCTGTGTG CCCTATGTG ATGCTGAACA AAAGAACTTA TTTTGAAGG 2040
 AAGGAAGGCC CTGTACAGTA GGATTTTGTG ACATGAATGG CAAATGTGAG AAACGAGTAC 2100
 AGGATGTAAT TGAACGATT TGGGATTTC TTAGCCAGCT GAGCATCAAT ACTTTTGAA 2160
 AGTTTGTAGC AGACAACATC GTTGGGTCTG TCCTGTGTTT CTCTTGATA TTTTGGATT 2220
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 35 CTCTGTTCAC CCCCAGTAAC GTGCAAAATG TGAGCAGCAT GGATTTCTGA TCGGTTCCGA 2340
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 GSCCACTACA CTCCAGCTG GGTGACAGAG TGAGATCTGC CTC

Seq ID NO: 354 Protein sequence
 Protein Accession #: NP_003174.2

60 1 11 21 31 41 51
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 GEPDSRVLAH IRDDVLIIRI NTDGAENIE FLWRVNDTK DKRMLVYKSE DIKNVSRLO 180
 65 PKVCGYLKVD NEELLFPGLV DREPPPELVH RVKRRADPDP MKNTCKLLV ADHFRFYRM 240
 RGEESTTINY LIELIDRVDD IYRNTSWDNA GPKGYGQIE QIRILKSPQE VKPGEKHYN 300
 AKSYPNEEKD AWDVIMLEQ FSPDIAERAS KVCLAHFTY QDFDMGTGL AYVGSPRANS 360
 HGGVCPKAY SPVGKNIYL NSGLTSTKNY GKTILTKHAD LVTTHLGHN PGAHPDGL 420
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 70 SRVDEGECD PGIMYLNNDT CCNSDCTLKE GVQCSDRNSP CCKNCQETA QKQCEAINA 540
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 KVCCRLSGR CVPYVDABEQ NLFLRKGP KC TVGFCDMNGK CERRVQDVIE RFWDFIDQL 660
 INTFGKFLAD NIVGSLVLF LIFNIPFSL VHCVDKLDK QYBSLSLPH SENVMLSSMD 720
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Seq ID NO: 355 DNA sequence
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Seq ID NO: 356 Protein sequence

Protein Accession #: NP_068604.1

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 GEPDSRVLAH IRDDVIRI NTDGAEYNIE PLNRFPVNDK DKRMLVYKSE DIKNVSR LQS 180
 PKVCGYKVD NEELLPKGLV DREPPPELVH RVKRRADPDF MKNTCKLLV ADHRFYRYMG 240
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 AKSYFNEERD ANDVRMLLEQ PSFDIABRAS KVLALHFTY QDFDMGTGL AYVGSFRANS 360
 HGGVCPKAY SPVVKKNYL NSGLTSTKNY GKTILTKRAD LVTTHELGN FGAEHDPDGL 420
 AECAPNEQD GKYVMPYIAV SGDHEHNMKF SNCSKQSIYK TIESKAQECF QERNKVCNG 480
 SRVDGEED PGIMYLNNDT CCNSDCTLKE GVQCSDRNSP CCRNCQFETA QKKQEAINE 540
 TCKGVSCTG NSSECPFPGN AEDDTVCLDL GKCKDGRKCP FCEREQQLBS CACNETDN 600
 KVCCRDLSGR CVFYVDABQK NLFLRKGP KC TVGFCDMNGK CKRRVQDVIE RFWDFFIDQLS 660
 INTFGKPLAD NIVGSVLVFS LIFWIPFSL VHCV

Seq ID NO: 357 DNA sequence

Nucleic Acid Accession #: NM_004994.1

Coding sequence: 20..2143

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 CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGCCTGCGC TGCTGCTTCT 240

5	CCAGAAGCAA	CTGTCCCTGC	COGAGACGGG	TGAGCTGGAT	AGGCCCAOCG	TGAAGGCCAT	300
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	CAAGTGGCAC	CACCACAACA	TCACCTATTG	GATCCAAAAC	TACTCGGAAG	ACTTGCOCGS	420
	GGCGGTGATT	GAOGACGCTT	TTGCCCGGCG	CTTGGCACTG	TGGAGGCGGG	TGACGCCGCT	480
	CACCTTCACT	CGCGTGTACA	GCGGGGACGC	AGACATCGTC	ATCCAGTTTG	GTGTGCGGGA	540
	GCACGGAGAC	GGGTATCCCT	TOGACGGGAA	GGACGGGCTC	CTGGCACACG	CCTTTCCTCC	600
	TGGCCCGGCG	ATTGAGGGAG	ACGCCCATTT	OGAOGATGAC	GAGTTGTGTT	CCCTGGGCAA	660
	GGGCGTGGTG	GTTCCAACTC	GGTTTGAAAA	CGCAGATGGC	GCGGCTTGCC	ACTTCCOCTT	720
10	CATCTTGGAG	GGCCGCTCCT	ACTCTGCTTG	CACCACCGAC	GGTGGCTCCG	ACGGCTTGCC	780
	CTGGTGCAGT	ACCAAGGCCA	ACTACGACAC	CGACGACCGG	TTTGGCTTCT	GCCCCAGOGA	840
	GAGACTCTAC	ACCCGGGACG	GCAATGCTGA	TGGGAAACCC	TGCCAGTTTC	CATTCACTTT	900
	CCAAGGCCAA	TCCCTACTCG	CCTGCAACAC	GGACGGTGGC	TCCGACGGCT	ACCGCTGGTG	960
	CGCCACCAAC	GCCAACTACG	ACCGGGACAA	GCTCTTGGGC	TTCTGCCCGA	CCCAGAGCTGA	1020
15	CTCGACGGTG	ATGGGGGGCA	ACTCGGCGGG	GGAGCTGTGC	GTCTTCCCTT	TCACTTTCTT	1080
	GGTAAGGAG	TACTCGACCT	GTACCAAGGA	GGGCGCGGGA	GATGGGCGCC	TCTGGTGCGC	1140
	TACCACCTCG	AACTTTGACA	GCGACAAGAA	GTGGGGCTTC	TGCCCGGACC	AAGGATACAG	1200
	TTTGTTCCTC	GTGGCGGGCG	ATGAGTTGCG	CCAGCGCTGG	GGCTTAGATC	ATTCTCTAGT	1260
	GCGCGAGGCG	CTCATGTACC	CTATGTACCG	CTTCACTGAG	GGGCCCCCTT	TGCATAAGGA	1320
20	CGACGTGAAT	GGCATCTCGG	ACCTCTATGG	TCCTCGCCCT	GAACTGAGC	CACGGCCCTC	1380
	AACCACCAAC	ACACCGCAGC	CCACGGCTCC	CCCGACGGTC	TGCCCCACCG	GACCCCCAC	1440
	TGTCCACCCC	TCAGAGCGCC	CCACAGCTGG	CCCCACAGGT	CCCCCTTCAG	CTGGCCCCAC	1500
	AGGTCCCCCC	ACTGCTGGCC	CTTCTACGGC	CACCTACTGTG	CCTTTGAGTC	CGGTGGACGA	1560
	TGCGCTGAAC	GTGAACATCT	TOGACGCCAT	CGCGGAGATT	GGGAACCAAG	TGTATTGTGT	1620
25	CAAGGATGGG	AAGTACTGGC	GATTCTCTGA	GGGCAGGGGG	AGCGGGCCGC	AGGGCCCCCTT	1680
	CCTTATCGCC	GACAAGTGGC	CCGCGCTGCC	CGCAAGCTG	GACTCGTCTT	TTGAGGAGCC	1740
	GCTCTCCAA	AAGCTTTTCT	TCTTCTCTGG	GCGCCAGGTG	TGGGTGTACA	CAGGCGCGTC	1800
	GGTGTCTGGC	CCGAGGCGCT	TGGACAAGCT	GGGCTTGGGA	GCGGACGTGG	CCAGGTGAC	1860
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30	GTTCGACGTG	AAGGCGCAGA	TGCTGGATCC	CCGAGCGGCC	AGCGAGGTGG	ACCGGATGTT	1980
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35	CAAACTGGTA	TTCTGTCTCT	GAGGAAAGGG	AGGAGTGGAG	GTGGGCTGGG	CCCTCTCTTC	2280
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Seq ID NO: 358 Protein sequence
Protein Accession #: NP_004985.1

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	ITYWIQNYSE	DLFRAVIDDA	FARAFALWSA	VTPLTFTRVY	SRDADIVIQF	GVAEHGCGYP	180
45	FDGKDGLLAH	AFPPGPGIQG	DAHFDDELW	SLGKGVVVP	RFGNADGAAC	HFFPIFEGRS	240
	YSACTTDRSG	DGLPWCSTTA	NYDTDDRFGF	CPSERLYTRD	GNADGKQCF	PFIFQGSYS	300
	ACTTDRSGDG	YRWCAATTANY	DRDKLFGFCP	TRADSTVMGG	NSAGELCVFP	FTPLGKEYST	360
	CTSEGRGDGR	LWCATTSNFD	SDKKMGPCPD	QGYSLFLVAA	HEFGHALGLD	HSSVPEALMY	420
	PMYRFTGEGP	LKDDVNGIR	HLYGPRPEPE	PRPPTTTTPQ	PTAPPTVCP	GPPTVHPSE	480
50	PTAGPTGPPS	AGPTGPTAG	PSTATTVPLS	FVDDACNVNI	FDALAEIGNQ	LYLFKDGKYN	540
	RFSBGRGSRP	QGPFLIADKW	PALPRKLDVS	FEEPLSKKLE	FFSGRVVWVY	TGASVLGPRR	600
	LDKLGLGADV	AQVTGALRSG	RGMILLFSGR	RLNRFVKAQ	MVDFRSASEV	DRMPGVPLD	660
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55 Seq ID NO: 359 DNA sequence
Nucleic Acid Accession #: NM_000213.1
Coding sequence: 127..5385

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	AAGAGGATGG	CAGGGCCACG	CCCGAGCCCA	TGGGCCAGGC	TGCTCCTGGC	AGCCTTGATC	180
	AGCGTCAGCC	TCTCTGGGAC	CTTGGCAAAC	CGCTGCAAGA	AGGCCCCAGT	GAAGAGCTGC	240
65	ACGAGTGTG	TCGCTGTGGA	TAAGGACTGC	GCCTACTGCA	CAGACGAGAT	GTTTCAGGGAC	300
	CGGCGCTGCA	ACACCCAGGC	GGAGCTGCTG	GCGCGGGGCT	GCCAGCGGGA	GAGCATGTGT	360
	GTATGGGAGA	GCAGCTTCCA	AATCACAGAG	GAGACCCAGA	TTGACACCAC	CCTGCGCGCG	420
	AGCCAGATGT	CCCCCAAGG	CCTGCGGGTC	CGTCTGCGGC	CCGGTGAGGA	GCGGCATTTT	480
	GAGCTGGAGG	TGTTTGAGCC	ACTGGAGAGC	CCCGTGGACC	TGTACATCCT	CATGGAATT	540
70	TCCAACCTCA	TGTCCGATGA	TCTGGACAAC	CTCAAGAAGA	TGGGCGAGAA	CCTGGCTCGG	600
	GTCTGAGGCC	AGCTCACCA	CGACTACACT	ATTGGAATTG	GCAAGTTTGT	GGACAAGTTC	660
	AGCGTCCCGC	AGACGAGCAT	GAGGCTGAG	AAGCTGAAGG	AGCCCTGGCC	CAACAGTGAC	720
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	AAATGTCAGG	GAGAGCGGAT	CTCAGGCAAC	CTGGATGCTC	CTGAGGGCGG	CTTGTGATCC	840
75	ATCCTGCAGA	CAGCTGTGTG	CACGAGGGAC	ATTGGCTGGC	GCCCGGACAG	CACCAACCTG	900
	CTGGTCTTCT	CCACCGAGTC	AGCCTTCCAC	TATGAGGCTG	ATGGCGCCAA	CGTGTGGGCT	960
	GGCATCATGA	GCGGCAACGA	TGAACGGTGC	CACCTGGACA	CCAGGGGAC	CTACACCCAG	1020
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	ATCATCCCCA	TCTTTGCTGT	CACCAACTAC	TCCTATAGCT	ACTACGAGAA	GCTTCAACAC	1140
80	TATTTCCCTG	TCTCTCACT	GGGGGTGCTG	CAGGAGGACT	CGTCCAACAT	CGTGGAGCTG	1200
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	CACATCCGCG	GGGGGGAAGT	GGGTATATAC	CAGGTGCAGC	TGCGGGCCCT	TGAGCACGCTG	1380
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 CTGGTCAACG ATGACAAACG ACCTATTGGG CCCATGAAGA AAGTGTGCTG TGCAACCCCT 3960
 45 AAGAACCAGA TGCTGCTTAT TGAGAACCTT CGGGAGTCCC AGCCCTACCG CTACACGGTG 4020
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 50 GGCAGCCAGA GCGCCAGCGT CTCOGATGAC ACTGAGCACC TGGTGAATGG CCGGATGGAC 4260
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 60 GCGCGAGAGC GTGAGGGTGT CATCACATT GAATCCAGG TGCAACCGCA GAGCCCACTG 4800
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 65 GCATTCCGGG TGGATGGAGA CAGCCCCGAG AGCCCGCTGA CCGTGGCGGG CCTCAGCGAG 5040
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 TACTG

Seq ID NO: 360 Protein sequence
 Protein Accession #: NP_000204.1

75

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1 11 21 31 41 51
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 EVFEFLESFV DLYILMDFSN SMSDDLNLK KMGQNLARVL SGLTSDYTIG FGKPFVDKVS 180
 PQTDMRPEKL KEPMFNSDPP FSPKNVISLT EDVDEFRNKL QGERISGNLD APEGGFDAIL 240
 QTAVCTRDIG WRFPDTHLLV FSTESAPHYE ADGANVLAGI MSRNDERCHL DTTGTYTYQR 300
 TDQYPSVPTL VRLLAKNHII PIPAVTNYSY SYTEKLHTYF FVSSLGVLEQ DSNINIVELLE 360
 EAFNRIRSNL DTRALDSPRG LRTEVTSKMP QKRTGSPFHI RRGEVGIYQV QLRALHVDG 420

5 THVQQLPEDQ KGNHILKPSF SDGLKMDAGI ICDVCTCELO KEVRSARCSF NGDFVCGQCV 480
 CSEGWSSGQC NCSTGSLSDI QPCLREGEDK PCSGRGEOQC GHCVCYGEGR YEGQFCEYDN 540
 FQCPRTSGLF CNDRGRCMSG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCEGR 600
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 LKRAEEVVVR CSFRDEDDDC TYSYTMEDGD APGPNSTVLV HKKKDCPPGS FWWLIPLLLL 720
 LLPLALLLLL LCKKYCACCK ACLALLPCCN RGHMVGFKED HYMLRENMA SDHLDTFMLR 780
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 KSQVSYRTQD GTAQGNRDYI FVEGELLFQF GEAWKELQVK LLELQEVDSL LRGRQVRRFH 1080
 VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPPHGDLAGP QNPNKAAGS 1140
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 15 AQGEGPSSSL VSCRTHQEVF SEPGRFAFNV VSVTVQLSW AEPATNGEI TAYEVCYGLV 1260
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 20 LPGSAFTLST PSAPGPLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCM AQGGGPAT 1620
 RVDGDSPEER LTVPLGSENV PYKFKVQART TEGFPEREG IITIESQDGG PFPQLGSRAG 1680
 LFQHLQSEY SSTTTHTSA TEPFLVDGPT LGAQHLEAGG SLTRHVTQEP VSRTLTSGT 1740
 LSTHMDQEFF QT

25 Seq ID NO: 361 DNA sequence
 Nucleic Acid Accession #: NM_013332.1
 Coding sequence: 1..63

30 1 11 21 31 41 51
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 35 GCAGAGGAGT AGGGTCTCT CAGCCATGAA GCATGTGTG AACCTCTACC TGTAGGTGT 240
 GGTAAGTACC CTACTCTCCA TCTTCGTTAG AGTGATGGAG TCCCTAGAAG GCTTACTAGA 300
 GAGCCCATCG CCGGGACCT CCGGACCAAC CAGAACCAA CTAGCCAAAC CAGAGCCAC 360
 CAAGGCGCTT CCAGACCATC CATCCAGAAG CATGTGATA GACCTCCTTC CATCTGGCC 420
 ATATTTTGA ACACCTGACCT AGACATGTCC AGATGGGAGT CCCATTCTTA GCAGACAAGC 480
 TAGACACCGT TGTAACCGA GAACATATTAC TAGGCCTTGA AGAACCTGTC TAACTGGATG 540
 40 CTCAATGCC CTGCAAGGCC TGTTAGGCC GGTTCGGTG GCTCATGCC GTAACTCTAG 600
 CACTTTGGGA GGCTGAGGTG GGTGGATCAC CTGAGGTGAG GAGTTGAGG CAGCCTCGC 660
 CAACATGGCG AAACCCCATC TCTACTAAA ATACAAAAGT TAGCTGGGTG TGGTGGCAGA 720
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 45 GAGGTGACG TGAACCGAGA TGCACTGCT GTACCCAGCC TGGGCCACAG TGCAAGACTC 840
 CATCTCAAAA AAAAAAAGAA AAAAAAAGC CTGTTAATG CACAGGTGTG AGTGGATTGC 900
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 TCCTCAGCAG TATGGCTCTG ACATCTCTTA GATGTCCCAA CTTCAGCTGT TGGGAGATGG 1020
 TGATAATTTT AACCTACTT CCTAAACATC TGTCTGGGTG TCCTTTAGTC TTGAATGTCT 1080
 50 TATGCTCAAT TATTTGGTGT TGAGCCTCTC TTCCACAAGA GCTCCTCCAT GTTTGGATAG 1140
 CAGTTGAAGA GTTGTGTGG GTGGGCTGTT GGGAGTGAGG ATGAGTGTGT CAGTGCCCAT 1200
 TTCTCATTTT ACATTTTAAA GTCTCTCTC CAACATAGTG TGTATTGGTC TGAAGGGGGT 1260
 GGTGGGATGC CAAAGCCTGC TCAAGTTATG GACATGTGG CCACCATGTG GCTTAAATGA 1320
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55 Seq ID NO: 362 Protein sequence
 Protein Accession #: NP_037464.1

60 1 11 21 31 41 51
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 MKHVLNLYLL GVVLTLLSIF VRVMSLEGL LESPSPGTSW TTRSQLANTE PTKGLPDHPS 60
 RSM

65 Seq ID NO: 363 DNA sequence
 Nucleic Acid Accession #: NM_023915.1
 Coding sequence: 250..1326

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 GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAC CAGGAATAAC CTATGCTGAA 180
 CCCAGCCTC AATCGTCCCC AAGTGTTCCT TGACACGCAT CTTTGCTTAC AGTGATCAC 240
 75 AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300
 CAAGAGATG ACATATCAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCCTCAC 360
 AATGAATTTG ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTGT GGCAGCATC 420
 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAC CAGCTTCATA 480
 TTCTATCTCA AAAACATAGT GGTTCAGAC CTCATAATGA CGCTGACATT TCCATTTCGA 540
 ATAGTCAATG ATGACGATT TGGACCTTGG TACTTCAAGT TTATCTCTG CAGATACACT 600
 80 TCAGTTTGT TTTATGCAA CATGTATACT TCCATCGTGT TCCCTGGGCT GATAAGCATT 660
 GATCGCTATC TGAAGGTGGT CAAGCCATT GGGGACTCTC GGATGTACAG CATAACCTTC 720
 ACGAAGGTTT TATCTGTTG TGTGTTGGTG ATCATGGCTG TTTTGTCTT GCCAATCATC 780
 ATCCTGACAA ATGATCAGCC AACAGAGGAC AATATCCATG ACTGCTCAA ACTTAAAGT 840
 CCTTTGGGGG TCAATAGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900
 GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960

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ATTACACTTT TCTGTCTGCG GTGTAATGTT TGCCTGGATC CAATAATTTA CTTTTTCATG 1200
TGTAGGTCAT TTTCAAGAAG GCTGTTCAAA AAATCAAATA TCAGAACCGAG GAGTGAAAGC 1260
ATCAGATCAC TGCAAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTCACTGAT 1320
GTGTAGGCTT TTTATTGTTT GTTGGAAATCG ATATGTACAA AGTGTAAATA AATGTTTCTT 1380
TTCATTATCC TTAATAAAAA AA

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Seq ID NO: 364 Protein sequence
Protein Accession #: NP_076404

1 11 21 31 41 51
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FYANMYTSIV FLGLISIDRY LKVVVKPFGDS RMYSTPTKV LSVCVWVIMA VLSLPNIILT 180
NGQPTEDNIH DCSLKLKPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQP 240
ISQSSSRKRIH NQSRIRVVAV FFTCFLPYHL CRIPPTFSHL DRLLDESAQK ILYYCKEITL 300
FLSACNVCLD PIIYFFMCRS PSRRLPKKSN IRTRESIRS LQSVRRSEVR IYYDYTDV

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Seq ID NO: 365 DNA sequence
Nucleic Acid Accession #: NM_005365.1
Coding sequence: 1..948

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TCCTCTGACA GCAAGGAGGA GGAGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCAGAGT 180
CCTCAGGAGG GCGCTTCTC CTCCATTTCG GTCTACTACA CTTTATGAGG CCAATTCGAT 240
GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGTTCGACCC AGCTCAGCTG 300
GAGTTCATGT TCCAAGAAGC ACTGAAATTG AAGGTGGCTG AGTTGGTTCA TTTCTGCTC 360
CACAAATATC GAGTCAAGGA GCCGGTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAAA 420
AATTACAAGC GCTACTTTCC TGTGATCTTC GGCAAGCCT CCGAGTTTAT GCAGGTGATC 480
TTTGGCACTG ATGTGAAGGA GGTGGACCCC GCCGGCCACT CCTACATCCT TGTCACTGCT 540
CTTGGCCTCT CGTGCATAG CATGCTGGGT GATGGTCATA GCATGCCCAA GGCCGCCCTC 600
CTGATCATTG TCCTGGGTGT GATCCTAACC AAAGACAAC TCGCCCTCTG AGAGGTTATC 660
TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAG AGCATGTGT CTACGGGGAG 720
CCGAGGAAGC TGCTCACCCA AGATTGGGTG CAGGAAAAC ACCTGGAGTA CCGGCAGGTG 780
CCCGGCACTG ATCCTGCGCA CTACGAGTTC CTGTGGGGTT CCAAGGCCCA CGCTGAAACC 840
AGCTATAGA AGGTCAATAA TTATTGGTTC ATGCTCAATG CAAGAGAGCC CATCTGCTAC 900
CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

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Seq ID NO: 366 Protein sequence
Protein Accession #: NP_005356.1

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1 11 21 31 41 51
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HKYRWKEPVI KAEMLESVIK NYKRYFFVIF GKASEFMQVI FGTDVKEVDP AGHSYILVTA 180
LGLSCDSMLG DGHSMFKAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VQKEEMFYPGE 240
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PSLYEEVLGE EQEGV

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Seq ID NO: 367 DNA sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86..1126

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1 11 21 31 41 51
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GTGCTACAGC TGGGTGCGA AAGCAGATGA CGATGCTCC CGAACAGA TGAAGACAGT 240
GAAGTGCGCG CCGGGCGTGG ACGTCTGCAC CGAGGCGGTG GGGGCGGTGG AGACCATCCA 300
CGGACAATTC TCGCTGGCAG TGCGGGGTTG CGGTTGCGGA CTCCCGGCA AGAATGACCG 360
CGGCTCGGAT CTTACGGGCG TCTGGCGTTC CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
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ATACCCGCCC AACCGCGTGG AGTGCTACAG CTGTGTGGCG CTGAGCGGGG AGGCGTGCCA 540
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CTTGACCGGC AAGCTCAACT TGAAGGACAG TAATGTGACT GTGTCTTCGC CTGTCCGGGG 660
CTGTGTCCAG GATGAATTTT GCACTCGGGA TGGAGTAACA GGCCCAAGGT TCACGCTCAG 720
TGGCTCTGTF TGCCAGGGGT CCGCTGTAA CTCTGACCTC CGCAACAAGA CTAATCTCTC 780
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GCCAGGCGCA ACCAGTCAAG CTCGAGACCA GGGAGTAGAA CACGAGGCTT CCGGGATGA 960
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CTTCTGCTGC GCTGTTTTCG GGCCTTGGGA AATAAAATAC CGTTGTATAT ATTCTGGCAG 1320

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5
GGGTGTTCTA GCTTTTGGAG GACAGCTCCT GTATCCTTCT CATCCTTGTC TCTCCGCTTG 1380
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GGTGGGACAA TGGCTCCCCA CTCTAAGCAC TGCCTCCCT ACTCCCGCA TCTTTGGGA 1560
ATCGGTTCCC CATATGTCTT CTTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC 1620
CTTATGCTCTG TGTGTGATCA GTTCTGCGCA CATAAATGCC TCAATAAGA TTTAATTACT 1680
TTGTATAGTG AAAAAAAA

10 Seq ID NO: 368 Protein sequence
Protein Accession #: NP_055215

15
1 11 21 31 41 51
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CTEAVGAVET IHGQPSLAVX GCGSGLPGKN DRGLDLHGLL AFIQLQCAQ DRCAKLNL 120
SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPFVVS CYNASDHVYK GCFDGNVLT 180
AANVTVSLPV RGCVDQDEFCT RDGVTGPGFT LSGSCCQGSR CNSDLRNKTY FSPRIPLVR 240
LPPPEPTTVA STTSVTSTTS AFVRPTSTTK PMPAPTSTQP RQGVHEASR DEEPRLTGGA 300
20 AGHQDRSNSG QYPKGGPQQ PHNKGCVAPT AGLAALLLAV AAGVLL

Seq ID NO: 369 DNA sequence
Nucleic Acid Accession #: NM_005329.1
Coding sequence: 1..1662

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CACTACCTGT CTTTGGGCT GTACGGGCGC ATCCTGGGCC TGCACCTGCT CATTAGAGC 180
CTTTTGGCT TCTTGGAGCA CCGGCGCATG CGACGTGCGG GCCAGGCCCT GAAGTGCGCC 240
TCCCGCGCGC GGGGCTCGGT GGCACCTGTC ATTGCGCGAT ACCAGGAGGA CCTGACTAC 300
TTGCGCAAGT GCGTGGCTC GGCACGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCATG 360
GTGGTGGATG GCAACCGCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG 420
GGCGGCACCG AGCAGGCGCG CTTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480
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TGCCAGGACC TGTTCAGTGA GACAGAGCTA GCCTTCTCTG TCTCTGGGGC TATACTGTAT 1560
GGCTGCTACT GGTGGGCGCT CCTCATGCTA TATCTGGCCA TCATGCGCCG GCGATGTGGG 1620
AAGAAGCCGG AGCAGTACAG CTTGGCTTTT GCTGAGGTGT GA

Seq ID NO: 370 Protein sequence
Protein Accession #: NP_005320.1

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VVDGNRQEDA YMLDIFHEVL GGTGAGFPV WRNPFHEAGE GETEASIQEG MDRVRDVVRA 180
STFSCIMQKW GGRKREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240
65 VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGFLGMY RNSLLQGFLE 300
DWYHQKFLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLWR LNQQTRWSKS 360
YFREWLKYNL WFKHKLHMT YESVVTGFFP FFLIATVIQL PYRGRINIL LFLITVQLVG 420
IIKATYACFL RGNAMIFMS LYSLLYMSSL LPAKIFALAT INKSGWGTSG RKTIVNFIG 480
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Seq ID NO: 371 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-7095

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CAGCTCCTCT GCTTTGCGCG CTTGGAATGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
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	AAATGCAATA	TGTATCTGTA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCACCTT	600
5	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGAATTTCAA	GTTTGGAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTC	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTGGGAA	GCAGGCTGCT	780
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Seq ID NO: 372 Protein sequence:

Protein Accession #: built from XP_031379

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25 Seq ID NO: 378 Protein sequence:
 Protein Accession #: EOS sequence

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55 Seq ID NO: 379 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 148-4632

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Seq ID NO: 380 Protein sequence:
 Protein Accession #: EOS sequence

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	INCESFKVTL	MASEHKCLSN	EELI IQDPFI	LEATQDDYVL	EVRHFQCPKW	PNPDSPISKT	1380
	FELISVKEEE	AANRDGPMIV	HDBHGGVTAG	TPCALTTLMH	QLEKENSVDV	YQVAKMINLM	1440
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	GAAGATTCAA	CTTCATCAGG	TTCAAGAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGATTAATTA	CACAGAGATA	CGTGTGTGAT	AATCTGAGAA	GACACCAAG	2220
60	TCCTTTTCTG	CAGGCCCACT	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCCCT	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAA	AGGATTGGGT	CTCCACGGTC	AACGTGGTAT	ACTGCGAGAC	AACCCAAACG	2400
	GTATACAATG	TGAGACACCC	TCTTCAACCT	TCCTACAGTA	GTGAAGTCTT	TCCTCTAGTC	2460
	ACCCCTTTGT	TGCTTGACAA	TCAGATCCCT	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT	2520
65	TCGGCCTTGC	ATGCTACGCC	TGTATTTCCC	AGTGTGATG	TGTCAATTGA	ATCCATCCTG	2580
	TCTTCTCTAT	ATGGTGACCC	TTTGCTTCCA	TTTTCTCTG	CTTCTCTCAG	TAGTGAATTG	2640
	TTTGGCCATC	TGCATACAGT	TTCTCAAAAT	CTTCCACAAG	TTACTTCAGC	TACCGAGAGT	2700
	GATAAGGTGC	CCTTGATATC	TTCTCTGCCA	GTGGCTGGGG	GTGATTGTCT	ATTAGAGCCC	2760
	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2820
70	TTTGGTAGTG	AATCTGGTGT	TCTTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCAACC	2880
	AGCAGTGATG	CCATGATGCA	TGCAGTCTCT	TCAGGGCCCTG	AACCTTCTTA	TGCTTGTCT	2940
	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTCCTTACA	GTTCGTCAAT	ACCTGTGCAT	3000
	GATTCTGTGG	GTGTAACCTA	TCAAGGTTCC	TTAATTAGAG	GCCTAGCCCA	TATACCAATA	3060
	CCTAAGTCTT	GGTAAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
75	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAACAT	TTCTTCAACT	GTTCCTGTAG	CTGAATTTAC	ATATACAACA	3240
	TCTGTGTTTG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAATGAG	3300
	ACTGAACCTG	AAATTCTCTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAGG	CACAGTCATG	3360
80	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3420
	ATTTCATGCA	CCAAGGCGAT	GTTTCCAGGG	TCCCTTGTCT	ATACCAACCAC	TAAGGTTTTT	3480
	GATCATGAGA	TTAGTCAAGT	TCCAGAAAAT	AACCTTTTCC	TTCAACCTAC	ACATACTGTC	3540
	TCTCAAGCAT	TTGCTGACAC	TTGCTTAAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
	TCCTCTGACC	CTGCTTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAG	TGAAGTATTG	CTACAACCTT	CTTTTCAGGC	TTCTGATGTT	3720
	GACACTCTGC	TTAAAACAGT	TCTTCCAGCT	GTGCCCAGTG	ATCCAATATT	GGTTGAAACC	3780

	CCCAAAGTTG	ATAAAATTAG	TTCTACAATG	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
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	ATGCACCTCT	CTTCACTTCA	AGGTTTGACC	ATTTCTCTATG	CAAGTGAGAA	ATATGAACCA	3960
5	GTITTTGTAA	AAAGTGAAAG	TTCCACCAAA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
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	TTTGCTACAC	CTGTTTTTAT	AATTGATGAA	CCATTAAATA	CACATAATAA	TAAGCTTATA	4140
	CATTCCGATG	AAATTTTAA	CTCCACCAAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
	ATTCCAACAG	TTGCTTCTGA	TACATTTGTA	TCTACTGATC	ATTCTGTTCC	TATAGGAAAT	4260
10	GGGCATGTTG	CCATTACAGC	TGTTTTCTCC	CACAGAGATG	GTTCGTGAAC	CTCAACAAAG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACCTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCGGGT	4380
	TTAGTGGGTG	TGGGTGAAGA	TGGTQACACT	GATGATGATG	GTGATGATGA	TGATGACAGA	4440
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	GACAGTCRAA	CTGGTATGGA	CAGAAGTCTC	GGTAAATCAC	CATCAGCAAA	TGGGCTATCC	4680
	CAAAAGCACAA	ATGATGGAAG	AGAGGAAAT	GACATTCAGA	CTGGTAGTGC	TCTGCTTCTC	4740
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20	ACTAATGAAA	AAGATGCTGA	TGGGATCCTG	GCAGCAGGTG	ACTCAGAAAT	AACCTCTGGA	4920
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25	TTAGAGGACA	GTGATCTCCC	TAGAGTTATA	TCCACACCTC	CAACACCTAT	CTTTCCAATT	5220
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	AGCTGTACTG	TTGACTTAGG	TATTACAGCA	GACAGCTCCA	ACCACCCAGA	CAACAAGCAC	5400
	AAGAATCCAT	ACATAAATAT	CGTTGCTTAT	GATCATAGCA	GGGTTAAGCT	AGCACAGCTT	5460
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	GGAAGGAGAA	AATGTGATCA	GTACTGGCCT	GCCGATGGGA	GTGAGGAGTA	CGGGAACCTT	5700
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35	AGAAACACAA	AAATAAAAAA	GGGCTCCAG	AAAGGAAGAC	CCAGTGGACG	TGTGTCACA	5820
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40	AATTATTGTT	TACAACTGTA	GGAGCAATAT	GTCTTCATTC	ATGATACACT	GGTTGAGGCC	6120
	ATACTTAGTA	AAGAACTGTA	GGTGTGAGC	AGTCATATTC	ATGCCTATGT	TAATGCATC	6180
	CTCATTCTCT	GACCAGCAGG	CAAAACAAGG	CTAGAGAAAC	AATTCAGCT	CCTGAGCCAG	6240
	TCAATATATA	AGCAGAGTGA	CTATCTGCA	GCCCTAAAGC	AATGCAACAG	GGAAGAAGAT	6300
	CGAATTTCTT	CTATCATCCC	TGTGGAAGA	TCAAGGGTTG	GCATTTTCAT	CCTGAGTGGG	6360
45	GAGGCACAG	ACTACATCAA	TGCTCTCTAT	ATCATGGGCT	ATTACACAG	CAATGAATTC	6420
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	CATAATGCC	AACGTGGTGT	TATGATTCCT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	6540
	GTTTACTGGC	CAATAAAGA	TGAGCCTATA	AATTGTGAGA	GCTTTAAGGT	CACCTTTATG	6600
	GCTGAAGAAC	ACAAATGTCT	ATCTAATGAG	GAAAACTTA	TAATTCAGGA	CTTTATCTTA	6660
50	GAGGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCACT	TTGAGTGTCC	TAAATGGCCA	6720
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	GCCATATAGG	ATGGGCCCTAT	GATTGTTTAT	GATGAGCATG	GAGGAGTGAC	GCGCAGGAAT	6840
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	ACCTCTCTGG	AGCAGTAATGG	TGCAGCATTG	CCTGATGGAA	ATATAGCTGA	GAGCTTAGAG	7080
	TCTTTAGTTT	AACACAGAAA	GGGGTGGGGG	GACTCACATC	TGAGCATTTG	TTTCTCTTCT	7140
	CTAAAAATTG	GAGGAAAAAT	CAGTCTAGTT	CTGTTATCTG	TTGATTTCCT	ATCACCTGAC	7200
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	TCTCAAGAT	GGAATTTGTT	TATTTTCTTC	TGTATTGATT	TAAACAGAAA	ATTTCAATTT	7380
	ATAGAGGTTA	GGAATTTCAA	ACTACAGAAA	ATGTTTGTGT	TTAGTGTCAA	ATTTTATAGT	7440
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65	TAAACACTC	TTCCATATGA	TATTCAACAT	TTTACAACCT	CAGTATTAC	CTAAAGTAGA	7560
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	FKASKITFEW	GKCMSSSDGS	ERHLEGGKFP	LEMQIYCFDA	DRFSFBEAV	KGKGLRLALS	180
80	ILFEVGTREN	LDPKAILDGV	ESVSRFGKQA	ALDPPILLAL	LPNSTDKYI	YNGSLTSPPC	240
	TDTVDMVIFK	DTVSISESQL	AVFCEVLTMQ	QSGVYMLADY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIEHAV	CSSEFENVOA	DPENYTSLLV	TWERPRVVDY	TMIEKFAVLY	QLLDGEDQTK	360
	HEPLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPFE	420
	LIGTEBIIKE	EBEGKDIIEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTHYNNRI	GTRYNEAKTN	480

	RSPTRGSEFS	GKGDVFNSTL	NSTSQPVTKL	ATEKDLSLTS	QTVTELPFHT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAESL	NTVSIETEEY	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITTYD	VLIPESARNA	SEDSTSSGSE	BSLKDPSEMG	NVWFPSGTDI	660
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	TEVTPHAFPT	SSRQQLVST	VNVVYSQTQ	PVYNGETPLQ	PSYSSSEVPFL	VTPLLLDNQI	780
	LNITPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAFL	PFSSASFSSSE	LFRHLHTVSQ	840
	ILPQVTSATE	SDKVPLHSL	PVAGDILLLE	PSLAQYSDVL	STTHAASETL	EPGSESGVLY	900
	KTLMPSQVEP	PSSDAMMHAR	SSGPEPSYAL	SDNEGSQHIF	TVSYSSAIPV	HDSVGVITYQG	960
10	SLFSGPSHIP	IPKSSLITPT	ASLLQPTHAL	SGDGEWSGAS	SDSEFLLPDT	DGLTALNISS	1020
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	LNASLQETSV	SISSTKGMFP	GLAHTTTKV	FDHEISQVPE	NMFSVQPTH	VSQASGDTSL	1140
	KPVLSEANSE	ASSDPASSE	LSPSTQLLPY	ETSASFSTEV	LLQPSFQASD	VDTLTKTVLP	1200
	AVPSDFILVE	TPKVDKISS	MLHLIVNSA	SSENMLHSTS	VPVFDVSPTS	HMHSASLQGL	1260
15	TISYASEKYE	PVLLKSESSH	QVPSLYSND	ELFQTANLEI	NQAHPPKGRH	VPATPVLSD	1320
	EPLNTLINK	IHSDEILTST	KSSVTGKVP	GIPTVASDTF	VSTDHVSPIG	NGHVAITAVS	1380
	PHRDGSVTST	KLLFPSPKATS	ELSHSAKSDA	GLVGGGEDGD	TDGDDDDDD	RDSGLSIIHK	1440
	CMSCSSYRES	QEKVMNDSIT	HENSLMDQNN	PISYSLSENS	EDNRVTSVS	SDSQTGMDRS	1500
	PGKSPSANG	SQKNDGKKEE	NDIQTGSALL	PLSPESKAWA	VLTSDEESGS	GGQTSDSLNE	1560
20	NETSTDFPSA	DTNKKDADGI	LAAGDSEITP	GFPQSPTSSV	TSENESEVPHV	SEAEASNSH	1620
	ESRIGLAEGL	ESEKKAIVPL	VIVSALTFIC	LVLVLGILY	WRKCFQTAHF	YLEDSTSPRV	1680
	ISTPPTPIFP	ISDDVGAIP	KHFPKHVADL	HASSGFTEEP	ETLKEFYQEV	QSCVTDLGIT	1740
	ADSSNHPDNK	HKNRYINIVA	YDHSRVKLAQ	LAEKDGKLT	YINANYVDGY	NRPKAYIAAQ	1800
	GLPKSTABDF	WRMIWEHNVE	VIVMITNLVE	KGRKCDQYW	PADGSEEEYGN	FLVTQKSVQV	1860
25	LAYTTNFTS	LRNTKIKKGS	QKGRPSGRVV	TQYHYTQWPD	MGVPEYSLPV	LTFVRKAAYA	1920
	KRHAUVGVVV	HCSAGVGRTO	TYIVLDSMLQ	QIQHEGTVM	FGFLKHRSQ	RNYLVQTEEQ	1980
	YVPIDHDLVE	AILSKETEVL	DSHILHAYNA	LLIPGPAGKT	KLEKQFQLLS	QSNIIQSDYS	2040
	AALKQCNREK	NRTSSIIIPVE	RSRVGISSLS	GBGTDIYNAS	YIMGYQSNSE	FIITQHPLH	2100
	TIKDFWRMWN	DHNAQLVVM	PDGQNAEDE	FVYWPKNDEP	INCESFKVTL	MAEHHKCLSN	2160
30	EEKLIQDPFI	LEATQDDYVL	EVRFHQCPKW	PNPDSPIKST	FELISVIEKE	AANRDGPMIV	2220
	HDEHGGVITAG	TFCALTTLMH	QLEKENSVDV	YQVAKMINLM	RPGVFADIEQ	YQFLYKVLIS	2280
	LVSTRQEEFN	STSLDSNGAA	LPDGNIAESL	ESLIV			

Seq ID NO: 383 DNA sequence

Nucleic Acid Accession #: NM_005688.1

Coding sequence: 126...4439

35							
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	AGAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCTC	GGGTATAGAA	180
	GTGTGAGGCA	GAGAACCAGC	ACTTCTGGGA	CGCACAGAGA	CCGTGAAGAT	TCCAAGTTCA	240
	GGAGAACTOG	ACCGTGGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCGGA	GCCGAGGGCC	300
45	TCTCTCTTGA	TGCTCTCATG	CATTCTCAGC	TCAGAACTCT	GGATGAGGAG	CATCCCAAGG	360
	GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACGAGC	420
	ACCCAGTGGG	CAATGCTGGG	CTTTTCTCCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
	CCCGTGTGGC	CCACAAGAAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
50	AAGTTGGGGC	AGACGCTGCT	TCCTTCGCGA	GGGTTGTGTG	GATCTTCTGC	CGCACCCAGC	660
	TCATCCTGTC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCACT	GGACCCAGCT	720
	TCATGGTGAA	ACACTCTCTG	GAGTATACCC	AGGCAACAGA	GTCTAACTCT	CAGTACAGCT	780
	TGTTGTGATG	GCTGGGCTCT	CTCTGACGG	AAATCGTGGG	GTCTTGTGCG	CTTGCACTGA	840
	CTTGGGCATT	GAATTACCGA	ACCGGTGTCC	GCTTGGCGGG	GGCCATCCTA	ACCATGGCAT	900
55	TTAAGAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
	TTTGTCTCAA	CGATGGGCGC	AGAAATGTTT	AGGCAGCAGC	CGTTGGCAGC	CTGTCTGGCTG	1020
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	GCTTCTCTGG	ATCAGCTGTT	TTTATCCTCT	TTTACCCAGC	AATGATGTTT	GCATCACGGC	1140
	TCACAGCATA	TTTCAGGAGA	AAATGCGTGG	CCGCCAAGGA	TGAACGTGTC	CAGAAGATGA	1200
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	GGGACTCTCT	CCACTCCAGT	ATCCAGAACT	CGCCCAAGCT	GACCCCAAAA	ATGAAAAAAG	1680
	ACAGAGGGGC	TTCCAGGGGC	AAGAAAGAGA	AGGTGAGGCA	GCTGCAGCGC	ACTGAGCATC	1740
70	AGGCGGTGCT	GGCAGAGCAG	AAAGGCCACC	TCCCTCTGGA	CAGTGACGAG	CGGCCAGGTC	1800
	CCGAAGAGGA	AGAAGGCAAG	CACATCCACC	TGGGCCACCT	GCGCTTACAG	AGGACACTGC	1860
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	GTGGAAAAAC	CTCTCTCATT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCTCT	AATGCTACTC	2040
	TGAGAGACAA	CATCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAA	TCTGTGCTGA	2100
	ACAGCTGTCT	CCTGAGGCTT	GACCTGGCCA	TTCTTCCGAC	CAGCGACCTG	ACGAGATTTG	2160
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	TGTGTAACCA	CAGTTTACAG	TACCTGGTTG	ACTGTGATGA	AGTGTATCTT	ATGAAAGAGG	2400
	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
80	CCATTTTTAA	TAACCTGTTG	CTGGAGAGGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
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	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
	GTCAGTGCC	CTGCTCAGTA	TATGGTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
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 40 GAGACGGGTG GGGGGCTGGA GACCATGCGA AGCGCGGTGA GTTCTCAGGG CTCTGSCCTT 5100
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Seq ID NO: 384 Protein sequence

Protein Accession #: NP_005679.1

1 11 21 31 41 51
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 VARHKGELSM EDVWSLSKHE SSDVNCRRLE RLWQELNEV GPDAASLRV VWIFCRTRI 180
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 75 VPHSVTVYI QAAGGFLAPL VIMALFMLNV GSTAFSTWWL SYWIKQSGSN TTVTRGNETS 900
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10     TGCGGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCGCGGGCG CAGGGGCAGC 240
      AAGGGCCTCG GGGCGGGGAG GAGGGGCCCG CGCGGGTCCG CATGGCGGCG CGGCTTCAGG 300
      GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGGAG AGCGCGCTGC TTGAGTTCTA 360
      CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
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15     CATACTGACT ATCCGACTGA CTGCTGCAGA CCACGCCCAA CTGCAGCTCT CCATCAGCTC 540
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      GGCTCAGCCT CCTCAGGGC AGAGGCGCTA AGCCAGCCT GCGGCCCTT CTTAGGTTCAT 660
      GCTCTCTCC CTAGGGAATG GTCCAGCAC GAGTGGCCAG TTCAATGTGG GGGCCTGATT 720
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Protein Accession #: NP_001318.1

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      PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAEIARRSLA QDAPPLFVPG 120
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Coding sequence: 52..459

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40     CGCATGGCG GTGCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGG CAGGAGGCG 300
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      ATCAGCTCCT GTCTCCAGCA GCTTTCCTG TGTATGTGGA TCACGCACTG CTTTCTGCC 420
      TGTGTTTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CCGCCCTTCC 480
      TAGGTGATGC CTCTCCCTT AGGGAATGCT CCCAGCAGA GTGGCCAGTT CATTGTGGGG 540
45     GCCTGATTGT TTGTGCTGG AGGAGGACGG CTTACATGTT TGTITCTGTA GAAATAAAG 600
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Seq ID NO: 388 Protein sequence
Protein Accession #: Eos sequence

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Seq ID NO: 389 DNA sequence
Nucleic Acid Accession #: NM_005562.1
Coding sequence: 90..3671

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65     GCTTCTGCTT CCTCTGCCC GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
      ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACTTCA CAGACAAACT GGTAAATGGAT 240
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70     CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGCAGCTG TAAACCAAGT GTGACAGGAG 420
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      AATGTGCACA GCGCCATCAA GATGTGTTA GCTCAGCCA ACGACTAGAC CTGTCTATT 840
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      TGAGTTACTT TGAGTATCGA AGGTTACTGC GGAATCTCAC AGCCCTCCGC ATCCGAGCTA 1140
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      TCTCTGAGC CCCAGCACCC TGGGTTGAAC AGTGTATATG TCCTGTTGGG TACAAGGGG 1260
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5	CAGTGATGCC	GGAGACGGAG	GAGGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTACCCGGTG	1560
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80	GGACDPDTGD	CYSGDENPDI	ECADCPIGFY	NDPFDPRSC	PCPCNPFSC	SUMPETEEVV	480
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 35 TATATATAGA TATGATATA TACATGTTT TCTATTAAA ATAGACAGTA AAATACTATT 1200
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 40 CTAATTATAC AAGGATGAAT TCTTTCAAT CTTCATGGT GCCCTTTTCA TATACTTATT 1440
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Seq ID NO: 392 Protein sequence
 Protein Accession #: AAD16433.1

1 11 21 31 41 51
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 LLOCCSPRET TSYTPRPPY KPAPSSGKDY V

Seq ID NO: 393 DNA sequence
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Coding sequence: 352..2820

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	CTGAGGAGCC	TTTCTGAGGA	GTAAAAAGAC	TACTGGCCTC	TGTGCCATGG	ATGATCTCTT	3660
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Seq ID NO: 394 Protein sequence
Protein Accession #: NP_006171.1

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	NFTRNKLSTL	SRKHFRHLDL	SELILVGNPF	TCSCDIMWIK	TLQBAKSSPD	TQDLYCLNES	180
	SKNIPLANLQ	IPNCGLPAN	LAAPNLTVBE	GKSITLSCSV	AGDPVPMYMW	DVGNLVSKRM	240
80	NETSHTQSL	RITNISDDSD	GKQISCVARN	LVGEDQDSVN	LTVHPAPTIT	FLESPTSDDH	300
	WCIPFTVKGN	PKPALQWFFN	GAILNESKYI	CTKHIVTNHT	EYHGCLQLDN	PTHMNNGDYT	360
	LIARNEYRGD	EKQISAPFMG	WPGIDDGANP	NYPDVIEDY	GTAANDIGDT	TNRSENPST	420
	DVTDKTRGRH	LSVYAVVVIA	SVVGFCLLVN	LFLLKLARHS	KFGMKGPASV	ISNDDDSASP	480
	LHHISNGSNT	PSSSEGGPDA	VIIGMTKIPV	IENPQYPGIT	NSQLKPDFTV	QHKRHNIVL	540
	KRELGEAGFG	KVFLABCYNL	CPEQDKILVA	VKTLLKADSDN	ARKDPHREAS	LLTNLQHEHI	600

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Seq ID NO: 396 Protein sequence
 Protein Accession #: AAL67965.1

1 11 21 31 41 51

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SKNIPLANLQ	IPNCGLPASN	LAAPNLVVEE	GKSITLSCSV	AGDPVPMYMW	DVGNLVSKHM	240
NETSHTQSL	RITNYSDDSD	GKQISCVAEN	LVGEDQDSVN	LTVHFAPTIT	FLESPTSDBH	300
WCIPPTVKGK	KXPALQWFYN	GAILNESKYI	CTKIHVINHT	EYHGCLQLDN	PTHMNGDYT	360
LIARNEYGKD	EKQISAHFMG	WPGIDDGANP	NYPDVIYEDY	GTAANDIGDT	TNRNSNEIPST	420
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KPDTFVQHIK	RHNIVLKREL	GEGAFGKVEL	AECYNLCPEQ	DKILVAVKTL	KDASDNARKD	600
FHREAEELTN	LQHEHIVKPY	GVCVBDPLI	MVPEYMKHGD	LNKFLRAHGF	DAVLMAEGNP	660
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DYYRVGGHTM	LPIRWMPPEP	IMYRKFTTES	DVWSLGVVLN	EIFTYKQKPW	YQLSNNEVIE	780
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Seq ID NO: 397 DNA sequence

Nucleic Acid Accession #: AB052906

Coding sequence: 74..814

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CTTCTTGATG	GGCATGGACA	GCACCCCTGA	GCCAAAGTGA	GGAGCACCAC	TGCCCATGTC	720
CTCAGGCACA	ACCCAATCTA	GGGCCACAGC	CACCAACCTC	ATCCTTTGCT	GCCTCCTCAT	780
CATCTCTCCC	TGCTTCATCC	TCCCTGGCAT	CTGAGGAGAG	TCTTTTAGAG	TGACAGGTTA	840
AAGCTGATAC	CAAAAGGCTC	CTGTGAGCAC	GGTCTTGATC	AAACTCGCCC	TTCTGTCTGG	900
CCAGCTGCCC	ACGACCTACG	GTGTATGTCC	AGTGGCCTCC	AGCAGATCAT	GATGACATCA	960
TGGACCAAT	AGCTCATTTA	CTGCCCTTGT	TCTTTTGCC	AACAATTTTA	CCAGCAGTTA	1020
TAGCTACAT	ATTATGCAAT	TTTCTCTTGG	TGCTACCTGA	TGGAAATCCT	GCACCTAAAG	1080
TTCTGGCTCA	CTAAACAAGA	TATATCATTT	TCTTTCTTCT	CTTTTGTGTT	GGAAAATCAA	1140
GTACTTCTTT	GAATGATGAT	CTCTTTCTTG	CAAAATGATAT	TGTCAATGAA	ATAATCAOCT	1200
TAGACTTCAG	ACCTCTGGGG	ATTCTTTCCG	TGTCTTGAAA	GAGAATTTTT	AAATTAATTTA	1260
ATAAGAAAAA	ATTATATATTA	ATGATTGTTT	CCTTTAGTAA	TTTATTGTTT	TGTACTGATA	1320
TTTAAATAAA	GAGTTCTATT	TCCCAAAAAA	AAAAAAAATA	AA		

Seq ID NO: 398 Protein sequence

Protein Accession #: BAB61048.1

50
55

1	11	21	31	41	51	
MAAAATKIL	LCLPLLLLLS	GWSRAGRADP	HSLCYDITVI	PKFRPGRWRC	AVQGVQDEKT	60
FLHYDCGNKT	VTPVSPGKX	LNVTTAWKAQ	NPVLREVVDI	LTEQLRDIQL	ENYTPKEPLT	120
LQARMSCEQK	ABGHSSGSWQ	PSFDGQIFLL	FDSEKRMWTT	VHPGARKMKE	KWENDKVVAM	180
SFHYFSMGDC	IGWLEDFLMG	MDSTLEPSAG	APLAMSSGTT	QLRATATTLL	LCCLLIILFC	240
PILPGI						

Seq ID NO: 399 DNA sequence

Nucleic Acid Accession #: NM_001898.1

Coding sequence: 57..482

60
65
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1	11	21	31	41	51	
GGCTCTCACC	CTCCTCTCCT	GCAGCTCCAG	CTTGTGCTCT	TGCTCTGAG	GAGACCATGG	60
CCCAGTATCT	GAGTACCTGC	CTGCTCCTGC	TGGCCACCTT	AGCTGTGGCC	CTGGCCTGGA	120
GCCCCAAGGA	GGAGGATAGG	ATAATCCGGG	GTGGCATCTA	TAACGCAGAC	CTCAATGATG	180
AGTGGGTACA	GCGTGCCCTT	CACCTCGCCA	TCAGCGAGTA	TAACAGGCC	ACCAAAAGATG	240
ACTACTACAG	ACGTCCGCTG	CGGGTACTAA	GAGCCAGGCA	ACAGACCGTT	GGGGGGGTGA	300
ATTACTTCTT	CGACGTAGAG	GTGGGCGGCA	CCATATGTAC	CAAGTCCAG	CCCAACTTGG	360
ACACCTGTGC	CTTCCATGAA	CAGCCAGAAC	TGCAGAGGAA	ACAGTTGTGC	TCITTTGAGA	420
CTACGAAAT	TCCTTGGGAG	AACAGAAAGT	CCCTGGTGAA	ATCCAGGTGT	CAAGAATCCT	480
AGGGATCTGT	GCCAGGCCAT	TGCAACAGC	CACCAACCCAC	TCCACCCCC	TGTAGTGCTC	540
CCACCCCTGG	ACTGTGTGGC	CCCAACCTGC	GGGAGGCTTC	CCCATGTGCC	TGCGCCAAGA	600
GACAGACAGA	GAAGGCTGCA	GGAGTCTTTT	GTTGCTCAGC	AGGGCGCTCT	GCCCTCCCTC	660
CTTCCTTCTT	GCTTCTAATA	GCCTGGTATC	ATGGTACACA	CCCCCCCACC	TCTTGCATTT	720
AAACAGTAGC	ATCGCC					

Seq ID NO: 400 Protein sequence

Protein Accession #: NP_001899.1

80

1	11	21	31	41	51	
MAQYLSTLLL	LIATLAVALA	WSPKEEDRII	PGGIYNADLN	DEWVORALHF	AISEYNKATK	60
DDYYRRPLRV	LRARQQTVGG	VNYFFDVEVG	RTICTKSQPN	LDTCAFHEQP	ELQKKQLCSF	120

EIVEVPWENR RSLVKSRCQS S

Seq ID NO: 401 DNA sequence

Nucleic Acid Accession #: NM_003976.2

Coding sequence: 299..961

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1	11	21	31	41	51	
CTCTGAGCTT	CTCTGAGCCT	TGTTTGCTCA	TCTGGAAAAA	GGGGATTAAA	CCATTACCT	60
CATGGAGTTG	TGAAGAATA	GCTGCAAGC	ACCTAACACA	TAGTAAGTT	CCCAGTGCAG	120
CTACTTCTGC	TGGGTTGAGT	CTAGCTGTGT	AGGCCCTTGT	TTCTCACCT	GGAGAACTG	180
GGGTGGCAGG	CCGGTCCCC	ACAAAAGATA	ACTCATCTCT	TAATTGTCAA	GCTGCCTCAA	240
CAGGAGGGTG	GGGGAACAGC	TCAACAATGG	CTGATGGGGG	CTCCTGGTGT	TGATAGAGAT	300
GGAACTTGGG	CTTGGAGGCC	TCTCAACGCT	GTCCCACTGC	CCCTGGCCTA	GGCGGCAGCC	360
TGCCCTGTGG	CCCACCTTGG	CCGCTCTGGC	TCTGCTGAGC	AGGCTCGCAG	AGGCCTCCCT	420
GGGCTCCGGG	CCCCGCAGCC	CTGCCCCCGG	CGAAGGCCCC	CCGCTGTGTC	TGGCGTCCCC	480
CGCCGGCCAC	CTGCGGGGGG	GACGCAACGC	CCGCTGGTGC	AGTGAAGAG	CCCGGGCGCC	540
CGCCGCGCAG	CCTTCTGGGC	CGCGCCCCCG	GCCTGCTGCA	CCCCCATCTG	CTCTTCCCCG	600
CGGGGGCCGC	GGGGGCGGG	CTGGGGGGCC	GGGCAGCCGC	GCTCGGGCAG	CGGGGGCGCG	660
GGGCTGCGCG	CTGCGCTCGC	AGCTGGTGCC	GGTGGCGCGG	CTCGGCCTGG	GCCACCGCTC	720
CGACGAGCTG	GTGCGTTTCC	GCTTCTGCGG	CGGCTCCTGC	CGCCGGCGGC	GCTCTCCACA	780
CGACCTCAGC	CTGGCCAGCC	TACTGGGGCG	CGGGGCCCTG	CGACCGCCCC	CGGGCTCCCG	840
CGCCGTGAGC	CAGCCCTGCT	GCGACCCAC	GCGCTACGAA	GCGGTCTCCT	TCTTGGACGT	900
CAACAGCAGC	TGGAGAACCG	TGGACCGCCT	CTCGCCAC	GCTGCGGCTG	GCTGGGCTCT	960
AGGGCTCGCT	CCAGGGCTTT	GCAGACTGGA	CCCTTACCGG	TGGCTCTTCC	TGCGTGGGAC	1020
CCTCCCGTAC	AGTCCCACTA	GCCAGCGGCC	TCAGCCAGGG	ACGAAGGCTC	CAAGAGCTGAG	1080
AGGCCCTCAG	CGGTGGGTGA	TGGATATCAT	CCCGAAGCAG	GTGAAGGGAC	AACCTGACTAG	1140
CAGCCCCAGA	GCCTTACCCC	TGGGATCCCC	AGCTTAAAG	ACACCAAGAG	CCTCAGCTAT	1200
GGAGCCCTTC	GGACCACTT	CTCAGACTG	CTGGCACTGG	CCAGGCTCTG	AACCTGGGAC	1260
CCCTCCTCTG	ATGAACACTA	CAGTGGCTGA	GGCATCAGCC	CCCGCCAGG	CCCTGTAGGG	1320
ACAGCATTTG	AAGGACACAT	ATTGAGTTG	CTTGGTTGAA	AGTGCTGTG	CTGGAACCTG	1380
CCTGTACTCA	CTCATGGGAG	CTGGCCCC				

Seq ID NO: 402 Protein sequence

Protein Accession #: NP_003967.1

35
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45

1	11	21	31	41	51	
MELGLGLST	LSHCPWPRRQ	PALWPTLAAL	ALLSSVAEAS	LGSAPRSPAP	REGPPPVLAS	60
PAGHLPGGRT	ARWCSGRARR	PPQPSPRPAP	PPPAPPSALP	RGGRARAGG	PGSRARAAGA	120
RGCRRLSQLV	FVRALGLGHR	SDELVRFRFC	SGSCRRRASP	HDLSLASLLG	AGALRPPPGS	180
RPVSPQCCRP	TRYEAVSFM	VNSTWRTVDR	LSATACGCLG			

Seq ID NO: 403 DNA sequence

Nucleic Acid Accession #: NM_057091.1

Coding sequence: 783..1445

50
55
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1	11	21	31	41	51	
ACTGGCCGCT	GAGAGAAGAA	TGGGTGGGAG	CAGAGAGCAG	CTGCTGCAGG	GCAGACAGCC	60
GGACCCCAAC	ATCTGCAGCT	ACCAGCAGTC	AGCCGCCCCA	CGCAGGGACC	GGCTTACCCC	120
TGCGTCCCCG	CCCTCACTCA	CTTCTCCCGG	CCCTCGGCCG	GGCCTCCAG	CTCTCTACTT	180
CGCGTGTCTA	CAAACTCAAC	TCCCGGTTTC	CGTGCCTCTC	CACCGCTCGA	GTTCCTACT	240
CTCCATATCC	GAGGGGCCCC	TCCAGCATC	TACCCGCCCT	CCAACTCCGG	GGGACCTAGC	300
CAAGCTAGGG	GGGACTGGAT	CCGACGGGTG	GAGCAGCCAG	GTGAGCCCCG	AAAGSTGGGG	360
CGGGGCGGGG	CGCTCCCGAG	CCCCACCCCG	GGATCTGGTG	ACGCTGGGGC	TGGAAATTTGA	420
CACCGGACGG	CTGCGGGCGG	GGGCAGGAGG	CTGCTGAGGG	ATGGAGTTGG	GCCCCGCCCC	480
CAGACAAGGC	CCGGGGGCTC	CGCCAGCAGC	AGGTCCCTCG	GGCCCCAGCC	CTGCTTGCCA	540
CCCGGGCCTG	GAGCCCCACA	CCGAGGGGTG	CAGACTGGCT	GCCAAAGCCA	CACCTTTGGC	600
TAAAAGAGGC	ACTGCCAGGT	GTACAGTCTT	GGGCATGGCG	TGTTTGAGCT	TGGGGGAGAG	660
GCCAGCACT	GGTCCCCGGA	AAGGTGCCTA	GAAGAACAAG	GTGCAGGACC	CGSTGCTGCC	720
TCAACAGGAG	GGTGGGGGAA	CAGCTCAACA	ATGGCTGATG	GGCGCTCCTG	GTGTTGATAG	780
AGATGGAAGT	TGGACTTGGA	GGCCTCTCCA	CGCTGTCCCA	CTGCCCTGG	CCTAGGCGGC	840
AGCCTGCCCT	GTGGCCCAAC	CTGGCCGCTC	TGGCTCTGCT	GAGCAGGCTC	GCAAGGGCTC	900
CCCTGGGCTC	CGCGCCCGCG	AGCCCTGCCC	CCCGGGAAGG	CCCCCGCCT	GTCTGGGCT	960
CCCCCGCCGG	CCACCTGCCG	GGGGGACGCA	CGCCCCCGTG	GTGCACTGGA	AGAGCCCGGC	1020
GGCCGCGCGC	GCAGCTTCT	CGGCCCGCGC	CCCGCCCGCC	TGCACCCCCA	TCTGCTCTTC	1080
CCCGGGGGGG	CCCGCGGGCG	CGGGCTGGGG	GCCCCGGCAG	CGCGCTCGGG	GCAGCGGGGG	1140
CGCGGGGCTG	CGCGCTGGCG	TGCACTGGG	TGCGGGTGGG	CGCGCTGGCG	CTGGGCCACC	1200
GCTCGAGCA	GCTGGTGGCT	TTCCGCTTCT	GCAGCGGCTC	CTGCGCGCGC	CGCGCTCTCT	1260
CACAGCACT	CAGCTGGGCC	AGCCTACTGG	GCGCGGGGCG	CCTGCGAGCG	CCCGGGGGCT	1320
CCCGGCCCGT	CAGCCAGCCC	TGCTGCCGAC	CCAAGCGCTA	CGAAGCGGTC	TCCTTCATGG	1380
ACGTCAACAG	CACCTGGAGA	ACCGTGGACC	GCCTCTCGCG	CACCGGCTGG	GGCTGCTGGG	1440
GCTGAGGGCT	CGCTCCAGGG	CTTTCAGAC	TGGAACCTTA	CGGTTGGCTC	TTCTGCTCTG	1500
GGACCTTCCC	GCAGAGTCCC	ACTAGCCAGC	GGCCTCAGCC	AGGAGCGAAG	GCCTCAAAGC	1560
TGAGAGGCC	CTACCGGTGG	GTGATGGATA	TGATCCCGGA	ACAGGTGAAG	GGACAACTGA	1620
CTAGCAGCCC	CAGAGCCCTC	ACCTTGCGGA	TCCAGCCCTA	AAAGACACCA	GAGACCTCAG	1680
CTATGGAGCC	CTTGGAGCCC	ACTTCTACA	GACTCTGGCA	CTGGCCAGCG	CTGAACTCTG	1740
GGACCCCTCC	TCTGATGAAC	ACTACAGTGG	CTGAGGCATC	AGCCCCCGCC	CAGGCCCTGT	1800
AGGAGCAGCA	TTTGAAGGAC	ACATATTGCA	GTGCTTGGT	TGAAAGTGCC	TGTGCTGGAA	1860
CTGGCTGTGA	CTCACTCATG	GGAGCTGGCC	CC			

Seq ID NO: 404 Protein sequence

Protein Accession #: NP_003967.1

1 11 21 31 41 51
 5 MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
 PAGHLPGGRT ARWCSGRARR PPPQSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
 RGCRLRSQLV PVRALGLGHR SDELVRPRFC SGSCRRARSP HDLSLASLLG AGALRPFPFGS 180
 RPVSQPCCRP TRYEAUSFMD VNSTWRTVDR LSATACGCLG

10 Seq ID NO: 405 DNA sequence
 Nucleic Acid Accession #: NM_057160.1
 Coding sequence: 1..714

1 11 21 31 41 51
 15 ATGCCCGGCC TGATCTCAGC CCGAGACAG CCCCTCCTTG AGGTCTCTCC TCCCCAAGCC 60
 CACCTGGGTG CCTCTTTCT CCTGAGGCT CCACCTGGTC TCTCCGCGCA GCCTGCCCTG 120
 TGGCCACCC TGCGCGCTCT GGCTCTGCTG AGCAGCGTGG CAGAGGCTTC CCTGGGCTCC 180
 20 GCGCCCCGCA GCCCTGCCCC CCGCGAAGGC CCCCCGCTG TCTGGCGTC CCGCGCCGCG 240
 CACCTGCCGG GGGGACGAC GGGCGCTGG TGCACTGGAA GAGCCCGCG GCGCGCCGCG 300
 CAGCCTTCTC GGGCCGCGCC CCGCGCGCT GCACCCCAT CTGCTCTTCC CCGCGGGGCG 360
 CCGCGCGCGC GGGCTGGGGG CCGGGGACG CGCGCTCGGG CAGCGGGGCG GCGGGGCTGC 420
 CGCCTGCGCT CGCAGCTGGT GCGGTGCGCG GCGCTCGGCC TGGGCCACCG CTCGACGAG 480
 CTGGTGGGTT TCGCTTCTG CAGCGGCTCC TCGCGCGCG CCGCTCTCC ACACGACCTC 540
 25 AGCCTGGCCA GCCTACTGGG CGCGGGGCG CTGCGACCG CCGCGGGCTC CCGCGCGCTC 600
 AGCCAGCCCT GCTGCGGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660
 ACGTGGAGAA CGTGGAGCG CCTCTCGCC ACCGCTCGG GCTGCGTGG CTGAGGGGCTC 720
 GCTCCAGGGC TTGTGAGACT GGACCCCTAC CGGTGGCTCT TCTGCTCTGG GACCTCCCG 780
 CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAG CCTCAAAGCT GAGAGGGCCC 840
 30 TACCGGTGGG TGATGGATAT CATCCCGAA CAGGTGAAG GACAACGAC TAGCAGCCCC 900
 AGAGCCCTCA CCTGCGGAT CCGAGCCTAA AAGACACCG AGACCTCAGC TATGGAGCCC 960
 TTGAGACCCA CTCTCAGAC ACTCTGGCAC TGGCCAGGCC TCGAACCTGG GACCCCTCT 1020
 CTGATGAACA CTACAGTGGC TGAGGCATCA GCGCCCGGCC AGGCCCTGTA GGGACAGCAT 1080
 35 TTGAAGGACA CATATTGCAG TTGCTGGTGT GAAAGTGCCT GTGCTGGAAC TGGCCTGTAC 1140
 TCACTCATGG GAGCTGGCCC C

Seq ID NO: 406 Protein sequence
 Protein Accession #: NP_476501.1

40 1 11 21 31 41 51
 MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS 60
 APRSPAPREG PPPVLASAPG HLPGRRTARW CSGRARPPPP QPSRPAPPPP APPSALPRGG 120
 45 RAARAGGPGS RARAAGARGC RLRSQLVPVR ALGLGHRSD ELVRFRCGSG CRRARSPHDL 180
 SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

Seq ID NO: 407 DNA sequence
 Nucleic Acid Accession #: NM_057090.1
 Coding sequence: 29..715

1 11 21 31 41 51
 50 CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACCTGGA CTGGAGGCC TCTCCAGCT 60
 GTCCCACTGC CCCTGGCCTA GCGGGCAGGC TCCACTGGT CTCTCGCGC AGCCTGCCCT 120
 55 TGGGCCACCC CTGGCGCTC TGCGCTCTGCT GAGCAGCGTC GCAGAGGCTC CCTTGGGCTC 180
 CCGCCCCGCG AGCCTGCCCC CCGCGAAGG CCCCCGCTG GTCTGGCGT CCGCGCCGCG 240
 CCACCTGCCG GGGGGACGCA CGGCGCGCTG GTGCACTGGA AGAGCCCGCG GCGCGCCGCG 300
 GCAGCCTTCT CGGCCCCGCG CCGCGCGGCG TGCACCCCA TCTGCTCTTC CCGCGGGGCG 360
 60 CCGCGCGCGC CGGCTGGGG GCGCGGCGC CCGCGCTCG GCAGCGGGG CCGCGGGGCTG 420
 CGCCTGCGC TCGCAGCTGG TCGCGGTGCG CGCGCTCGGC CTGGGCCACC GCTCGACGA 480
 GCTGGTGGT TTCCGCTTCT GCAGCGGCTC CTGCGCGCG GCGCGCTCTC CACACGACCT 540
 CAGCCTGGCC AGCCTACTGG GCGCGGGGCG CTGCGACCG CCGCGGGCTC CCGCGCCCTG 600
 CAGCCAGCCC TGCTGCGGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG AGTCAACAG 660
 65 CACCTGGAGA ACCGTGGACC GCCTCTCGCG CACCGCCTGC GGCTGCCTGG GCTGAGGGCT 720
 CGTCCAGGG CTTTGCAGAC TGGACCCCTA CCGGTGGCTC TTCTGCTG GACCCCTCCC 780
 GCAGAGTCCC ACTAGCCAGC GGCTCAGCC AGGGAAGAAG GCCTCAAAGC TGAAGGGCCC 840
 CTACCGGTGG GTGATGGATA TCATCCCGA ACAGGTGAGG GGACACTGA CTAGCAGCCC 900
 CAGAGCCCTC ACCCTGCGGA TCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC 960
 70 CTGCGACCC ACTTCTACA GACTCTGGCA CTGGCCAGGC CTGAAACCTG GGAACCCCTC 1020
 TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCC CAGGCCCTGT AGGGACAGCA 1080
 TTTGAAGGAC ACATATTGCA GTTGTCTGGT TGAAAGTGCC TGTGCTGGA TGGCCTGTGA 1140
 CTCACCTATG GAGCTGGCCC C

75 Seq ID NO: 408 Protein sequence
 Protein Accession #: NP_476431.1

1 11 21 31 41 51
 80 MELGLGGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60
 GPPPVLASPA GHLPGGRTAR WCSGRARRPP PQPSRPAPPP PAPPSALPRG GRAARAGGPG 120
 SRARAAGARG CRLRSQLVPR RALGLGHRSD ELVRFRCGSG SCRRARSPHD LSLASLLGAG 180
 ALRPPPGSRP VSQPCCRPTR YEAVSFMDVN STWRTVDRLS ATACGCLG

Seq ID NO: 409 DNA sequence
Nucleic Acid Accession #: Bos sequence
Coding sequence: 1..1746

5	1	11	21	31	41	51	
	ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	60
	GCCTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCAGGT	GGAGTGCACC	120
	GGGGCACGCA	TTGTGGGGT	GCCCACCCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
10	CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCCCCGTTC	TCAATATCTC	AGCCCTCATC	240
	GCCCTGAGGA	TTGAGAAGAA	TGAGCTGTCC	CGCATCACGC	CTGGGGCCIT	CGGAAACCTG	300
	GGCTGCTGTC	GCTATCTCAG	CCTGCCAAC	AACAAGCTGC	AGGTTCCTCC	CATCGGCCCTC	360
	TTCCAGGGCC	TGGACAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCACT	GTTGCAGATC	420
	CAGCCGCCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCCAC	480
15	CTGGAATACA	TCCCTGACGG	AGCCTTCGAC	CACCTGGTAG	GACTCACGAA	GCTCAATCTG	540
	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCCCTCGGC	TTATGAGAA	CAGGCTCACG	GATATCCCCA	TGGGCACITT	TGATGGGCTT	660
	GTAAACCTGC	AGGAACCTGC	TCTACAGCAG	AACAGATTG	GACTGCTCTC	CCCTGGTCTC	720
	TTCCACAACA	ACCAACAACCT	CCAGAGACTC	TACCTGTCCA	ACAAACCAT	CTCCAGCTG	780
20	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTGGGG	CCCATGCCCA	ACCTGCGGGA	GCITTTGGCTC	900
	TATGACAACT	ACATCTCTTC	TCTACCGGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCCGTATTC	TTAGCCGCAA	TCAGATCAGC	TTCACTCTCC	CGGCTGCCTT	CAACGGGGCTA	1020
	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATTGC	1080
25	TTCCGCATGT	TGGCCAACTC	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTCGCCAA	CGTCAATGCG	CTCATGGCCA	TCCAGCTGCA	GAACAACCCAG	1200
	CTGGAAGACT	TGCCCTCGGG	CATCTTCGAT	CACCTGGGGA	AACGTGTGTA	GCTGGGGCTG	1260
	TATGACAATC	CCTGAGAGTG	TGACTCAGAC	ATCCTTCCGC	TCCGCAACTG	GCTCCTGCTC	1320
	AACCCAGCTA	GGTTAGGGAC	GGACACTGTA	CCTGTGTGTT	TCAGCCGAGC	CAATGTCCGA	1380
30	GGCCAGTGCC	TCATTATCAT	CAATGTCAAC	GTTCCTGTTT	CAAGGTGCCA	TGTCCCTGAG	1440
	TGCCCTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
	TCGCTCTCTT	CTACCACTGA	GCTAACCCAGC	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	ATTCAAGTCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCACAGG	CGGGCTGGCC	1620
	ATTGCCGCCA	TGTGAATTGG	CATTGTGCGC	CTGGCCTGCT	CCCTGGCTGC	CTGGCTGGCC	1680
35	TGTTGCTGCT	GCAAGAAAGAG	GAGCCAGCT	GTCTGTATGC	AGATGAAGGC	ACCCCAATGAG	1740
	TGTTAAAGAG	GCAGGCTGGA	GCAGGGCTGG	GGAAATGATG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGAATTCT	CTTTCTGGCC	1860
	CTAGATAAAG	GTGTGCCTAC	CTCTTCCTGA	CTTGCTTGAT	TCTCCCGTAG	AGAAGCAGGT	1920
	CGTGCCGGAC	CTTCTTACAA	TCAGGAAGAT	AGATCCCACT	GGCCATGGCA	AAAGCCCTGG	1980
40	GGATTTCGCA	TCTATACCCC	TGGGCTTCCT	TCGAGAGGGC	TCTTCTTCCA	AATCCTCCCC	2040
	ACCTGTCTCT	CAGAACACGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGGCTT	CTGTAGACTC	2100
	AGTTAGTCCA	CAGCCTGCTC	ACTTGTGGGG	AATAGTTCTC	CGCTGAGATA	GCCCCCTCTG	2160
	CCTAAGTATT	ATGTAAGTTG	ATTTCCCTTC	TTTTGTTTCT	CTTGTTTGTG	CTATGGCTTG	2220
	ACCCAGCATG	TCCCTTCAAA	TGAAAGTTCT	CCCCCTGATT	TTCTGCTCCT	GAAGGCAGGG	2280
45	TGAGTTCTCT	GCTAATACAG	GACTTCAAAC	CATTTAACCTG	GTTCCTTAAG	AGCCGCTCAAT	2340
	CAGCCTGGTT	TTGGGGATGC	TATGAAAGAG	AGAAGGAAAA	TCATGCCGCT	CAGTTCTCTG	2400
	AGACAGAAGA	GCGGTCTATCA	GTGTCTCACT	TGTGATTTTT	ATCTGGAAAA	GGAGAAACA	2460
	CCCCAGCACA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAACTGCA	AACCTTGCTT	2520
50	TGAAAGTTT	AGCCCTTTAA	GGAAATGAAAT	CATGTAGAAT	TTTGCACTTC	TAAAAACATT	2580
	AAAATCAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCTGGGGGG	TCCTGTGTTT	2640
	CACCCCTAGA	GTTTGTTTTA	AAATTTTAA	TTGAAGCATG	TGAAGTGATC	STGCAGAAAA	2700
	GTGGGAACAT	GATAGTGTAT	GGCTTGGTGG	ATTTTCACAA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCCTGGGC	TTTTCCGAGA	2820
55	GGAGATGGGG	GCTTCTGAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGGA	GCCAGGACGG	2880
	TCCCCCCACA	GTCAAGCTGT	GCAAAGGCCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	ATGGGAGACT	GTGGCCTGAA	CAGGAGATTT	TATTATATCT	GGAGACCTTG	3000
	AGAGAOCCTG	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGACG	CCACACCTTC	TTCCCTGCCA	GCAAGTTGTC	TGCGCTCAT	CGGAGGCCCC	3120
	TCCGCTGGA	GCCTTCTATG	GACGTGATAT	GCCTGTATCT	GTTTTAAATT	TTCAATCTTC	3180
60	ACTTAGGGGA	AGTGAATGCG	CTCAGAGATG	AGATCCTTTA	ATTGAAAAAG	AAGTGTAAAG	3240
	GAATCTAGTG	TCTTTCTAAT	GTGGTAAAAAT	TCTCCATCAA	CATCACAGTC	AGCTGGCAGC	3300
	TGAATCTCAG	AATCTCAGTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACTAGTG	3360
	GTCTGGGGGG	TCCTCGGAGC	TCCTCCTGCG	TGTGGTCTGG	TTAGGAGTTG	AGTTGTTTGC	3420
	TCAGGGGTTA	TTCTCCTCCT	CGAGTCACAG	TCACAAGAAAT	ACCTGCCTTC	TCTGGCTTTC	3480
65	CTGCTATACA	CATATTCACA	TGGGCTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGCTTTT	3540
	CTTGGACAA	CTGGCCCATG	TTACAGTGAA	ATGGAGAATT	TCAGGTCTCC	ACGTCTGCCC	3600
	AGGAAAGAAC	TTCACTGAC	TCCACGGGGA	TCTGGAATTC	CACGACCAAT	CCCGATCGGC	3660
	TCTTATTAGC	TCCCGCTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
	TGGGCTCTTA	TTAGCTCCCC	GCTCCACAG	ACACCTGTGA	TCTGGAATTC	TACCACCAAT	3780
70	CCCGATCGGC	TCTTATTAGC	TCCCGCTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCACG	TGCTGACCCAG	TTTTCCCTTC	CAGTTCTCTG	ACAAAAAGTG	TCCAGAGGGC	3900
	TGTTTGCAAA	CACCTAGTGCA	CTTTGTAGCT	TTTCACTCTC	TGTCCAGGG	AATCTAGGAG	3960
	AGATGAGGCC	CGTCAAGAGTC	AAGAGATGTC	ATCCCCCAG	GGTCTCCAG	GCATTTCAC	4020
	ACTATTGGTG	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCACA	GGAAAGTGGC	4080
75	CCAGAGCATG	GCACATGAGC	ATCACCCGCT	GATGGTGGCC	TGCTGTGCTT	GGTGCCAACA	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTTGGCCAC	AGACCTGTGC	4200
	GGTGTCTCTG	TGAGTGGCCT	CCAGATGTCT	TTGTGCATAG	GCACAAGTGG	GCCAGGGCTG	4260
	GAGGAGGGTG	GGAAACCTCA	TCAATCCGTC	GGCCCTGCCA	ATCTTAACCC	AGAACCCCTTA	4320
	GGTATTCTCTG	GCAGTAGCCA	TGACATTGGA	GCACCTTCTT	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCCACT	GTCTCAGATG	GACACCAACC	AGGAGCACCC	TAGGTGAGGG	GTGAGGGCCC	4440
80	CCTTATGTGA	ACCTCTTGCC	TCTTCTTTTC	TCCCATCAGA	GTGGTGTGAT	GGAGCCATTG	4500
	GCCTCTCTTT	CTTCAGCGGG	CCCTTCAACC	TCTCTGACCC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGA	GTCTCTTTTC	CAACAGGATG	ATGCATTTCG	TCAATTCCTA	4620
	GGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGTACAGA	GTTCAAGTTT	4680

CCTCTCTGTT TACAGCTCCT TGACAGTCCC ACGCCCATCT GGAGTGGGAG CTGGGAGTTA 4740
 GTGTTGGAGA AGAAACAACA AAAGCCAATT AGAACCACTA TTTTAAAAA GTGCTTACTG 4800
 TGCACAGATA CTCTTCAAGC ACTGGACGTG GATTCTCTCT CTAGCCCTCA GCACCCCTGC 4860
 GGTAGGAGTG CCGCCTCTAC CCACCTTGTA TGGGGTACAG AGGCACCTGC TCTTCTGCAT 4920
 GGTGTTCAAT AGGCTGGGAG TTTTATTAT CTCTTCAAAC TTTGTACAAG AGCTCATGGC 4980
 TTGCTCTGGG CTTCCTGTCAT TAAACCAAAG GAAATGGAAG CCAITCCCCT GTTGCTCTCC 5040
 TTAGTCTTGG TCATCAGAAC CTCACCTTGGT ACCATATAGA TCAAAAGCTT TGTAAACCACA 5100
 GGAAAAAATA AACTCTTCCA TCCCTTAAAG AATAGAATAG TTTGTCCCTC TCATGGGAAT 5160
 TGGGCTGTAT GTATATTGTT CTTCCTCCTT AGAATTAGA GATACAAGAG TTCTACTTAG 5220
 AACTTTTCAT GGACACAATT TCCACAACCT TTCAGATGCT GATGTAGAGC TATTGGGAAA 5280
 GAACTTCCAA ACTCAGGAAG TTTGCAGAGA GCACAGAGCT AGAGATAACT CGGGACCCAG 5340
 AGTTGGTCGA CAGATGTTAG ATGTATCCTA GCTTTTAGCC ATAAACCACT CAAAGATTCA 5400
 GCGCCAGAT CCCACAGTCA GAACTGAATC TGCCTTGTG GGAAGCCAGC AGTGGCCCTG 5460
 GGAAGGAAGC CATGGCTGTG GTTCAGAGAG GGTGGGCTGG CAAGCCACTT CCGGGGAAAA 5520
 CTCCTTCCGC CCCAGGTTTC TTCTTCTCTT AAGGAGAGAT TGTCTCACC AACCCGCTGC 5580
 CTTCATGCTG CCTTCAAAGC TAGATCATGT TTGCCTTGT TAGAGAAATTA CTGCAATCA 5640
 GCGCCAGTGC TTGGCGATGC ATTTACAGAT TTCTAGGCC TCAGGGTTT GTAGAGTGTG 5700
 AGCCCTGGTG GGCAGGGTGT GGGGGTCTGT CTCTGCTGG ATGTGCTTG TAATCCATTT 5760
 GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 410 Protein sequence

Protein Accession #: BAB84587.1

1 11 21 31 41 51
 MPLKHYLLLL VGCQAWGAGL AYHGCPSSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60
 LNTHTIELNE SPFLNISALI ALRIEKNELS RITPGAFENL GSLRYLSLAN NKLQVLPGL 120
 FQGLDSLESL LLSSNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAPD HLVLTLKLN 180
 GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTDFGL VNLQELALQ NQIGLLSPGL 240
 FHNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRLEWL 300
 YDNHISLPLD NVFSNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLGDNV 360
 FRMLANLQNI SLQNNLRQL PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCBLRL 420
 YDNFWRCDSD ILPLRNWLLL NQPRIGTDTV PFCFSPANVR GQSLIIINNV VAVPSVHVPE 480
 PPSYPETPWY PDTSPYDPT SVSSTTELTS PVEDYDILT IQVTDERSVW GMTQAQSGLA 540
 IAAIVIGIVA LACSLAACVG CCCCCKRSQA VLMQMKAPNE C

Seq ID NO: 411 DNA sequence

Nucleic Acid Accession #: XM_098151

Coding sequence: 1..447

1 11 21 31 41 51
 ATGATGCATT TGCTCAATTC TCAGGGCTGG AATGAGCCGG CTGGTCCCCC AGAAAGCTGG 60
 AGTGGGGTAC AGAGTTCACT TTTCTCTCT GTTACAGCT CCTTGACAGT CCCACGCCCA 120
 TCTGGAGTGG GAGCTGGGAG TCAGTGTGG AGAAGAAACA ACAAAAGCCA ATTAGAACCA 180
 CTATTTTAA AAAGTGTCTA CTGTGCACAG ATACTCTTCA AGCACTGGAG GTGGATTCTC 240
 TCTCTAGCCC TCAGCACCCC TGCGGTAGGA GTGCCGCCCT TACCCACTTG TGATGGGTA 300
 CAGAGGCACT TGCTCTCTG CATGGTGTTC AATAGGCTGG GAGTTTATT TATCTCTTCA 360
 AACTTTGTAC AAGAGCTCAT GGCTTGTCTT GGGCTTCTG CATTAAACCA AAGGAATATG 420
 AAGCCATTCC CCGTGTGCTC TCCTTAG

Seq ID NO: 412 Protein sequence

Protein Accession #: XP_098151

1 11 21 31 41 51
 MMELNLSQGW NEPAGPPESW SGVQSSVFLS VYSSLTVPRP SGVGAGSQCW RRNKSQLEP 60
 LFLKSAICAQ ILPKHWIWL SLALSTPAVG VPPLPTCDGV QRHLLFCMVF NRLGVLFISS 120
 NFWQLMAQL GLSSLNQKRW KPFPCCSP

Seq ID NO: 413 DNA sequence

Nucleic Acid Accession #: NM_002658.1

Coding sequence: 77..1372

1 11 21 31 41 51
 GTCCCGCAG CGCGCTGCGG CCTCCTGCTC GCAGGCCACC GAGGCGCGCG CGCTCTAGCG 60
 CCGGACCTC GCCACCATGA GAGCCCTGCT GCGCGCGCTG CTCTCTGCG TOCTGGTCTG 120
 GAGCGACTCC AAAGGCAGCA ATGAACCTCA TCAAGTTCCA TOGAAGTGT ACTGTCTAAA 180
 TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCACATT CACTGGTGA ACTGCCCAA 240
 GAAATTGCGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300
 TCACTTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCGCTGCC TGCCCTGGAA 360
 CTCTGCCACT GTCCCTTCAGC AAAGCTACCA TGCCACAGA TCTGATGCTC TTCAGTGGG 420
 CCTGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGGCGACCTT GGTGCTATGT 480
 GCAGGTGGGC CTAAGCGCG TTGTCCAGA GTGCATGGTG CATGACTGCG CAGATGGAAA 540
 AAGCCCTCC TCTCCTCCAG AAGAATTAAA ATTTAGTGT GGCCAAAAGA CTCTGAGGCC 600
 CCGCTTTAAG ATTATGGGG GAGAAATCAC CACCATCGAG AACGAGCCCT GGTTTGCGGC 660
 CATCTACAG AGGCACCGGG GGGGCTCTGT CACTAAGTGT TGTGGAGGCA GCCTCATCAG 720
 CCTTGCTCG GTGATCAGCG CCACACACTG CTTCATTGAT TACCCAAAGA AGGAGGACTA 780
 CATGCTTAC CTGGGTGCTC CAAGGCTTAA CTCACACAGC CAGGGGAGGA TGAAGTTTGA 840
 GGTGGAAAAC CTATCTCTAC ACAAGGACTA CAGCGCTGAC ACGCTTGTCT ACCACAAGA 900
 CATGCTCTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCGGACTAT 960
 ACAGACCAT TGCTGCGCTC CGATGTATAA CGATCCCGAG TTTGGCACA GCTGTGAGAT 1020
 CACTGGCTTT GGAAGAGAGA AFTCTACGA CTATCTCTAT CCGGAGCAGC TGAATATGAC 1080

5 TGTGTGAAG CTGATTTCCC AC0GGGAGTG TCAGCAGCCC CACTACTACG GCTCTGAAGT 1140
 CACCACCAAA ATGCTATGTG CTGCTGACCC CCAATGGAAA ACAGATTCTT GCCAGGGAGA 1200
 CTCAGGGGGA CCCCTGCTCT GTTCCCTCCA AGGCGCATG ACTTTGACTG GAATTGTGAG 1260
 CTGGGGCCGT GGAGTGTGCC TGAAGGACAA GCCAGGCGTC TACACGAGAG TCTCACACTT 1320
 CTTACCCCTG ATCCCGAGTC ACACCAAGGA AGAGAAATGG CTGGCCCTCT GAGGGTCCCC 1380
 AGGGAGGAAA CGGGCACCAC CGCTTTCTT GCTGGTTGTC ATTTTTCAG TAGAGTCATC 1440
 TCCATCAGCT GTAAGAAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGGAT TTGCCTGTGG 1500
 CACCACCAAG GTGAACGACA ATAGCTTTAC CCTCACGGAT AGGCCTGGGT GCTGGCTGCC 1560
 10 CAGACCCCTT GGCCAGGATG GAGGGGTGGT CCTGACTCAA CATGTTACTG ACCAGCAACT 1620
 TGTCTTTTTC TGGACTGAAG CCTGCAGGAG TTAAGGAGGG CAGGGCATCT CCTGTGCATG 1680
 GGCTGGAAGG GAGAGCCAGC TCCCCGAGCC GGTGGGCATT TGTGAGGCC ATGTTTGAGA 1740
 AATGAATAAT TTCCCAATTA GGAAGGTGTA GCAGCTGAGG TCTCTTGAGG GAGCTTAGCC 1800
 AATGTGGGAG CAGCGGTTTG GGGAGCAGAG AACTAACGA CTTAGGGCA GGGCTCTGAT 1860
 15 ATTCATGAA TGTATCAGGA AATATATATG TGTGTGTATG TTTGCACACT TGTGTGTGG 1920
 GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTCTCT 1980
 AAAGTGTGTG GACTGTGATG CCACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGTCACTC 2040
 CTGGGGCCCT TGGGTCCCC CAGGTGACAG TGCCCTGGGA TGTACTTATT CTGCAGCATG 2100
 ACCGTGACCC AGCAGTGTCT CAGTTTCACT TTCACATAGA TGTCCTTTTC TTGGCCAGTT 2160
 20 ATCCCTTCTT TTATGAGTCT TCCATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT 2220
 ACACGAATA TTTATATTTC ACTATTTTAA TTTATATTTT TGTAAATTTA AATAAAGTG 2280
 ATCAATAAAA TGTGATTTTT CTGA

Seq ID NO: 414 Protein sequence
Protein Accession #: NP_002649.1

25 1 11 21 31 41 51
 MRALLARLLL CVLVVSDSKG SNELHQVPSN CDCLNGGTCV SNKYFSNIHW CNCPKRFGGQ 60
 HCEIDSKRKC YEGNGHFYRG KASTDTMGRP CLPWN SATVL QQTYHAHERSD ALQLGLGRHN 120
 30 YCRNPDRRR PWCYVQVGLK PLVQECMVHD CADGKOPSSP PEELKFCQCG KTLRPRPKII 180
 GGEFTTIEHQ PWFPAIYRRH RGGSVTVYCG GSLISPCWVI SATHCPIIDY KKEDYIVYLG 240
 RSLNSNTQG EMKFEVENLI LHKDYSADTL AHNDLALLK IRSKEGRCAQ PSRTIQTICL 300
 PSMYNDPQFG TSCEITGPGK ENSTDYLYPE QLKMIIVVKLI SHRECOQPHY YGSEVTTKML 360
 CAADPQWKTD SCQDSSGGPL VCSLQGRMTL TGI VSWGRGC ALKDKPGVYT RVSHFLPWIR 420
 35 SHTKEENGLA L

Seq ID NO: 415 DNA sequence
Nucleic Acid Accession #: NM_024422.1
Coding sequence: 202..2907

40 1 11 21 31 41 51
 CGCCAAAGGA AAAGCCCTT GGATGAGAGG CAGGCGCTTC AGAGAAGCTA AGAAAAGCAC 60
 CTCTCCGCGC GCCCCACCTC CTCGCGCTCG CGCTCCTCCT GAGCAGCGGG CCCAGACTGC 120
 45 GCTCCGSCCG CGGCGCTCGC CCGCGGAGC CCTCCTACCC CGGCCGACG CTGGGCGCGC 180
 GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCTC CGGCTCCTG GAACGGAGCC 240
 CTCTGCCGCG TGCTCCTGCT GACCCCTCGC ATCTTAATAT TTGCCAGTGA TGCCCTGCAA 300
 AATGTGACAT TACATGTTCT CTCCAACTA GATGCGGAGA AACTTGTGG TAGAGTTAAC 360
 50 CTGAAGAGT GCTTTACAGC TGCAAACTA ATTCAATCAA GTGATCCTGA CTCCCAATT 420
 TTGGAGCTG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGTCCTCGGA GAAGAGAAAT 480
 TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAGA AGAAATATT TGTCTTTTGG 540
 GAGCATCAA CAAGGTCTT AAAGAAAAGA CATACTAAG AAAAGTTCT AAGGCGGCGC 600
 AAGAGAAGAT GGGCTCCAAAT TCCTTGTTCG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660
 55 CTTTCTCTTC AACAGGTTCA ATCTGACAGC GCCCAAACT ATACCATATA CTATTCCATA 720
 AGAGGTCTCG GAGTTGACCA AGAACCTCG AATTATTTT ATGTGGAGAG AGACACTGGA 780
 AACTTGTATT GTACTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
 TTTGCAACAA CTCCAGATGG GTATACTCCA GAACCTCCAC TGCCCTTAAT AATCAAAATA 900
 GAGGATGAAA ATGATAACTA CCAATTTTT ACAGAAAGAA CTTATACTTT TACAATTTTT 960
 60 GAAAATTGCA GAGTGGGCCT TACTGTGGGA CAGTGTGTG CTACTGACAA AGATGAGCCT 1020
 GACACAGTGC ACACACGCTC GAAGTACTCC ATCATTTGGC AGGTGCCACC ATCACCCACC 1080
 CTATTTTCTA TGCATCCAAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
 GAGTTAAATG ACAAGTACCA GTTGAAAATA AAGTACAAG ACATGGATGG TCAGTATTTT 1200
 GGTCTACAGA CACCTTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCCTTGCCA 1260
 65 ACATTACTCT GTACTTCTTA TGTGACATCA GTGGAAGAAA ATACAGTTGA TGTGGAAATC 1320
 TTACAGGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAACCTGGAG AGCTAATTAT 1380
 ACCATTTTAA AGGGCAATGA AATGGCAAT TTTAAATTTG TAACAGATGC CAAAACCAAT 1440
 GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG 1500
 70 CAAATTGGTG TAGTTAATGA AGCTCCATTT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560
 AGCACAGCAA CAGTTACTGT TAATGTAGAA GATCAGGATG AGGGCCCTGA GTGTAAACCT 1620
 CCAATACAGA CTGTTGSCAT GAAAGAAAAT GCAGAAAGTG GAACAACAAG CAATGGATAT 1680
 AAAGCATATG ACCCAGAAAC AAGAAAGTAG AGTGGCATAA GSTATAAGAA ATTAACATGAT 1740
 CCACACGGGT GGGTCAACAT TGATGAAAAT ACAGGATCAA TCAAGTTTT CAGAAGCCTG 1800
 GATAGAGAGG CAGAGACCAT CAAAAATGGC ATATATAATA TTACAGTCTT TGCATCAGAC 1860
 75 CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGACGT GAATGATAAC 1920
 AGCCCATTTA TACTTAAAAA GACAGTGATC ATCTGCAAAAC CCACCATGTC ATCTGCGGAG 1980
 AITGTTGCGG TTGATCCTGA TGAGCCTATC CATGGCCCAT CCTTTGACTT TAGTCTGGAG 2040
 AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAATGA TACAGCAGCA 2100
 CGTCTTCTCT ATCAGAAATG TCCTCCATTT GGCTCATATG TAGTACCTAT AACAGTGAGA 2160
 80 GATAGACTTG GCATGCTTAG TGTCACTTCA TTGGATGTTA CACTGTGTGA CTGCATTACC 2220
 GAAAATGACT GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGGA 2280
 AAGTGGGCCA TCCTTGTCAAT ATTGTTGGGC ATAGCATTGC TCTTTTGCAT CCGTTTACG 2340
 CTGGTCTGTG GGGCTCTCGG GACGTCTAAA CAACCAAAAG TAATTCTCGA TGAATTAGCC 2400
 CAGCAQAACC TAATTGTATC AAACACAGAA GCTCCTGGAG ATGACAAAGT GTATTCTGCG 2460
 AATGGCTTCA CAACCCAAAC TGTGGGGGCT TCTGCTCAGG GAGTTTGTGG CACCGTGGGA 2520

5 TCAGGAATCA AAAACGGAGG TCAGGAGACC ATCGAAATGG TGAAGGAGG ACACCAGACC 2580
 TCGGAATCCT GCCGGGGGGC TGGCCACCAT CACACCTGG ACTCCTGCAG GGGAGGACAC 2640
 ACGGAGGTGG ACAACTGCAG ATACACTTAC TCGGAGTGGC ACAGTTTAC TCAGCCCCGT 2700
 CTGGGTGAAA AAGTGTATCT GTGTAAATCAA GATGAAATC ACAAGCATGC CCAAGACTAT 2760
 GTCCGTGACAT ATAACATAGA AGGAAGAGGA TCGGTGGCTG GGTCTGTAGG TTGTGTGAGT 2820
 GAACGACAAG AAGAAGATGG GCTTGAATTT TTGGATAATT TGGAGCCCAA ATTTAGGACA 2880
 CTAGCAGAAG CATGCATGAA GAGATGAGTG TGTCTAATA AGTCTCTGAA AGCCAGTGGC 2940
 TTTATGACTT TTAATAAAAA TTACAAACCA AGAATTTTTT AAAGCAGAAG ATGCTATTGT 3000
 10 TGGGGGTTTT TCCTCATTA TTTGGATGGA ATCTCTTGG TCAATATGCAC ATTTACAGAG 3060
 AGACACTATA AACAGTACA CAAATTTTTT AATTTTTTACA TATTTTTTAAA TTACTTATCT 3120
 TCTATCCAAG GAGGTCTACA GAGAAATTAA AGTCTGCCTT ATTTGTTACA TTTGGGTATA 3180
 ATGACAACAG CCAATTTATA GTGCAATAAA ATGTAATTAA TTCAAGTCTT TATTATAGAC 3240
 TATTTGAAGC ACAACCTAAT GGAATAATTG AGAGACCTTG CTTTAACATT ATCTCCAGTT 3300
 15 AATTAAGTGT TCATGTGGTG CTTGGAACCT GTTGTTTTCC TGAACATCTA AAGTGTGTAG 3360
 ACTGCATCTT TGCTATTATT TTATTCTTGT AATGTGACCT TTTCACTGTG CAAAGGAGA 3420
 TTTCTAGCCA GGCATTGACT ATTACAATTT CATT

Seq ID NO: 416 Protein sequence

Protein Accession #: NP_077740.1

20 1 11 21 31 41 51
 MEAARPSGSW NGALCRLLLL TLAILIFASD ACKNVTLEVP SKLDAEKLVG RVNLKECFTA 60
 ANLIHSSDPD FQILEDGSVY TTNITLLSSE KRSPTILLSN TENQEKKIP VFLEHQTKVL 120
 25 KRRHTKEKVL RRAKRRWAPI PCSMLENSLG PFPLFLQQVQ SDTAQNYTIY YSIRGPGVDQ 180
 EPRNLFYVER DTGNLYCTRP VDREQYESPE IIAFATTPDG YTPFLPLPLI IKIEDENDNY 240
 FIFTEETTF TIFENCVRGT TVGQVCATDK DEPDTHMTRL KYSIIGQVPP SPTLFSMHPT 300
 TGVIITTSQ LDRELDKYQ LKIKVQMDMG QYFGLQTTST CIINIDVDND HLPFTTTSY 360
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNPKIVTDA KTNESVLCV 420
 30 KPLNYEEKQQ MILQIGVNE APPSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVP RSLDREAEI 540
 KNGIYNITVL ASDQGGRTCT GTLGIILODV NDNSPFIPKK TVIICKPTMS SAEIVAVDPD 600
 BPIHGPFDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFSGSYVPI TVDRDLGMSS 660
 VTSLDVTLCD CITENDCTHR VDRIGGGGV QLKGWAILAI LLGIALLFPI LEFTVCGASG 720
 35 TSQKPVIFD DLAQNLIVS NTEAPGDDKV YSANGFTTQT VGASAGVGC TVGSGIKNGG 780
 QETIEMVKGQ HQTSESCRGA GHHTLDSR GGHTEVDNCR YTYSEWSFT QPRLGEKVYL 840
 CNQDENHKEIA QDYVLTNYE GRGSVAGSVG CSEREQEDG LEFLDNLEPK FRTLAEACMK 900
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Seq ID NO: 417 DNA sequence

Nucleic Acid Accession #: NM_004949.1

Coding sequence: 202..2745

45 1 11 21 31 41 51
 GCGCAAGGA AAAGCCCTT GGTAGAGAG CAGGCGCTTC AGAGAAGCTA AGAAAAGCAC 60
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 GCTCGGCGCG CGGCGCTCG CCGCGGAGC CCTCTACCC CGGCGCGAG CTCGGCCGCG 180
 50 GACCTGCCCC GAGCCCTCT CATGGAGGA GCCCGCCCT CCGGCTCTCG GAACGGAGCC 240
 CTCGCGCGCG TGCTCTGCT GACCTCGCG ATCTTAATAT TTGCCAGTA TGCCCTGCAA 300
 AATGTGACAT TACATGTTC CTCCAACTA GATGCGGAGA AACTGTGTGG TAGAGTTAAC 360
 CTGAAAGAGT GCTTTACAGC TGCAAACTA ATTCAATCAA GTGATCTCTA CTTCCAAATT 420
 55 TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGTCCTCGGA GAAGAGAAGT 480
 TTTACCATAT TACTTTCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGCTTTTTTG 540
 GAGCATCAA CAAAGGTCTT AAAGAAAAGA CATACTAAG AAAAGTTCTT AAGGCGCGCC 600
 AAGAGAAGAT GGGCTCCAAT TCCTGTGTCG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660
 CTTTTCCTTC AACAGGTTC ATCTGACAG GCCCAAACT ATACCATATA CTATTCCTA 720
 AGAGTCTCTG GAGTTGACCA AGAACCTCG AATTATTATT ATGTGGAGAG AGACACTGGA 780
 60 AACTGTGATT GTACTCGTCC TGTAGATGT GAGCAGTAG AATCTTTGA GATAATTGCC 840
 TTTGCAACAA CTCTCAGTGG GTATACTCCA GAACCTCCAC TGCCCTAAT AATCAAAATA 900
 GAGGATGAAA ATGATACTA CCCAATTTT ACAGAAGAAA CTTATCTTT TACAATTTTT 960
 GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020
 GACAAGATGC ACACACGCTT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCAACCCACC 1080
 65 CTATTTTCTA TGATCTCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
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 GGTCTACAGA CAACCTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCACCTGCCA 1260
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 70 TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAACCTGGAG AGCTAATTAT 1380
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 75 CCAATACAGA CTGTTGCTAT GAAAGAAAAT GCAGAAGTGG GAACAACAAG CAATGGATAT 1680
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 CCAACAGGGT GGGTCACCAT TGATGAAAAT ACAGATCAA TCAAGTITT CAGAAGCCTG 1800
 GATAGAGGG CAGAGACCAT CAAAAATGGC ATATATAATA TTACAGTCTT TGCATCAGAC 1860
 CAAGAGAGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGAGCT GAATGATAAC 1920
 80 AGCCCATTA TACCTAAAA GACAGTGATC ATCTGCAAC CCACCATGTC ATCTGCGGAG 1980
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 AAGTGGCCCA TCCTTGCAAT ATTGTTGGGC ATAGCAATTG TCTTTTGCAT CCTGTTTACG 2340

5 CTGGTCTGTG GGGCTTCGG GAGCTCTAAA CAACCAAAAG TAATCTCTGA TGATTAGCC 2400
 CAGCAGAACCC TAATGTATC AAACACAGAA GCTCCTGGAG ATGACAAAGT GTATTCTGCG 2460
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 10 AGATGGGCTT GAATTTTGG ATAATTGGA GCCCAAATT AGGACACTAG CAGAAGCATG 2940
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 15 AGTACACAAA TTTTCAATT TTTACATATT TTTAAATTAC TTATCTTCTA TCCAAGGAGG 3180
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 GTGGTGCTTG GAAACTGTGT TTTTCTGAA CATCTAAAGT GTGTAGACTG CATTCTTGCT 3420
 20 ATTATTTTAT TCTGTGAATG TGACCTTTTC ACTGTGCAA GGGAGATTTC TAGCCAGGCA 3480
 TTGACTATTA CAATTCATT

Seq ID NO: 418 Protein sequence
Protein Accession #: NP_004940.1

25 1 11 21 31 41 51
 MEAARPSGSW NGALCRLLLL TLAILIFASD ACKNVTLHVP SKLDAEKLVG RVNLKECFDA 60
 ANLIHSSDPD FQILEDGSVY TINTILLSSE KRSPTILLSN TENQEKKIP VFLEHQTKVL 120
 30 KRRHTRKEVL RRAKRWAPI PCSMLENSLG PFPLFLQQVQ SDTAQNYTIY YSIRGPGVDQ 180
 EPRNLFFVER DTGNLYCTRP VDREQYESPE ILAFATPDG YTPELPLPLI IKIEDENDNY 240
 PIFTEETTFP TIFENCVRGT TVGQVCATDK DEPDTHMTRL KYSLIGQVPP SPTLFSMHPY 300
 TGWITTTSSQ LDRELIDKYQ LKIKVQDMQG QYFGLQTTST CIINIDVDND HLPFTFRTSY 360
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKGNB NGNFKIVIDA KTNBGLVLCV 420
 35 KPLNVEEKQQ MILQIGVVNE APPSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480
 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI 540
 KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIPKK TVIICKPTMS SABIIVAVDPD 600
 EPIHGPPFPD SLBSSTSEVQ RMWRLKAIND TAARLSYQND PPFQSYVVPF TVRDLGMSS 660
 VTSLDVTLCD CITENDCTHR VDPRIIGGGV QLGKWAIALI LLGIALLLPCI LPTLVCGASG 720
 40 TSQKPKVIPD DLAQQLNIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG 780
 QETIEMVKGQ HQTSESRCGA GHHHTLDSR GGHTEVDNCR YTYSEWHSFT QPRLGEESIR 840
 GHTLIKN

Seq ID NO: 419 DNA sequence
Nucleic Acid Accession #: NM_002722.1
Coding sequence: 14..301

50 1 11 21 31 41 51
 ACTCTGGACT COGGATGGCT GCGGCACGCC TCTGCTCTC CTGCTGCTC CTGTCCACCT 60
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 ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCAGTA TGCAGCTGAT CTCCGTAGAT 180
 ACATCAACAT GCTGACCAGG CCTAGGTATG GGAAAGACA CAAAGAGGAC ACGCTGGCCT 240
 TCTCGGAGTG GGGGTCCCGG CATGCTGCTG TCCCCAGGGA GCTCAGCCCG CTGACTTAT 300
 55 AATGCCACTC TCTGCTCTCT ACGACTCCAT GAGCAGCGCC AGCCAGCTC TCCCTCTGCG 360
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 AAGCC

Seq ID NO: 420 Protein sequence
Protein Accession #: NP_002713.1

60 1 11 21 31 41 51
 MAAARLCLSL LLLSTCVALL LQPLLGAQGA FLEPVYPGDN ATPBQMAQYA ADLRRYINML 60
 TRPRYGRKHK EDTLAFSEWG SPFAAVPREL SPLDL

Seq ID NO: 421 DNA sequence
Nucleic Acid Accession #: NM_032545.1
Coding sequence: 46..718

70 1 11 21 31 41 51
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 75 CTATCAAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGTTG CCACTCAGAA 180
 GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCAATTC GGAGAGGTGA CTGGGAGGCG 240
 CGAGGCGCTG GGGCGGAGG AGCCGCTCCC CTACTCCCGG GCTTTCGAG AGGGTGGGTC 300
 CGGCGGGCGG CGCTGCTGCA GGAACGGCGG TACCTGGGTG CTGGGAGCT TCTGCGTGTG 360
 CCGGCGCCAC TTCACGGGCC GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGCGC 420
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 80 CCTGCACTGC CTCCCTCTCC AGACGCTGCA CCGCTGTGAC CCGAAAGACT TCCTGGGCTC 540
 CCAAGCTCAC GGGCGGAGCG CGGGGGGCGC GCCAGGCTG CTACTCTTGC TGCCCTGCGC 600
 ACTCTGCAC CGCTCTCTGC GCCCGGATGC GCCCGGCAC CCTGGGTCCC TGGTCCCTTC 660
 CGTCTCCAG CGGGAGCGGC GCCCTGCGG AAGGCGGGA CTTGGGCATC GCCTTTAATT 720
 TTCTATGTTG TAAATAATAG ATGTGTTAG TTTACGTAA GCTGAAGCA TGGGTGAATA 780

TTTTTATTGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA 840
AAAAAA

Seq ID NO: 422 Protein sequence
Protein Accession #: NP_115934.1

1 11 21 31 41 51
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10 VTGSAEGWGP EEPLFYSRAP GEGASARPRC CRNGGTCVIG SFCVCPAHT GRYCEHDQRR 120
SEGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHANGP SAGGAPSLLL 180
LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRPGRPLG HRL

Seq ID NO: 423 DNA sequence
Nucleic Acid Accession #: NM_006533.1
Coding sequence: 72..467

1 11 21 31 41 51
20 AGGGAGAGAG GGAGGGGAGG AAATTGGAGA CCCCAGCACC CCCTTGCTCA CTCTCTTGCT 60
CACAGTCCAC GATGGCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCCT 120
TCTCCGGACC TGGTGTGAGG GGTGGTCTTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180
CGGACCAGGA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC 240
CGACTCGCG ATTCTGAGC ATTACCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300
25 AGGGCCGTGG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360
CTGCTCGCTG GGGCTATTTC CCCAGTAGCA TTGTCCGAGA GGACCAAGCC CTGAAACCTG 420
GCAAGTCGA TGTGAAGACA GACAAATGGG ATTTCTACTG CAGTGAGCT CAGCCTACCG 480
CTGGCCCTGC CGTTTCCCTT CCTTGGGTTT ATGCAATAC AATCAGCCCA GTGCAAAC

Seq ID NO: 424 Protein sequence
Protein Accession #: NP_006524.1

1 11 21 31 41 51
35 MARSLVLCGV IILLSAFSGP GVRGGPMPKL ADRKLCADQE CSHPISMAVA LDYMAPDCR 60
FLTIHRGQV VYFSKLKGRG RLPWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD 120
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Seq ID NO: 425 DNA sequence
Nucleic Acid Accession #: NM_080870.1
Coding sequence: 3..710

1 11 21 31 41 51
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AAGGGAAAAA CACACCAATC CCAGAAAAGC CTACAGAAAA CTGGGGAAAC ACCCACTGA 180
CCAATGAGAC CATAAAAGCC CCAGTAAAGT CCACAGAAAA CCCAGAAAAA ACAGCAGCAG 240
TCACAAAGAC TATAAAACCT TCAGTCAAGG TCACAGGAGA CAAATCTCTC ACTACTACCT 300
50 CTCTCTCATCT AAATAAACT GAAGTTACTC ATCAGGTGCC CACTGGTTCT TTCACCTCA 360
TTACATCTAG AACGAAGCTG AGTTCTATCA CATCAGAAGC CACAGGAAAC GAGAGCCATC 420
CATACCTCAA TAAAGATGGC TCACAGAAAG GTATCCACGC TGGACAGATG GGAGAGAATG 480
ATTCACTCCC TGCAATGGCC ATAGTTATTG TGGTCTCTGT GGCTGTGATT CTCCTCCTGG 540
TGTTCTCTGG CCTGATCTTC TTGGTCTCCT ATATGATGCG GACACGCCGC ACATAAACC 600
55 AGAACACCCA GTACAATGAT GCAGAGGATG AGGGTGGGCC CAATTCTCTC CCGGTCTACC 660
TGATGAGACA GCAGAACTCTT GGCATGGGCC AGATCCCTTC CCCACGGTGA TCTTGGAGTA 720
GGGCCCCAGC CCTGGCTCTT CCATGCTCTG CCCCCTTCTT GGATGAGGAA COGGACTCAC 780
AATTTCATTT TCCGGGACTA CAGGAAGGGC AGAGAATACT GACGGTTACC AGTATTAACC 840
CTTCATCTGT TCTTGAACT GGTGGGGAA TGAGGTGATA AGCAAGGAGG GTGTAAGTTT 900
60 AGGGGACAAA GAAGAAGAA TGAATAATAC GAGCAGACAT TCTCTGTAGA AGGTAATGGT 960
CTGAGAATGA AAAGGTGTTT GATGGACATG TTGTGGGGGC ACCAATGCAG AACACTGCAC 1020
TGAGTCTTAA AGGAAGGACA GGAGCCTTAT AGGCAATGCC CCAGACTGAC TTGTGAGTGG 1080
GGTTTATGGG GAAAGGGAGG GACTGAGGCG AGAGTCTCTG GGTTCAGGA CAGCATTATG 1140
TTATTTCCAT TCACTATTAC TTAAGAGTTT GTGTGTAAC AGGCTCATCT CTGAGTTCTC 1200
65 AGGACCTTG CCCCCACCC CATTTTTTTA ATGAAAAA AAAACAAAAA AACCGATCC 1260
AAGAAGAAAA GAGAATTAT TTCTCTCTCC ACTCTCTCCA TGCCCTGGAG AAAAAAAGT 1320
CCAGAAGAAA TCATAAATAT CTCTCATCTA CATGGTTGCT TCCTCTCTCT CCCAAATCCC 1380
TTAGTTTCTT TAAATGTCTA CAGTGGACGC CCTGTGGT TGGCTGTCTG GGTGTGGGT 1440
70 GGACACGCAA GGAGGGGATT TTTATTGGC CAGCAGTCTC ACCCACTGAT CTCCACCCCA 1500
GACCTTCCCT GATTGGTGTG TCAGCATTGA TTTTCTGTG TCTTCCACCA AAAGCCAGCT 1560
GTAGCTTTAT CTGGTAAAG TTACCATCT TCTCTACTGT CCCCATTCTC TCTCTOCCA 1620
CCTTCACCCC AGATTCAGT TTTCTCTCT GTAGGCATT CATCTGTGTG TGTTTCTGG 1680
75 ATTTTCTCTC TCTCTCTTA TGGCATTTT ACCTTATTAC TGATTGGGTA GAGGGGAAA 1740
AGGAGATGA TGATGATAGT TTCTTCTGT CTATTGACCT TTTTATAAT AAAGTATAAC 1800
ATGT

Seq ID NO: 426 Protein sequence
Protein Accession #: NP_543146.1

1 11 21 31 41 51
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TETIKAPVKS TENPETAARV TKTIKPSVKV TGDKSLTTTS SHLAKTEVTH QVPTGSFTLI 120
TSRTELSSIT SEATGNESHV YLNKDGSKQK IHAGQMGEND SPPAWAIVTV VLVAVILLV 180

Seq ID NO: 427 DNA sequence
Nucleic Acid Accession #: XM_069480.1
Coding sequence: 1..4383

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GCATATGTCA	GCCTAATGTA	CGGTATCAAG	AAGCCGTACG	AGTTCOAGAG	GGAGATGAGT	180
CTGGGGGTG	CTGTGGTCTC	TGTGACCCCT	TACAGCAGCC	ACCATGAGGG	GGAGGCTGCC	240
AGCCAGGCGT	ACTCTTGTCA	AATGAAAGCT	TCTTGGGGGG	CAGGTTGCTAC	TACATTTCCAA	300
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GGCAATCTAC	AGACCAAGCA	AAAAAGCACA	CTTTTTCAG	AAAAAATCAG	AGCAGCCTCA	900
AAAAACACAT	ACAGAGACAC	AGGAACCCCA	GAGAGTCCAG	AAAAAATCTA	AGATTCCAGA	960
ACAACAGTTG	CCTCAGACAA	GCTCCTGACA	AAACTACATA	AAAAATACAT	AGAGACCTAT	1020
TCAGGCCAAT	AGCTCACACA	ATCTCTAGCA	GAGCTCAGAG	AACATGAGGG	AGAGCAGGCC	1080
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GAGAACACCA	CACATCTCCC	AGCAGAGCCT	ACAGAAATAT	GAGAAAGGAC	AGCCCAATGAG	1200
AAACCCGACG	CACTTCCGAC	AGGGCTCACA	GAAATAGAGG	AAATGACAGC	CAATGAGAAAT	1260
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ACACCATCCC	CAGCAGGGCC	TACAGAAATC	AGAGAAACGA	CAGCCAAAGG	GAGAGACCCA	1620
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TCGCCAGCAG	AGGCTCAGAA	AAATGACAGA	AGGACCCCAT	TTGCATATGA	GAAAACCCCA	1740
TCCTCCTCAG	CAGAGCCTAC	AGAACACGGA	GAAGAGACCC	CATGTGCCAA	TGAGAACACC	1800
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ACCATCATCT	CCTCAGCAGA	GCTCAGACAA	CACAGAGAAA	GGACTCCACT	GGCCAATGAG	2040
AAACACCAAC	CTCCCGCCGC	AGGCGCTACA	GAAATATAGG	AAAGGACAGC	CAATGAGAAC	2100
ACACACCAT	CCCCAGCAGG	GCTCAGACAA	AATAGAGAAA	TGACAGCCAA	CGAGAGAACCC	2160
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TCATCCCCAG	CAGAGCCTAC	AGAAAATGGA	CAAGAGACCC	CATTGTGCCA	TGAGAAAAACC	2280
ACATCATCCC	CAGCAGAGCC	TACAGAACAT	GAGAAAGGGA	CCCCACTGCG	CAATGAGAAC	2340
ACCACCATCT	CCCCAGCAGA	GCTCAGACAA	AATAGAGAAA	GGACAGCCAA	TGAGAGAACCC	2400
ACACCATATC	CAGCAGAGCC	TACAGAAATC	AGAGAAAGGA	GAGCCAAATG	GAACACCCCA	2460
CCATCCCCAG	CAGAGCCTAC	AGAAAATGGA	GACAGGACTC	CATTGTGCCA	TGAGAGAACCC	2520
ACACCATATC	TAGCAGAGCC	TACAGAAATC	GGAGAAAGGA	CCCCACTTGC	CAATGAGAAC	2580
ACCACATCTC	CCTCAGCAGA	GCTCAGACAA	CACGACGAAA	GAGCTCCACT	GGCCAATGAG	2640
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ACCACCAAT	TCCCAGCAGA	GCTCAGACAA	AATAGAGAAA	GCACAGCCAA	TGAGAGAACCC	2760
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CTATCCCCAG	CAGAGCCTAC	AGAAAATGGA	GAATGTAGCC	CATTGGCCAA	TGAGAGAACCC	2880
ACATCATCCC	CAGCAGAGCC	TACAGAAATC	GAGAAAGGGA	CCCCACTTAC	CAATGAGAAC	2940
ACCACCATCT	CCTCAGCAGA	GCTCAGACAA	CATGAGAGAAA	GGACCCCACT	GGCCAATGAG	3000
ATCACCAATC	CATCCGAGCA	AGAGCCTACA	GAACTGGAG	AAAGGATAGC	CAATGAGAAC	3060
GCCACACCAT	CCCCAGCAAA	GCTCAGACAA	CATGAGAGAA	GCACAGTCAA	TGAGGACCAAC	3120
ACACCATCTC	CAGCAGAGCC	TACAGAAATC	GGAGAAAGGA	CCCCACTGCG	CAATGAGAAC	3180
ACACCAACAT	CCCCAGCAGA	GTCTCAGAAA	CTATGAGAAA	GGACAGCCCA	TGAGAGAACCC	3240
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Seq ID NO: 428 Protein sequence
Protein Accession #: XP_069480.1

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LGCGCGSVTP YSSHHEGEAA SQRYSCQMKa SWGAGATTFO EYQKTGELST SDHIFPLTPG 120
LVYSIPFDHI VLHSGQRPEP LPKSTETHEQ KRHCNTRHS KPTDKPTGNS KTIDHKSSTD 180
NHEAPPTSEE NSSNQKQDPM IRNQRSVDPa DSTTTHKESA GKQHITPAK SKINCRKSTT 240
KSTVTRKSD KTRGRPLEKSM STLDKSTSS HKTITSPHNS GNSQTKQKST SPPEKITAAS 300
KTTYKITGTP EESEKTEDSR TTVASDKLLT KTKNIQETI SANELTQSLA EPTHEGGRTA 360
NENNTSPAE PTERNERTAN ENTTLSPAEP TENRERTANE NTAPFPAGPT ENREMTANEN 420
TTLFPAEPT EHGERTANENT TSPAEPT EHGERTANENT TSPAEPT EHGERTANENT 480
TSSSAESTEH GERTPLANEN TTPSPAEPTE NRERTANENT TSPAGPTEN RETTAN EKTT 540
LSPVEPTENR ETTANEKTTT SPAEPTENGQ RTPFANEKTT SSSAEPT EHGERTPLANENT 600
TSPSPAEPTE RERTANEKTT TSPAEPTENG DRTPLANEKTT TSPSPAEPTE GQRTPFANEK 660
TTSSSAEPTE HEERTPLANE NTTSPAEPTE ENRERTANEN TTPSPAEPTE NREMTANEKTT 720
TLFPAEPTEN RERTANEKTT SSPAEPTENG QRTPFANEKTT TSPSPAEPTE GERTPLANEN 780
TTLSPAEPTE NRERTANEKTT TFPFPAEPTEN RERTANENTTT PSPAQPTENG DRTPLANEKTT 840
TPSLAEPTE GRTPPFANEK TTSSSAEPTE HAERTPLANE NTTSPAEPTE ENRERTANEK 900
TTQFPAEPT NRESTANEKTT TFPFPAEPTEN REWTANENTTT LSPAEPTEHE EMTPLANEKTT 960
TLSPAEPTE GRTPPFANEK TTPSPAEPTE HGERTPLANE ITTPSRAEPT EHGERIANEK 1020
ATPSPAKPT EGETTVNEDT TSSSAEPTE GERTPLANEN TTPSPAEPTE EHGERIANEK 1080
TSPSPAEPTE GERTPSANEK TTPSPAEPTE HEEMTPSANE NTTSPVKT EHGERTPLAN 1140
EKITLSEPEG TEHGAKTTS NEKITPSLAK PTEHGERITS PNDKITSSAA ESTEHRDRAT 1200
SANVITPAPA EPIKHAKTTS LAHEKMTQVT EKSTHEPEKT TSTTEKTRT PEKPTLYSEK 1260
TICTKGKQTP VPEKPTENLG NTTLTETIK APVKSTENPE KTAAVTKTIK PSVKVTGDKS 1320
LTTTSSHLNK TEVTHQVPTG SFTLITSRTK LSSITSEATG NBSHPYLNKD GSKGHIHAGQ 1380
MGENDSPFAM AIVIVLVAV ILLVFLGLI FLVSYMMRTR RTLTQNTQYN DAEDSGGPNs 1440
YFVYLMQQN LGMGQIPSPR

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Seq ID NO: 429 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..10674

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GGGGCCCGCG GGAGTATCCC CGGCGCGCCC GCTCTGGGCG ACGAAGCGCG GGGGAGCAGA 180
GTGGAGCGCG TGGGCGCAGC GTTCCGCGCA CGCTGCGGCG TGCTGCGGGA GCTCAGCGAG 240
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50 GAGCACTGTT ACCTGCTACA CAGTTTGA GAATTTGAGG CTTTAGCTCG CCGGCGATTG 780
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55 ATTCCATGTC CTGATGAAAA TCACACCTCT CCACCTGGA GACATCCCC TGAAGACTGT 1080
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CTCGCGCAGC CGAAGACATG CCACATCAGC TGTCTACAA GGGAAATGTT ATATAAGACA 1380
ACATGTTTGG TTGCTGTGTA TGAAGGTGAC AGACTAGAA GCAAGTATAA GCTTACTTGT 1440
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TTTCAGATGC CCAAGATGT CATCATATC CCCCACAACT GTGGCAAGCA GCCAGCCAAA 1560
65 TTTGGGACGA TCTGCTATGT AAGTTGCGGC CAAGGTTTCA TTTTATCTGG AGTCAAAGAA 1620
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70 GCTATCGTAT ACACGGCAAC TGACCTATCC GGCACACAGG CCAGCTGCAT TTTCCATATC 1920
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5	AATTGCCCTT	TGGGAACCTA	TTATAATCTG	GAACATTCCA	CCTGTGAAAG	CTGCCGGATC	3060
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Seq ID NO: 430 Protein sequence
 Protein Accession #: PGENESH predicted

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 Coding sequence: 1..390

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 CACAACAACA ATTCAGATT TATTCCCAA AGTGATGAAG AAAATGAGGG TTCCCAATAC 1440
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TATATGAGTC AGTTACTACT TACAGGTGAT AACTTGCAAT CTATTGGAAG ATAAAGTTGT 3000
CAAACTGTGC AAGAAATGAGA AAAGCCAAAT TAGAAAATCC TATGTCCTAG TTTCTTACC 3060
AAGGATAATT AAATATATCA CTAAGAGCTT TATATATTGA TTATATATTG TTGCAACTG 3120
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TTGTAGGGTG CTCATGGTGT GTTTTATTA TTATTACTCA GATTCCACAG TGGCAAGAAA 4380
CATCATCTTA CATAATGGA AACATTACA TCAAATCCCA CTTACTTTAA TGCGAAGCTG 4440
GAGATAATTT ATGGTATTGT ATTGTAACAC ATTAATGAAA ACTTTTTTAC AGTTGAGTGA 4500
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Seq ID NO: 434 Protein sequence
Protein Accession #: NP_009162.1

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1 11 21 31 41 51
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MVLISIPVTI YYNVILAYSL YMFASFQSE LPWKNCSWS DENCSRSPIV THCNVSTVNK 180
GIQEIIMNK SWVDIMNFTC INGSBIYQPG QLPSEQYWNK VALQRSSGMN ETGVIVWYLA 240
LCLLLAWLIV GAALFKGIKS SGKVVPYPTAL PFYVVLILL VERATLEGAS KGISYYIGAQ 300
SNPTKLKEAE VWKDAATQIP YSLSVANGGL VALSSYNKPK NNCPSDAIVV CLTNCLTSVF 360
AGPAIFSIIG HMAHISGKEV SQVVKSGFDL APIAYPEALA QLPFGPPWSI LFFFMLLTLG 420
LDSQFASLET ITTTIQDLFP KVMKMRVPI TLGCCLVFL LGLVCVTQAG IYVHLIDHF 480
CAGWGLLIAA ILELVGIWI YGNNRFIEDT EMMIGAKRWI FNLWHRACWF VITPILLIAI 540
PIWSLVQFHR PNYGAIPYPD WGVALGWOMI VFCIIWIPIM AIKIIQAKG NIFQRLISCC 600
RPASNWGPYL BQHRGERYKD MVDPKKBADH EIPTVSGSRK PE

Seq ID NO: 435 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 51..1085

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1 11 21 31 41 51
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TTCTAACTTT CTGGAACCCA CCCACCACCT CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
ATGTGACAGA GGGGAAGGAG GTTCTTCTAC TCGCCACAA CCGGCCAG AATCGTATTG 240
GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
TAGGAATCA ACAAGCTACC CCAGGGCCCG CATACAGTGG TOGAGAGACA ATATACCCCA 360
ATGCATCCCT GCTGATCCAG AAGGTACCC AGAATGACAC AGGATCTAT ACCCTACAAG 420
TCATAAAGTC AGATCTGTG AATGAAGAAG CAACCGACA GTTCCATGTA TACCCGAGC 480
TGCCCAAGCC CTCATCTCC AGCAACAAC CCAACCCCT GGAGGACAAG GATGCTGTG 540

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CCTTCACCTG TGAACCTGAG GTTCAGAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
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 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720
 ACCGCACTGA CCGAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780
 CCTCAAGAGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840
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 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020
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 TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCTT 1140
 GAATTCCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGCTCTG 1200
 CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA 1260
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 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860
 CTGACTCATT CTTTATTCTA TTTAGTTGG TTTGTATCTT GCTCAAGGTG CGTAGTCCAA 1920
 CTCTTGGTAT TACCCTCTTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
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 GGCTGGAATT ACAAAACCTA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
 ATAAAGCCCC CAATGTGTG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATCTC CAACTGAAAT 2220
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 TGTTCCTGT TCCCAATTG ACAAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
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 TAGCTCTATA ACT

Seq ID NO: 436 Protein sequence
 Protein Accession #: AA59907.1

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1 11 21 31 41 51
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 NRIGYSWYKQ ERVDNGSLIV GYVIGTQQAT PGPAYSGRET IYPNASLLIQ NVTONDTGTFY 120
 TLQVIKSDLV NEEATGQPHV YPELKPSPIS SNNSNFVEDK DAVAFTEPE VQNTYLVWV 180
 NGQSLPVSFR LQLSNGNMTL TLLSVKRNDG GSYECEIQNP ASANRSDPVT LNVLYGPDVP 240
 TISPSKANYR PGENLNLSCB AASNPPAQYS WFINGTFQOS TOELFIPNIT VNNSGSYMCO 300
 AHSNATGLNR TTVTMITVSG SAFPVLSAVAT VGITIGVLAR VALI

Seq ID NO: 437 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 1355..1657

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 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAACCTA ACAGACTACC CCAGGGCCCC CATACAGTGG TCGAGAGACA ATATACCCCA 360
 ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480
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 CCTCAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840
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 GAATTCCTCT AGCTCCTCCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGCTCTG 1200
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5 CTGACTCATT CTTTATTCTA TTTTAGITGG TTTGTATCTT GCCTAAGGTG GGTAGTCCAA 1920
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10 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTTAACCAA TGTATTTATT TCTGTGGTTC 2400
TGTTTCCTTG TTCCAATTGG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
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TAGCTCTATA ACT

15 Seq ID NO: 438 Protein sequence
Protein Accession #: AAA59908.1

1 11 21 31 41 51
MDSFSQDVKT RLLIMIRLLP PFNLSLLMPA SFAMQDDAVI SISQEVASEG NLTECQIYLV 60
NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELD

25 Seq ID NO: 439 DNA sequence
Nucleic Acid Accession #: M18728.1
Coding sequence: 2370..2501

1 11 21 31 41 51
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30 CCTCAGCCCC TCCTCTGAGA TTGCATGTCC CTTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120
TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
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TAGGAATCTA ACAAGCTACC CCAGGGCCCC CATACAGTGG TCGAGAGACA ATATACCCCA 360
ATGATCTCCT GCTGATCCAG AACGTACCC AGAATGACAC AGGATTCTAT ACCCTACAAG 420
35 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480
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CCTTCACCTG TGAACCTGAG GTTCAGAAAC CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
GCCTCCCGGT CAGTCCCGAG CTGCAGCTGT CCAATGGCAA CATGACCCCTC ACTCTACTCA 660
40 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAT ACAGAACCCA GCGAGTGCCA 720
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45 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020
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GAATCTCTCT AGCTCTCTCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
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50 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAAGTAGAGA CAGTCAAACT 1320
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60 CTGACTCAIT CTTTATTCTA TTTTAGITGG TTTGTATCTT GCCTAAGGTG GGTAGTCCAA 1920
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65 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220
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ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCTCT TACTTTAACT 2340
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TGTTTCCTTG TTCCAATTGG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
70 CTATCACTGT ACTTGTAGAG TGGTGTCTCT TTAATTCATA AATCACAAT AAAAGCCAAT 2520
TAGCTCTATA ACT

75 Seq ID NO: 440 Protein sequence
Protein Accession #: AAA59909.1

1 11 21 31 41 51
MLTNVPIVSV LFPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS

80 Seq ID NO: 441 DNA sequence
Nucleic Acid Accession #: NM_002381.2
Coding sequence: 64..1524

1 11 21 31 41 51

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5		CTGCTGCTGC	TGCCCTCCGC	CGCCCCCGAC	CCCGTGGCCC	GCCCCGGCTT	COGGAGGCTG	180
		GAGACCCGAG	GTCCCGGGGG	CAGCCCTGGA	CGCCGCCCT	CTCCTGCGGC	TCCCGACGGC	240
		GCGCCCGCTT	COGGGACGAG	CGAGCCTGGC	CGCGCCCGCG	GTGCAGGTGT	TTGCAAGAGC	300
		AGACCCCTGG	ACCTGCTGTT	TATCATTGAT	AGTTCTCGTA	GCGTACGGCC	CCTGGAATTC	360
		ACCAAAGTGA	AAACTTTTGT	CTCCCGGATA	ATCGACACTC	TGGACATTGG	GCCAGCCGAC	420
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		ACCATGTCAG	GCTGAGCCAT	CCAGACAGCA	ATGGACGAAG	CCTTCACAGT	GGAGGCGAGG	600
		GCTCGAGAGC	CCTCTCTTAA	CATCCCTAAG	GTGGCCATCA	TTGTTACAGA	TGGGAGGCC	660
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15		GTGGGGTGG	ACCGGGGAGA	CATGGCGTCC	CTCAAGATGA	TGGCCAGTGA	GCCCCAGAG	780
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		GAAACCTTCT	GTGGCTGGA	CCCTGTGTGT	CTTGGAAACAC	ACCAAGTGCCA	GCACTGTGCG	900
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		AATGAAGACA	GGAAAACTTG	TTCAGCTCAA	GATAAATGTG	CTTTGGGTAC	CCATGGGTGT	1140
		CAGCAATATT	GTGTGAATGA	CAGAACAGGG	TCCCATCATT	GTGAATGCTA	TGAGGGCTAC	1200
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		GGTTGCCAGC	ACATTGTGTG	GAGTGTAGGG	GCGCATCCT	ACCACGTGTA	TTGCTATCCT	1320
25		GGCTACACCT	TAAATGAGGA	CAAGAAAAACA	TGTTCAAGCCA	CTGAGGAAGC	ACGAAGACTT	1380
		GTTTCCACTG	AAGATGCTTG	TGGATGTGAA	GCTACACTGG	CATTCCAGGA	CAAGGTGAGC	1440
		TCGTATCTTC	AAAGACTGAA	CACTAAACTT	GATGACATTT	TGGAGAAGTT	GAAAAATAAT	1500
		GAATATGGAC	AAATACATCG	TTAAATGCT	CCAATTTCTC	ACCTGAAAAT	GTGGACAGCT	1560
		TGGTGTACTT	AATACTCATG	CATTCTTTTG	CACACCTGTT	ATTGCCAATG	TTCTGCTTAA	1620
30		TAATTGTGCA	TATCTGTAT	TAATGCTTGA	ATATTACTGG	ATAAATTTGA	TGAAGATCTT	1680
		CTGCAGAAAT	AGCATGATTT	TTCCAAGGAA	ATACATATGC	AGATACTTAT	TAAGAGCAAA	1740
		CTTTAGTGTC	TCTAAGTTAT	GACTGTGAAA	TGATTGGTAG	GAAATAGAAT	GAAAAGTTTA	1800
		GTGTTTCTTT	ATCTACTAAT	TGAGCCATTT	AATTTTAAAT	TGTTTATATT	AGATAACCAT	1860
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35		TTATTACTGA	GAGTGCAAAT	TGTACAAGGT	ATTTACACAT	ACAACCTCAT	ATAACTGAGA	1980
		TGAATGTAAT	TTTGAACGT	TTAACACTTT	TTGTTTTTTG	CTTATTTTGT	TGGAGTATTA	2040
		TTGAAGATGT	GATCAATAGA	TTGTAATACA	CATATCTAAA	AATAGTTAAT	ACAGATCAAG	2100
		TGAACATTTAC	ATTGCCATTT	TTAATTCATT	CTGGCTTTTG	AAAGAAATGT	ACTACTAAAG	2160
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40		CTTTATTATT	TGCTTCAGG	ATCCAAGTGA	CAAAGTTATA	TATTTATAAA	ATTGCTATAA	2280
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		AGTGCTGGGA	TTACAGGCTT	GAAAGTCTAA	CTTTTTTTTA	CTTATATATT	TGATACATAT	2400
		AAATCTTTTG	GCTTTGAAAC	TTGCAACTTT	GAGAACAAAA	CAGTCCCTTA	AATTTTGCAC	2460
		TGCTCAATTC	TGTTTTTCGT	TTGCATTGTC	TTAATATAA	TAAAGTTAT	TACCTTTACA	2520
45		TATTATCATG	TCTATTTTGG	ATGACTCATC	AATTTGTGCT	ATTAAAGATA	TTTCTTTAAA	2580
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Seq ID NO: 442 Protein sequence
Protein Accession #: NP_002372.1

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55		RVAVVNYAST	VRIEFQLQAY	TDKQSLKQAV	GRITPLSTGT	MSGLAIQTAM	DEAFTVRAGA	180
		REPSSNIPKV	AIIVTDGRPQ	DQVNEVAARA	QASGIELYAV	GVDRADMASL	KMMASEPLEE	240
		HVFYVETYG	IEKLSSRFQE	TFCALDPCVL	GTHQCQHVCI	SDGEGKHRC	CSQGYTLNAD	300
		KKTCALDR	ALNTHGCEHI	CVNDRSGSYH	CECYEGYTLN	EDRKTCQASD	KCALGTHGQ	360
		HICVNDRTGS	HHCBCYBGYT	LNADKKTCVS	RDKCALGSHG	CQHICVSDGA	ASYHCDYCPG	420
60		YTLNEDKKT	SATEARRLV	STEDACGCEA	TLAPQDKVSS	YLQRLNLTLD	DTLEKLKINE	480
		YQYHR						

Seq ID NO: 443 DNA sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

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70		GAGCAAGCGC	CAGGACCGCG	CCCCTGCTCC	CGCGGCAGCT	CCTGGAGCGC	GGACCTGGAC	180
		AAGTGCATGG	ACTGCGGCTC	TTGCAGGGCG	CGACCGCACA	GCGACTCTGT	CCTGGGCTGC	240
		GCTGCAGCAC	CTCCTGCCCC	CTTCCGGCTG	CTTTGGGCCA	TCCTTGGGGG	CGCTCTGAGC	300
		CTGACCTTGG	TGCTGGGGCT	GCTTTCTGGC	TTTTTGTGCT	GGAGACGATG	CGCAGGAGGA	360
		GAGAAGTTCA	CCACCCCAT	AGAGGAGACC	GGCGGAGAGG	GCTGCCACGC	TGTGGCGCTG	420
75		ATCCAGTGTG	AATGTGCCCC	CTGCCAGCGG	GGGCTCGCCC	ACTCATCATT	CATTCTATCA	480
		TTCTAGAGCC	AGTCTCTGCC	TCCAGACGCG	GGGGGAGGCC	AAGCTCTCTC	AACCACAGAG	540
		GGGGTGGGGG	GCGGTGAATC	ACCTCTGAGG	CCTGGGCCCA	GGGTTCAGGG	GAACCTTCCA	600
		AGGTGCTTGG	TGCTGGGCTG	TCTGGCTCCA	GAACAGAAAG	GGAGCCTCAC	GCTGGCTCAC	660
80		ACAAACACAG	TGACACTGAC	TAAGGAACTG	CAGCAATTGC	ACAGGGGAGG	GGGGTGCCTT	720
		CCTTCCCTTAC	AATCTGGGGG	CCAGGCTGAC	TTGGGGGGCA	GACTTGACAC	TAGGCCCCAC	780
		TCACCTCAGAT	GTCCTGAAAT	TCCACCAAGG	GGGTCAACCT	GGGGGGTTAG	GGACCTATTT	840
		TTAACACTAG	GGGCTGGCCC	ACTAGGAGGG	CTGGCCCTAA	GATACAGACC	CCCCCAACTC	900
		CCCAAGCGG	GGAGGAGATA	TTTATTTTGG	GGAGAGTTTG	GAGGGGAGGG	AGAATTTATT	960

AATAAAAGAA TCCTTAACTT TAAAAAATA AAAAAA

Seq ID NO: 444 Protein sequence
 Protein Accession #: NP_057723.1

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1 11 21 31 41 51
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 SDFCLGCAAA PPAFRLWLP ILGGALSLTP VLGLLSGFLV WRRRCRRREKF TPIIETGGE 120
 GCPAVALIQ

Seq ID NO: 445 DNA sequence
 Nucleic Acid Accession #: AF322916.1
 Coding sequence: 50..4300

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10 Seq ID NO: 446 Protein sequence
 Protein Accession #: AAG49577.1

1 11 21 31 41 51
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 TICQLLIDRG APVNSRDQKN RTALMLGCEY GCRDAVEVLI KNGADISLLD ALGHDSYYA 240
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 20 ESLRTIEALK NRPKYFESDH LGSGSHFSNR KEDMLLKQGG MYMADSQCTS PGIPAHMQSR 420
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 CERVKEDSDE QIKQLEDALK DVQKRMYSSE GKVKQMTHF LALKEHLTSE AASGNHRLTE 540
 ELKDQLKDLK VKYEGASAEV GKLRNQIKQN EMIVEEFKRD EGKLIENKR LQKELSMCEM 600
 25 EREKGRKVT EMEGQAKELS AKLALSIPAE KPENMKSSLS NEVNEKAKKL VEMEREHEKS 660
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 KVLNDNLKLL EQAHNLTIEI KHYVPLKVS EDMKSHDAI IDDLNRKLLD VTQRYTEKKL 780
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 30 IHALTSENIN LKQMSNQYV PVKTHEEVRM TINDTLAKTN RELLDVKKKF EDINQEPVKI 900
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 35 CYEKEQQTVT KLHQLLENQK NSSVPLAEHL QIKEAPEKEV GIIKASLREK EESQNKMEK 1200
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40 Seq ID NO: 447 DNA sequence
 Nucleic Acid Accession #: NM_003020.1
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Seq ID NO: 448 Protein sequence
 Protein Accession #: NP_003011.1

70 1 11 21 31 41 51
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80 Seq ID NO: 449 DNA sequence
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 Coding sequence: 79..2538

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5 CAACAGACCT CACATCTTTC TTCTTATGAA ATTATAACTC CTTGGAGATT AACTAGAGAA 240
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 TTATTTTGA AATACAAAAT ATACTAAAAG AGTGTGTGTG TATTCACGCA GTTACTCGCT 3180
 TCCATTTTTA TGACCTTTCA ACTATAGGTA ATAACTCTTA GAGAAATTAA TTTAATATTA 3240
 GAAATTTCTAT TATGAATCAT GTGAAAGCAT GACATTGTT CACAATAGCA CTATTTTAAA 3300
 55 TAAATTATAA GCTTTAAGGT ACGAAGTATT TAATAGATCT AATCAAATAT GTTGATTCT 3360
 GGCTATAATA AAGCAGGAGC AATTATAAAA TCTTCAATCA ATTGAACCTT TACAAAACCA 3420
 CTTGAGAATT TCATGAGCAC TTTAAAATCT GAACTTTCAA AGCTTGCTAT TAAATCATTT 3480
 AGAATGTTTA CTTTACTTAA GGTGTGCTGG GTCATGTAAA ATATTAGACA CTAATATTTT 3540
 60 CATAGAAATT AGGCTGGAGA AAGAAGGAAG AAATGGTTTT CTTAAATACC TACAAAAAAG 3600
 TTACTGTGGT ATCTATGAGT TATCATCTTA GCTGTGTTAA AAATGAATTT TACTATGGC 3660
 AGATATGGTA TGGATCGTAA AATTTTAAGC ACTAAAAAT TTTTCATAAC CTTTCATAAT 3720
 AAAGTTTAAAT AATAGGTTTA TTAAGTGAAT TTCAATAGTT TTTTAAAGT GTTTTGTGTT 3780
 TGTGTATATA TACATATACA AATACACAT TTACAATAAA TAAATACTT GAAATTTCTA 3840
 AAAAAA AAAA AAAA

Seq ID NO: 450 Protein sequence
 Protein Accession #: NP_003807.1

65
 70 1 11 21 31 41 51
 | | | | |
 MGS GARFPPSG TLRVRWLLLL GLVGPVLGAA RPFQQTSHL SSYEIITPWR LTRRERREAPR 60
 PYSKQVSYVI QABGKEHIIH LERNKDLLPE DFVVYTYNKE GTLITDHFNI QNHCHYRGYV 120
 EGVNSSLIAL SDCEPGLRLL HLENASYGIE PLQNSSHFEH IYRMDVYK EPLKCGVSNK 180
 DIEKETAKOE EEEPPMTQL LRRRAVLPO TRYVELFIVV DKERYDMNGR NQTAVREEMI 240
 LLANYLDSMY IMLNIRILV GLIEWTNGNL INIVGGAGDV LGNFVQWREK FLITRRRHDS 300
 75 AQLVLKKGFG GTAGMAFVGT VCSRSHAGGI NVFGQITVET PASIVAHELG HNLGNHDDG 360
 RDCSCGAKSC IMNSGASGR NFSSCSAEDF EKLTLNKGKN CLLNIPKPE AYSAPOGKN 420
 LDVAGEECDG GTFKCEBLDP CCBGSTCKLK SFAECAYGDC CKDCRFLPGG TLCKGKTSEC 480
 DVPEYCNSS QFQPFDFVIQ NGYPOQNKKA YCYNGMCQYY DAQCQVIFGS KAKAARKDCF 540
 IEVNSKGRDF GNCGFSNGEY KKCATGNALC GKLQCNVQE IPVFGIVPAI IQTPSRGKTC 600
 80 WGVDFQLGSD VPDGMVNEG TKCGAGKICR NFQCDVASVL NYDCDVQKKC HGHGVCSNK 660
 NCHCENGWAP PNCECTGYGG SVDSGPTYNE MNTALRDGLL VFPFLIVPLI VCAIFIFIKR 720
 DQLWRSYFRK KRSQTYESDG KNQANPSRQP GSVPRHVSFV TPPREVPIYA NRPVAPTAA 780
 KQPQPPSRP PPPQPKVSSQ GMLIPARPAP APPLYSSLT

Seq ID NO: 451 DNA sequence
Nucleic Acid Accession #: NM_016650.1
Coding sequence: 196..789

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      GGTTCACATA TATGCAGATG TCTCGATATA GGAATGAAAT TACGTCTTTG GAACCACTTA 60
      AATAAGTCAA ATATACTTGG AGCTTTAAAA ATTAAGAGGA GAGAGATTCTG AGCACCTTTT 120
      CTGCTGCCAT GACAACCATG CAAGGAATGG AACAGGCCAT GCCAGGGTTG GCCTGGTGTG 180
10     CCCCAGCTGG GAAACATGGC TGTCATACAT TCACATCTGT GGAAAGGATT GCAAGAGAAG 240
      TTCTGGAAGG GAGAACCCAA AGTCTTGGG GTTGTGCAGA TTCTGACTGC CCTGATGAGC 300
      CTTAGCATGG GAATAACAAT GATGTGTATG GCATCTAATA CTTATGGAAG TAACCCCTATT 360
      TCGGTGCATA TCGGTACAC AATTGGGGG TCAGTAATGT TTATTATTTC AGGATCCCTG 420
      TCAATTGCAG CAGGAATTAG AACTACAAA GGCCTGGTCC GAGGTAGTCT AGGAATGAAT 480
15     ATCACCAGCT CTGACTGGC TGCATCAGGG ATCTTAATCA ACACATTAG CTTGGCGTTT 540
      TATTCACTCC ATCACCCTTA CTGTAACATC TATGGCAACT CAAATRAATG TCATGGGACT 600
      ATGTCCATCT TAATGGGTCT GGATGGCATG GTGCTCCTCT TAAGTGTGCT GGAATTCCTG 660
      ATGTCTGTGT CCTCTCTGCT CTTTGGATGT AAGTGTCTCT GTTGTACCCC TGGTGGGGTT 720
      GTGTAAATCT TGCCATCACA TTCTCAGATG GCAGAACAG CATCTCCAC ACCACTTAAT 780
20     GAGGTTTGAG GCCAACAAA GATCAACAGA CAAATGCTCC AGAAATCTAT GCTGACTGTG 840
      ACACAAGAGC CTCACATGAG AAATTACCAG TATCCAACTT CGATACTAGT AGACGTGTG 900
      ATATTATTAT TATATGTAAAT CCAATTATGA ACTGTGTGTG TATAGAGAGA TAATAAATTC 960
      AAAAATATGT TCTCATTTT TTCCCTGGAA CTCAATAACT CACTTCACTG GCTCTTTATC 1020
25     GAGAGTACTA GGAGTTAAAT TAATAAATA TGCAATTAAT GAGGCCACAG GAAAAA

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Seq ID NO: 452 Protein sequence
Protein Accession #: NP_057734.1

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30     1      11      21      31      41      51
      |      |      |      |      |      |
      MAVIHSMLWK GLQEKFLKGE PKVLGVVQIL TALMSLSMGI TMMCMASNTY GSNPISVHIG 60
      YTIWGSVMFI ISGSLSIAAG IRTTKGLVRG SLGMNITSSV LAASGILINT FSLAFYSFHH 120
      PYCNYYGNSN NCHGTMSILM GLDGMVLLLS VLEFCIAVSL SAFGCKVLCC TPGGVVLILP 180
35     SLSHMAETAS PTLPLENV

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Seq ID NO: 453 DNA sequence
Nucleic Acid Accession #: NM_002091.1
Coding sequence: 56..503

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40     1      11      21      31      41      51
      |      |      |      |      |      |
      AGTCTCTGCT CTTCCAGGCC TCTCCGGCGC GCTCCAAGGG CTTCOCCTCG GACCATGCG 60
      CGGCAGTGAG CTCCCGCTGG TCCTGCTGCG GCTGGTCTCT TGCCTAGCGC CCCGGGGGCG 120
      AGCGGTCCCG CTGCTGCGGG GCGGAGGGAC CGTGTGACCC AAGATGTACC CGCGCGGCAA 180
      CCACTGGGCG GTGGGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTTCTGTTTC 240
      TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
      GAATTGTGCT GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCACCCCAA 360
      GGCCTTGGGC AATCAGCAGC CTTGCTGGGA TTCAGAGGAT AGCAGCAACT TCAAGATGT 420
      AGGTTCAAAA GGCAGAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
      CCCCAGCTG AACCAAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC 540
      TAAGAGACTG AGTTCTGCAA GCATCAGTTC TAOGATCATC CAACAGATT TCCTTGTGCA 600
      AAATAITGGA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTGATTTT CAAGCAGCAT 660
      CTTCTGGTTT AAACCTGTGT GCTGTGAACA ATTGTGAAA AGAGTCTTCC AATTAATGCT 720
      TTTTATATC TAGGCTACCT GTTGGTTAGA TTCAGGCCCC CGAGCTGTTA CCATTCACAA 780
55     TAAAAGCTTA AACACAT

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Seq ID NO: 454 Protein sequence
Protein Accession #: NP_002082.1

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60     1      11      21      31      41      51
      |      |      |      |      |      |
      MRGSELPLVL LALVLCIAPR GRAVPLPAGG GTVLTMYPR GNHWAVGHLM GKSTGESS 60
      VSRGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPQ PKALGNQPPS WDSSEDSNFK 120
65     DVGSKGKVR LSAFGSQRER RNPQLNQ

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Seq ID NO: 455 DNA sequence
Nucleic Acid Accession #: NM_016522.1
Coding sequence: 265..1299

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70     1      11      21      31      41      51
      |      |      |      |      |      |
      GCGAAGCAG CAGGAGGGA GCCCCTTTG GCGTCTCTCC GTGGAACCGG TTTTCGAGG 60
      CTGGCAAAAG CCGAGGCTGG ATTTGGGGGA GGAATATTAG ACTCGAGGA GTCTGCGCGC 120
      TTTTCTCTCT CCGCGGCTCT CCGGTGCGCG GGGTTCACC GCTCAGTCCC CGCGCTCGCT 180
      CCGCACCCA CCACTTCTCT GTGCTGCGCC GGGGGCGTG TGCCGTGCGG CTGCCGAGT 240
      TCGGGGAAGT TGTGGCTGTC GAGAAATGGG GTCTGTGGGT ACCTGTTCTT GCCCTGGAAG 300
      TGCTCTGTGG TCGTGTCTCT CAGGCTGCTG TTCTTGTATC CCACAGGAGT GCCCGTGGGC 360
      AGCGGAGATG CCACTTCCC CAAAGCTATG GACAACTGTA CGGTCCGCA GGGGGAGAGC 420
      GCCACCTCA GGTGACTAT TGACAACCGG GTCAACCGGG TGGCTCGCT AAAACGACGC 480
      ACCATCTCT ATGCTGGGAA TGACAAGTGG TGCTGGATC CTCGCTGGT CTTTCTGAGC 540
      AACACCCAAA GCGAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
      TACACCTGCT CGGTGAGAC AGACAACAC CCAAGACCT CTAGGGTCCA CCTCATTTG 660
      CAAGTATCT CCAAAATTGT AGAGATTCT TCAGATATCT CCATTAAATG AGGGAACAA 720
      ATTAGCCTCA CCTGCATAGC AACTGGTAGA CCAGAGCCTA CGTTACTTTG GAGACACATC 780

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TCTCCCAAAG CGTTGGCTT TGTGAGTGAA GACGAATACT TGGAAATTCA GGGCATCACC 840
CGGGAACAGT CAGGGGACTA CGAGTGCAGT GCCTCCAATG ACGTGGCCGC GCCCGTGGTA 900
CGGAGAGTAA AGGTCAACGT GAACTATCCA CCATACATTT CAGAAGCCAA GGGTACAGGT 960
GTCCCGGTGG GACAAAAGGG GAACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020
TTCCAGTGGT ACAAGGATGA CAAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080
AACAGACCTT TCCTCTCAAA ACTCATCTTC TTCAATGTCT CTGAACATGA CTATGGGAAC 1140
TACACTTGGG TGGCCTCCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTTGGT 1200
CCAGGCGCCG TCAGCGAGGT GAGCAACGGC ACGTCGAGGA GGGCAGGCTG CGTCTGGCTG 1260
CTGCTCTTTC TGGTCTTGCA CCTGCTTCTC AAATTTTGAT GTGAGTGCCA CTCCCCACC 1320
CGGAAAGGCG TGCCGCCACC ACCACCACCA ACACAACAGC AATGGCAACA CCGACAGCAA 1380
CCAACTCAGT ATATACAAT GAAATTAGAA GAAACACAGC CTCATGGGAC AGAAATTTGA 1440
GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTTT AAAAAAGAAA TTGAAATTTG 1500
CCTTGAGATC ATTTAGGTAC AATGGAGTTT TCTTTTCCCA AACGGGAAGA ACACAGCACA 1560
CCCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG 1620
GGCTCAGCCT CTCTGCCCCA AGACTGCCCC CACGTGGAAC ATTCTGGAGC TGGCCATCCC 1680
AAATTCATC AGTCCATAGA GACGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT 1740
CGGGCCCAAG CGTGGCGCTG CGGGCACTTT GGTAGACTGT GCCACCAAGG CGTGTGTTGT 1800
GAAACGTGAA ATAAAAAGAG CAAAAAAGAG AAAAAAAGAG

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Seq ID NO: 456 Protein sequence
Protein Accession #: NP_057606.1

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1 11 21 31 41 51
| | | | |
MGVGYLFLP WKLVVLSLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60
NRVTRVAMLN RSTILYAGND KWCLDPRVVL LSNQTQYYSI BIGNVDVYDE GPYTCSVQTD 120
NHPKTSRVHL IVQVSPKIVE ISSDISINEG NNISLTCIAT GRPEPTVTWR HISP KAVGFV 180
SEDEYLEIQG ITRQSGDYB CSASNDVAAP VVRVVKVTVN YPPYISEAKG TGVFVGQKGT 240
LQCEASAVPS AEFQWYKDDK RLIEGKKGVK VERNRPFSLK IFFNVSEHDY GNYTCVASNK 300
LGHTNASIML FGPFAVSEVS NGTSRRAGCV WLLPLLVLHL LLKF

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Seq ID NO: 457 DNA sequence
Nucleic Acid Accession #: NM_012261.1
Coding sequence: 203..1045

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1 11 21 31 41 51
| | | | |
GATTGTCTCT GCCAGCAGCT GTGGGTGCGG CGCTCGACAC CGAGTCTAG CTAGGGGCTC 60
ACAGAATACG CGCTCCCTCC CTCCCCCTTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC 120
CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG 180
CCTCATTCGG GGCCTGCGA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG 240
ACTTCGAGTT CTCTGATGT TGTTCATAC AATGGCTCAA ATCATGGCAG AACAGAAGT 300
GGAAATCTCT TCAGGCCCTT CCACTAACCC TGAAAAAGAT ATATTGTGG TGGGGGAAA 360
TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG 420
GGCCAGCAAC TACGTAGATC TGATCACAGA ACAGGCGGAT ATGCAATTGA CCGGGGAGC 480
TGAGGTGAAG GGCCGCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTCTT GGGTGGATCG 540
CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAAGCCAC AACATGTCCA AGGGACCTGA 600
GGCGACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660
CAAAAGCGCA GTCACTGCTG GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCTTGGT 720
CACCCCGCGT GGAAGTCTT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCTCTAG 780
TGATCCGCGT AAGAGCGTCA CCTGATCCT GTCTGCGGTC CACATCCAC CTTTGTGACAT 840
TATCTCAGAT TTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900
GGAAAGAAC TTGCCCCGTA TTTTGGGGCT CATCTTGGGC CTGTCATCA TGGTAACACT 960
CGCGATTTC CAGTCCACC ACAAAATGAC TGCCAACAG GTGCAGATCC CTCGGGACAG 1020
ATCCCAATAT AAGCATATGG GCTAGAGGCC GTTAGGCAGG CACCCCTTAT TCCTGCTCCC 1080
CCAACCTGAT CAGGTAGAAC AACAAAAGCA CTTTTCATC TTGTACAGCA GATACACCAA 1140
CATAGCTACA ATCAAAACAG CCGTGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200
AACCCACGGA AGGGGGAGAG AGGGTCTCAG ACAGCTTTCG TGCTCATGTT GGCTTGGCTT 1320
ATGCTGGGGA GGAGGGGAGG AGGGTCTCAG ACAGCTTTCG TGCTCATGTT GGCTTGGCTT 1320
TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCCAA AGTTTAGGGA 1380
TTGAAAACAT GCTTCTTTGA GGAGGAAACC CCTTTAGGTT CAGAAGAATA TGGGGTGCCT 1440
TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAACC 1500
TCATGCTCCC TGCAGCAAGA CCGCTGAAAG TGATTCAATG TCTGGCTGG CATCTGTCAT 1560
GTTTAGTGAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG 1620
AAAAAGACTA ATGTAACATAT GCAGAGTTGT TTGGACTTCT TCCTGTGCCA GGTCCAAGTC 1680
GGGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AARTGAATA AAACACACTA 1740
TTCTCTGGC

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Seq ID NO: 458 Protein sequence
Protein Accession #: NP_036393.1

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80

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1 11 21 31 41 51
| | | | |
MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKIDIFVV RENGTTCLMA 60
EPAAKFIVPY DVNASNYVDL ITEQADIALT RGAEVKGRGC HSQSELQVFW VDRAYALKML 120
FVKESHNM SK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHELS ALVTPAGKSY 180
EQQAQQTISL ASSDPQKVTM MILSAVHIQF FDIISDFVFS BEHKCPVDER BQLEBTLPLI 240
LGLILGLVIM VTLAIYHVH KMTANQVQIP RDRSQYKHM

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Seq ID NO: 459 DNA sequence
Nucleic Acid Accession #: NM_001169.1
Coding sequence: 85..870

1 11 21 31 41 51

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TAGGAGATAA	GAGTATCTTG	CACAGCAGGT	GCAGGTTTCC	CAGCAGCTCA	GGCAAGAGTC	60
CGATGTTTGT	GCCTATCTGAT	CCTGATGTCT	GGAGAGATAG	CCATGTGTGA	GCCTGAATTT	120
GGCAATGACA	AGGCCAGGGA	GCCGAGCGTG	GGTGGCAGGT	GGCGAGTGTG	CTGGTACGAA	180
CGGTTTGTGC	AGCCATGTCT	GGTGGAACTG	CTGGGCTCTG	CTCTCTTCAT	CTTCATCGGG	240
TGCCTGTGCG	TCATTGAGAA	TGGGACGGAC	ACTGGGCTGC	TGCAGCCGGC	CCTGGCCAC	300
GGGCTGGCTT	TGGGGCTCGT	GATTGCCACG	CTGGGGAAAT	TCAGTGGTGG	ACACTTCAAC	360
CCTGCGGTGT	CCCTGGCAGC	CATGCTGATC	GGAGGCCCTCA	ACCTGGTGAT	GCTCCTCCCG	420
TACTGGGTCT	CACAGCTGCT	CGGGGGGATG	CTCGGGGCTG	CCTTGGCCAA	GGTGGTGAGT	480
CCTGAGGAGA	GGTTCCTGAA	TGCATCTGGG	GCGGCTTTG	TGACAGTCCA	GGAGCAGGGG	540
CAGGTGGCAG	GGGCGTTGGT	GGCAGAGATC	ATCCTGACGA	CGCTGTGGC	CCTGGCTGTA	600
TGCATGGGTG	CCATCAATGA	GAAGACAAAG	GGCCCTCTGG	CCCGTTCTC	CATCGGCTTT	660
GCCTGCACCG	TGGATATCCT	GGCTGGGGGC	CCTGTGTCTG	GAGGCTGCAT	GAATCCCGCC	720
CGTGCCTTTG	GACCTGCGGT	GGTGGCCAAC	CACTGGAACT	TCCACTGGAT	CTACTGGCTG	780
GGCCCACTTC	TGGCTGGCCT	GCTTGTGGA	CTGCTCATTA	GGTGCTTCAT	TGGAGATGGG	840
AAGACCCGCC	TCATCTGAA	GGCTCGGTGA	GCAGAGCTCG	TGGGATTCCCT	GCTGCTCCAG	900
GTGTCTCTAG	CTCAGCTGTC	CCAGACTGAG	GACAGGGGAG	TTCCTGCATT	TCTGCCCAGG	960
GCAGAGGCC	AGAGGAGCGA	CCCCCTGCTT	CCACTGCTTG	GGCCTGCTTT	CTCAGATAGA	1020
CTGACTGCTG	AGGAGGCTCT	AGGTTCTTGG	AATTCCTTTG	TGCTCATCAG	AGACCCAGC	1080
CTGGGGAACA	CGCTGCCCGC	ACTGCCCAGA	GAGCAGTGCA	AACACCAAA	CACGAGCGTG	1140
TTTCTTGAGA	GGAATGTCCC	CGAGTTGGAC	AAGGAGGCTG	TTTCTGCACA	TCAGCTCATT	1200
TCCCGCACCC	CATTCTTGCG	TTGATTGCTT	TGTTGGGGGC	CTGGCCACTT	CCTTGTCTCT	1260
CAAGCTGACA	ATTCTCACTT	TGCAATAAAT	AGTCCAGTGT	TTCTTTCAT		

Seq ID NO: 460 Protein sequence
Protein Accession #: NP_001160.1

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MSGEIAMCEP	EFGNDKAREP	SVGGRWRVSW	YERFVQPCLV	ELLGSALFIF	IGCLSVIENG	60
TDITGLIQPAL	AHGLALGLVI	ATLGNISGGH	FNPVSLAAM	LIGGLNLVLM	LPYVWSQLLG	120
GMLGAALAKV	VSPERFWNA	SGAAPVTQVE	QGQVAGALVA	EIILTLLAL	AVCMGAINEK	180
TKGPLAPPSI	GFAVTVDILA	GGFVSGGCMN	PARAFGPVAV	ANHNWFHWIY	WLGPLLALGL	240
VGLLIRCFIG	DGKTRLILKA	R				

Seq ID NO: 461 DNA sequence
Nucleic Acid Accession #: NM_003226.1
Coding sequence: 2..226

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45
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GATGCTGGGG	CTGGTCTGCG	CCTTGTCTGC	CTCCAGCTCT	GCTGAGGAGT	ACGTGGGCCT	60
GCTGTCAAAC	CAGTGTGCGG	TGCCGGCCAA	GGACAGGGTG	GACTGCGGCT	ACCCCCATGT	120
CACCCCCAAG	GAGTGCAACA	ACCGGGGCTG	CTGCTTTGAC	TCCAGGATCC	CTGGAGTGCC	180
TTGGTGTTC	AAGCCCCCTGA	CTAGGAAGAC	AGAATGCACC	TTCTGAGGCA	CCTCCAGCTG	240
CCCCTGGGAT	GCAGGCTGAG	CACCTTGCC	CGGCTGTGAT	TGCTGCCAGG	CACGTGTCAT	300
CTCAGTTTTT	CTGTCCCTTT	GCTCCCGGCA	AGCTTTCTGC	TGAAAGTTCA	TATCTGGAGC	360
CTGATGTCTT	AACGAATAAA	GGTCCCATGC	TCCACCCG			

Seq ID NO: 462 Protein sequence
Protein Accession #: NP_003217.1

55
60

MLGLVLALLS	SSSABEYVGL	SANQCAVPK	DRVDCGYPHV	TPKECNNRGC	CFDSRIPGVP	60
WCFKPLTRKT	ECTF					

Seq ID NO: 463 DNA sequence
Nucleic Acid Accession #: NM_002993.1
Coding sequence: 64..408

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GGCAGAGACC	AGTCTCCGGG	CCTCCACCCA	GCTCAGGAAC	COGGAACCC	TCTCTTGACC	60
ACTATGAGCC	TCCCGTCCAG	COGCGCGGCC	CGTGTCCCGG	GTCCTTCGGG	CTCCTTGTGC	120
GGCTGCTGCG	CGCTGCTGCT	CCTGCTGACG	COGCGGGGCG	CCCTGCGCAG	CGCTGGTCTT	180
GTCTCTGCTG	TGCTGACAGA	GCTGCGTTGC	ACTTGTTTAC	CGGTACGCT	GAGAGTAAAC	240
CCCAAAACGA	TTGGTAAACT	GCAGGTGTTC	COGCGAGGCC	CGCAGTGCTC	CAAGGTGGAA	300
GTGTAGAGCT	CCCTGAAGAA	CGGGAAGCAA	GTTTGTCTGG	ACCGGAAGC	CCCTTTTCTA	360
AAGAAAGTCA	TCCAGAAAT	TTTGGACAGT	GGAAACAAGA	AAACTGAGT	AACAAAAAAG	420
ACCATGCATC	ATAAAATTGC	CCAGTCTTCA	GCGGAGCAGT	TTTCTGGAGA	TCCCTGGACC	480
CAGTAAGAA	AGAAGGGAAG	GTTTGGTTTT	TTTCCATTTT	CTACATGGAT	TCCCTACTTT	540
GAAGAGTGTG	GGGGAAGCC	TAOGCTTCTC	CCTGAAGTTT	ACAGCTCAGC	TAATGAAGTA	600
CTAATATAGT	ATTTCACATA	TTTACTGTTA	TTTACCTGTA	TAAGTTATTG	AACCCCTTGG	660
CAATTGACCA	TATTGTGAGC	AAAGAATCAC	TGGTTATTAG	TCTTTCATAG	AATATTGAAT	720
TGAAGATAAC	TATTGTATTT	CTATCATACA	TTCTTAAAG	TCTTACCGAA	AAGGCTGTGG	780
ATTTCGTATG	GAATAAATGT	TTTATTAGTG	TGCTGTTGAG	GGAGGTATCC	TGTTGTTCTT	840
ACTCACTCTT	CTCATAAAT	AGGAAATATT	TTAGTTCTGT	TTTCTTGGGG	AATATGTTAC	900
TCCTTACCTT	AGGATGCTAT	TTAAGTTGTA	CTGTATTAGA	ACACTGGGTG	TGTCATACCG	960
TTATCTGTGC	AGAATATATP	TCCTTATTCA	GAATTTCTAA	AAATTTAAGT	TCTGTAAGGG	1020
CTAATATATT	CTCTTCTAT	GGTTTATGAT	GTTTGAITGC	TTCTTAGTAT	GGCATAATGT	1080
CATGATTTAC	TCATTAAACT	TTGATTTTGT	ATGCTATTTT	TTCACTATAG	GATGACTATA	1140

5
 ATTCTGGTCA CTAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC 1200
 TGATTGCTAA TTACATAGA AATGTATTCT CTITGGTTTT TAAATAAAG CAAAATTAC 1260
 AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTGAA CAATTGAAAT ATAAATTCAT 1320
 CATTATGTC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
 TTTAAAGGTT TTGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
 AAATGCACT TTTATTTTTT CTTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCAAT 1500
 TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAA AAAA

10
 Seq ID NO: 464 Protein sequence
 Protein Accession #: NP_002984.1

15
 1 11 21 31 41 51
 MSLPSSRAAR VPGPSGSLCA LLALLLLLTTP PGFLASAGFV SAVLTELRCT CLRVTLRVNP 60
 KTIQKLQVFP AGPQCSKVEV VASLRNGKQV CLDPBPAPFLK KVIQKILDSG NKKN

20
 Seq ID NO: 465 DNA sequence
 Nucleic Acid Accession #: NM_002038.2
 Coding sequence: 108..500

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 1 11 21 31 41 51
 GAACCGTTTA CTCGCTGCTG TGCCCATCTA TCAGCAGGCT CCGGCTGAA GATTGCTTCT 60
 CTTCTCTCCT CCAAGGTCTA GTGACGGAGC COGCGCGCGG CGCCACCATG CGGCAGAAGG 120
 CGGTATCGCT TTCTTGTGTC TACCTGCTGC TCTTCACCTG CAGTGGGGTG GAGGCAGGTA 180
 AGAAAAAGTG CTCGGAGAGC TCGGACAGCG GCTCOGGGTT CTGGAAGGCC CTGACCTTCA 240
 TGGCCGTGCG AGGAGGACTC GCAGTCGCGG GGCTGCCCGC GCTGGGCTTC ACCGGCGCGG 300
 GCATCGCGGC CAACTCGGTC GCTGCCTCGC TGTATGAGCTG GTCTGCGATC CTGAATGGGG 360
 CGCGCGTGCC CGCGCGGGGG CTAGTGGCCA CGCTGCAGAG CCTCGGGGCT GGTGGCAGCA 420
 GCGTGTGCTAT TATGTATATT GGTGCCCTGA TGGGCTACGC CACCCACAAG TATCTCGATA 480
 GTGAGGAGGA TGAGGAGTAG CCACGAGCTC CCAGAACCTC TTCTTCCTTC TTGGCCTAAC 540
 TCTTCAGATT AGGATCTAGA ACTTTGCCTT TTTTTTTTTT TTTTTTTTTT TTTGAGATGG 600
 GTTCTCACTA TATTGTCCAG GCTAGAGTGC AGTGGCTATT CACAGATGCG AACATAGTAC 660
 ACTGACGCTT CCAACTCCTA GCCTCAAGTG ATCCTCTCTG CTCACCTCC CAAGTAGGAT 720
 TACAAGCATG GCGGACGAT GCCCAGAAAT CAGAACTTTC TCTATCACTC TCCCAACAA 780
 CCTAGATGTG AAAACAGAAT AAATTCACCC CAGAAAA

40
 Seq ID NO: 466 Protein sequence
 Protein Accession #: NP_002029.3

45
 1 11 21 31 41 51
 MRQKAVSLFL CYLLLFCTSG VEAGKKKCSB SSDSGSGFWK ALTFMAVGGG LAVAGLPALG 60
 FTGAGLAANS VAASLMSWSA ILNGGGVPAG GLVATLQSLG AGGSSVVIGN IGALMGYATH 120
 KYLDSSEDEE

50
 Seq ID NO: 467 DNA sequence
 Nucleic Acid Accession #: NM_003469.2
 Coding sequence: 92..1945

55
 60
 65
 70
 75
 80
 1 11 21 31 41 51
 GAAACGGCCC GAGAAGCTCG CCGGAGAAC GGGGAGGAAT ATGCTGTGGA GCTCCTCTGC 60
 CATATAAACA AAAAGAGGAA ATCTTTCAAA CATGGCTGAA GCAAAAGACC ACTGGCTTGG 120
 AGCAGCCCTG TCTCTTATCC CTTTAAATTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT 180
 TCAGAGAAAC CAGCTGCTCT AGAAAGAAC AGACCTCAGG TTGAAAAATG TCCAAAAGTT 240
 TCCAGTCTCT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCCGAG AACCAAGCTCA 300
 TAAGGAAGAA AGCAGCCCGA ATTATAATCC CTACCAAGGT GTCTCTGTCC CCTTCAGCA 360
 AAAAGAAAT GGCATGAAA GCCACTTGCC CGAGAGGGAT TCACTGAGTG AAGAAGACTG 420
 GATGAGAATA ATACTCGAAG CTTTGAGACA GGCTGAAAT GAGCCTCAGT CTGCACCAAA 480
 AGAAAAAAG CCCTATGCCT TGAATTCAGA AAAGAACTTT CCAATGGACA TGAGTGATGA 540
 TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCTATGTA 600
 TGAAGAGAA TCCAGGGATA ACCCTTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA 660
 TACTCTCAA AGCCTTGCTA CATTGGAATC TGTCTTCCAA GAGCTGGGGA AACTGACAGG 720
 ACCAAACAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACCTTATA CGGATGATGA 780
 AGATGATATC TACAAGGCTA ATAACATTGC CTATGAAGAT GTGGTCGGGG GAGAAGACTG 840
 GAACCCAGTA GAGGAGAAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAGA 900
 GAATATAGGA AAAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGGCAT 960
 CCAGGAAGAA GATCTTCGGA AAGAGAGTAA AGACCAACTC TCAGATGATG TCTCCAAAGT 1020
 AATTGCCTAT TTGAAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA 1080
 AAATGGGAAA AGGGCCACCA GGCTTTTGA GAAACCTCTT GATTCTCAGT CTATTATCA 1140
 GCTGATTGAA ATCTCAAGGA ATTACAGAT ACCCCAGAA GACTTAATTG AGATGCTCAA 1200
 AACTGGGGAG AAGCGAATG GATCAGTGA ACCGGAGCGG GAGCTTGACC TTCTGTGTA 1260
 CTTAGATGAC ATCTCAGAGG CTGACTTGA CCATCCAGAC CTGTTCCAAA ATAGGATGCT 1320
 CTCCAAGAGT GGTACCCCTA AAACACCTGG TGTGTCTGGG ACTGAGGCC TACCAGACGG 1380
 GCTCAGTGTG GAGGATATTT TAAATCTTTT AGGGATGGAG AGTCAGCAA ATCAGAAAAC 1440
 GTCGTATTTT CCCAATCCAT ATAACCAGGA GAAAGTCTG CCAAGGCTCC CTTATGGTGC 1500
 TGGAAAGTCT AGATCGAACC AGCTTCCCAA AGCTGCCTGG ATTCACATG TTGAAAACAG 1560
 ACAGATGCAA TATGAAAACC TGAACGACAA GGATCAAGAA TTAGGTGAGT ACTTGGCCAG 1620
 GATGCTAGTT AAATACCCCTG AGATCATTAA TTCAAAACCA GTGAAGCGAG TTCTCGSTCA 1680
 AGGCTCATCT GAAGATGACC TGCAGGAAGA GGAACAAATT GAGCAGGCCA TCAAGAGCA 1740
 TTTGAATCAA GGCAGCTCTC AGGAGACTGA CAAGCTGGCC CCGGTGAGCA AAAGTTTCCC 1800
 TGTGGGGCCC CCGAAGAAATG ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT 1860
 AATGAAAGTG CTGGAATACC TCAATCAAGA AAAGGCAGAA AAGGGAAGGG AGCATATTGC 1920

5 TAAGAGAGCA ATGAAAAATA TGTAAGCTGC TTTCATTAAT TACCCTACTT TCATTCTCTC 1980
CACCCCAAGC AAATCCCAAC ATTTCTCTTC AGTGTGTGA CTTCATCTCT GTTAACACTG 2040
TAATATCTTT AAATGATGTA CAGGCAGATG AAACCAGGTC ACTGGGGAGT CTGCTTCATT 2100
TCCTCTGAGC TGTATCTCTG TGTATGGATA TGTGTAATG TTATGACTCC TTGATAAAAA 2160
ATTTATTATG TCCATTATTC AAGAAAGATA TCTATGACTG TGTTTAATAG TATATCTAAT 2220
GGCTGTGGCA TTGTTGATGC TCACATATGA TAAAAAGTG TCCTATAATT CTATTGAAAG 2280
TTTTTAATAT TTATTGAATT ATTTTGTAC TGTCTGTAGC GTTTTGTGGA GACTCTGGAC 2340
AAAAAATAA AGCATTATAA ATATA

10 Seq ID NO: 468 Protein sequence
Protein Accession #: NP_003460.1

15 1 11 21 31 41 51
MAEARKTHWG AALSLIPLIF LISGAEAAAF QRNQLQKEP DLRLNVQKF PSEPMIRALE 60
YIENLRQQAQ KEESPDPYNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRIILEALRQ 120
AENEPQSAKP ENKPYALNNE KNPPMDMSDD YETQQWPERK LKHMQFPMPY EENSRENPFK 180
RTNBIVEEQY TQSLATLES VFQELGKLTG PNNQKRERMD EQKLYTDE DDIYKANNIA 240
YEDVVGGEW NPVEEKIESQ TQEEVRSKE NIGKNEQIND EMKRSQGLGI QEEDLRKESK 300
20 DQLSDDVSK IAYLRLVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIEISRLQI 360
PPEDLIEMLK TGEKPNGSVE PERELDLFVD LDDISEADLD HPDLFQNRML SKSGYFKTPG 420
RAGTEALFDG LSVEDILNLL GMESAANQKT SYFPNPNQOE KVLPRLPYGA GRSRSNQLPK 480
AAWIPHYENR QMAYENLNDK DQELGEYLAR MLVKYFEIIN SNQVKRVPQG GSSEDDLQEE 540
25 EQIEQAIKEH LMQSSQEDT KLAPVSKRFP VGPPKNDTTP NRQYWDLL MKVLEYLNQE 600
KAEKGRSHIA KRAMENM

30 Seq ID NO: 469 DNA sequence
Nucleic Acid Accession #: NM_006398.1
Coding sequence: 19..516

35 1 11 21 31 41 51
GGCCCCCTGT CTGCAGAGAT GGCTCCCAAT GCTTCCTGCC TCTGTGTGCA TGTCCGTTCC 60
GAGGAATGGG ATTTAATGAC CTTTGTATGCC AACCCATATG ACAGCGTGAA AAAAATCAAA 120
GAACATGTCC GGTCTAAGAC CAAGGTTTCT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC 180
AAGATCTTAA AGCCACGGAG AAGCCTCTCA TCTTATGGCA TTGACAAAGA GAAGACCATC 240
CACCTTACCC TGAAGTGGT GAAGCCAGT GATGAGGAGC TGCCCTTGTG TCTGTGGAG 300
TCAGGTGATG AGGCAAGAG GCACCTCCTC CAGGTGOGAA GGTCCAGCTC AGTGGCACAA 360
GTGAAAGCAA TGATCGAGAC TAAGACGGGT ATAATCCCTG AGACCCAGAT TGTGACTTGC 420
40 AATGGAAGA GACTGGAAGA TGGGAAGATG ATGGCAGATT ACGGCATCAG AAAGGGCAAC 480
TTACTCTTCC TGGCATCTTA TTGTATTGGA GGGTGACCAC CCTGGGGATG GGGTGTGGC 540
AGGGGTCAAA AAGCTTATTT CTTTAACTCT CTACTCAAC GAACACATCT TCTGATGATT 600
TCCCAAAATT AATGAGAATG AGATGAGTAG AGTAAGATTG GGGTGGGATG GGTAGGATGA 660
45 AGTATATTGC CCAACTCTAT GTTCTTTGA TTCTAACACA ATTAATTAAG TGACATGATT 720
TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTAA GGCAAAATAG AGCATTC

Seq ID NO: 470 Protein sequence
Protein Accession #: NP_006389.1

50 1 11 21 31 41 51
MAPNASCLCV HVRSEWDLM TFDANFYDSV KRIKEHVRSK TKVPVQDQVL LLGSKILKPR 60
RSLSSYSDIK ERTIHLTLKV VKPSDEELPL FLVESGDRAK RHLLQVRRSS SVAQVKAMIE 120
55 TKTGIIPETQ IVTCNGKRL E DGMADYGI RKGNNLFLAS YCIGG

Seq ID NO: 471 DNA sequence
Nucleic Acid Accession #: XM_094741.1
Coding sequence: 1..948

60 1 11 21 31 41 51
ATGAAGGCCA ACTACAGCGC AGAGGAGCGC TTTCTCTGCT TGGGTTTCTC CQACTGGCCT 60
TCCCTGCAGC CGTCTCTCTT CGCCCTTGTC CTCTGTGCT ACCTCTCTGAC CTTGACGGGC 120
65 AACTCGGCGC TGTGTCTGCT GGCCTGCGC GACCCGCGCC TGACACGCC CATGTACTAC 180
TTCTCTGCTC ACCTGGCCTT GGTAGAGCGG GGCCTCACTA CTAGCGTGGT GCCCGCGCTG 240
CTGGCCAACC TGGCGGAGCC AGCGCTCTGG CTGCGCGCA GCCACTGCAC GGCCAGCTG 300
TGGCATCGC TGGCTCTGGG TTGGGCGGAA TGGCTCTCC TGGCGGTGAT GGCTCTGGAC 360
CGCGCGCGC CAGTGTGCGG CCGCTGCGC TATGCGGGGC TGTCTCTCCC GCGCTATGT 420
70 CGCACGCTGG CCAGCGCCTC CTGGCTAAGC GGCCTCACCA ACTCGGTTGC GCAACCGCG 480
CTCTGCGCTG AGCGCGCGCT GTGCGCGCCC CGCTCTGCTG ACCACTTCAT CTGTGAGCTG 540
CGCGCGTTC TCAAGCTGGC CTGCGGAGGC GACGGAGACA CTACCGAGAA CCAGATGTTT 600
GCGCGCGCG TGGTCACTCT GCTGCTGCGG TTGCGGTCA TCTGCGCTC CTACGCTGCC 660
75 GTGGCGCGG CTGTCTGTTG CATGCGGTTG AGCGGAGGCC GGAGGAGGCC GGTGGGACG 720
TGTGGGTCCC ACCTGACAGC CGTCTGCGCT TTCTACGGCT CGGCATCTA CACCTACCTG 780
CAGCGCGCG AGCGCTACAA CCAGGCACGG GGCAAGTTGG TATCGCTCTT CTACACCTG 840
GTCAACCTG CTCTCAACC GCTCATCTAC ACCCTCAGGA ATAAGAAATG GAAGGGGCA 900
GCGAGGAGC TGCTGCGGAG TCTGGGAGA GGCCAGGCTG GGCAGTGA

80 Seq ID NO: 472 Protein sequence
Protein Accession #: XP_094741.1

1 -11 21 31 41 51
MKANYSABER FLLGLPDSWP SLQPVLPALV LLCYLLTLTG NSALVLLAVR DPLRHTPMY 60

FLCHLALVDA GFTTSVVPPL LANLRGPALW LPRSHCTAQL CASIALGSAB CVLLAVMALD 120
 RAAAVCRPLR YAGLVSPRLC RFLASASWLS GLTNSVAQTA LLAERPLCAP RLLDHFICEL 180
 PALLKLACGG DGTDTTENQMF AARVVILLLE FAVILASYGA VARAVCCMRP SGGRRRAVGT 240
 CGSHLTAVCL FYGSAITYYL QPAQRYNQAR GKFVSLFYTV VTPALNPLIY TLRNKKVKGA 300
 ARRLRLSLGR GQAGQ

Seq ID NO: 473 DNA sequence
 Nucleic Acid Accession #: NM_001062.1
 Coding sequence: 76..1380

1 11 21 31 41 51
 | | | | |
 GCTCTCATT CCTTCTGCC ATCACTTAAT AAATAGCCAG CCAATTTCATC AACATTCTGG 60
 TACACTGTGG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTTACTGTGT 120
 TCTTTTATTC CAAGCCAACT ATGOGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC 180
 CTAAACCTC TGTTGAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTC 240
 AATGTTGTGT TGTCCCTCAA ACTTGTGGA ATCCAGATCC AAACCTGAT GCAAAAGATG 300
 ATCCAAACAA TCAATACAA TGTGAAAAGC AGATTGTGAG ATGTAAGCTC GGGAGAGCTT 360
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAACGCTG AGGAAAACCT AATATATGAT 420
 TACCACCTGA CTGACAAGCT AGAAAATAAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA 480
 CACAATGGCA CTCCCTGAC TAACACTAC CAGCTCAGCC TGGACGTTTT GGCCTTGTGT 540
 CTGTTCAATG GGAACACTAC AACCOCGAA GTTGTCAACC ACTTCACTCC TGAAAATAAA 600
 AACTATTATT TTGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CCTGGCTCTG 660
 ACCGTGTGA AGAAGAGTCT AATAAATGGG CAGATCAAAG CAGATGAAGG CAGTTTAAAG 720
 AACATCAGTA TTTATACAAA GTCACCTGTA GAAAAGATTC TGTCTGAGAA AAAAGAAAAT 780
 GGTCCTATTG GAAACACATT TAGCACAGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA 840
 GACTATTATA ATGAAAATGA CTGGAATTGC CAACAACTC TGAATACAGT GCTCAGCGAA 900
 ATTTCTCAAG GAGCAATCAG TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG 960
 GGAAAAGACT TCTTGATAT TAACAAAGAC TCTTCTTGG TCTCTGCTT AGGTAACCTC 1020
 AACATCTCG CTGATGAGCC TATAACTGTG ACACCTCCTG ACTCACAATC ATATATCTCC 1080
 GTCATTTACT CTGTGAGAA CAATGAAACA TATTTCAACA ATGTCACGTG GCTAAATGGT 1140
 TCTGTCTTCC TCAGTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACTAT ATTTGGTTTC 1200
 ACAATGGAGG AGCGCTCATG GGGGCCCTAT ATCACTGTA TTCAGGGCCT ATGTGCCAAC 1260
 AATAATGACA GAACCTACTG GGAACCTCTG AGTGGAGGCG AACCCTGAG CCAAGGAGCT 1320
 GGTAGTACG TGTGCCGCAA TGGAGAAAC TTGGAGGTTT GCTGGAGCAA ATACTAATAA 1380
 GCCCAAACT TCCTCAGCTG CATAAAATCC ATTTGCACTG GAGTTCATG TTTATTGTCC 1440
 TTATGCTTC TTCTTCAATT ATCCAGTAC GAGCAGGAGA GTTAATAACC TCCCTTCTC 1500
 TCTCTACATG TTCAATAAAA GTTGTGAAA GATTAAC

Seq ID NO: 474 Protein sequence
 Protein Accession #: NP_001053.1

1 11 21 31 41 51
 | | | | |
 MRQSHQLPLV GLLLFSPFIP QLCICEVSE ENYIRLKP LL NTMIQSNYR GTSAVNVVLS 60
 LKLVGIQIQT LMQRMIQIQL YNVKSRLSDV SSGELALIL ALGVCRNAEE NLIYDYHLTD 120
 KLENKPQAEI ENMEAHNGTP LTNYYQLSLD VLALCLFNGN YSTAEVNVHF TPENKNYYFG 180
 SQFSVDTGAM AVLALTCVKK SLINGQIKAD EGSLKNISYI TKSLVEKILS EKKENGLIGN 240
 TFSITGEAMQA LPSVSDYVNE NDWNQQTILN TVLTEISQGA FSNPNAAQV LPALMGKTF 300
 DINKDSSCVS ASGNFISAD EPITVTPFDS QSYISVNVSV RINETYFTNV TVLNGSVFLS 360
 VMEKAQIMND TIFGPTMEER SWGPYITCIQ GLCANNNDRT YWELLSSGGE LSQAGSYV 420
 RGENLEVRW SKY

Seq ID NO: 475 DNA sequence
 Nucleic Acid Accession #: NM_004852.1
 Coding sequence: 89..1546

1 11 21 31 41 51
 | | | | |
 GCCCGCGGCC GCCCGGGGCC CTGATGAGCT GAATGAAGGC TGCTACACC GCCTATOGAT 60
 GCCTACACAA AGACCTAGAA CGTGCSCCAT GAACCCGAGG CTGACAATGG AAAGTCTGGG 120
 CACTTTGCAC GCGCGCGCGC GCGGCGGCGG TGGCGGGGGG GCGGCGGGGG GCGGCGGGGG 180
 CGGCGCGGGG GCGCGGGGCC ATGAGCAGGA GCTGCTGGCC AGCCCCAGCC CCCACCAAGC 240
 GCGCGCGGGC CGCGCTGGCT CGCTGCGGGG COCTCGCGCG CCTCCAACCG CGCACCAAGG 300
 GCTGGGCAOG GCGGCAAGCG GCGCAGCGGC GCGCTCGCGC TCGGCCATGG TCACCAGCAT 360
 GGCCCTOGATC CTGGACGGCG GCGACTACCG GCCCGAGCTC TCCATCCCGC TGCACCAAGC 420
 CATGAGCATG TCTTGGAGCT CGTCTCGGCC TGGCATGGGG ATGAGCAACA CCTACACCAC 480
 GCTGACACCG CTCCAGCGGC TGCCAACCAT CTCCACGCTG TCTGACAAAT TCCACCAACC 540
 TCACCCGCAC CACCATCCGC ACCACCAACA CCACCAACAC CACCAAGCGC TGTCCGGCAA 600
 CGTCAGCGCG AGCTTCAACC TCATGCGCGA CGAGCGCGGG CTCOCGGCCA TGAACAACT 660
 CTACAGTCCC TACAAGGAGA TGCCCGGCAT GAGCCAGAGC CTGTCCCGCG TGGCCGCCAC 720
 GCGCTGTGGC AACCGGGCTAG GCGGCTTCCA CAACGCGCAG CAGAGTCTGC CCAACTACGG 780
 TCCGCGCGGG CAGGACAAAA TGCTCAGCCC CAACCTGAGC GCGCACCACA CTGCTATGCT 840
 GACCGCGGGT GAGCAACACC TGTCCCGCGG CCTGGGCACC CCACCTGCGG CCATGATGTC 900
 GCACCTGAAC GGCCTGCACC ACCCGGGCCA CACTCAGTCT CAOGGGCGGG TGCTGGCACC 960
 CAGTGGCGAG CGGCCACCTT CGTCTCATC GGGCTCGCAG GTGGCCACGT CGGGCCAGCT 1020
 GGAAGAAATC AACACCAAGG AGGTGGCCCA GCGCATCACA GCGGAGCTGA AGCGCTACAG 1080
 TATCCCCAG GCGATCTTTG GCGAGGGGT GCTGTGCGG TCTCAGGGGA CTCTCTCGGA 1140
 CCTGCTCGGG AATCCAAAAC CGTGGAGTAA ACTCAAACT GGCAGGGAGA CCTTCCGAG 1200
 GATGTGGAAG TGGCTTCAGG AGCCCGAGTT CCAGCGCATG TCCGCTTAC GCGTGGCAGC 1260
 GTGCAACGCG AAGACGAGAG AACCAACAA AGACAGGAAC AATTCCAGAG AGAAGTCCCG 1320
 CCGTGTGTTT ACTGACCTCC AACCGCGAAC ACTCTTGCC ATCTTCAAGG AGAACAAACG 1380
 CCGTCAAGG GAGATGCAGA TCACCAATTC CCAGCAGCTG GCGCTGGAGC TCACCAACGT 1440
 CAGCAACTTC TTATGAAGG CCCGCGCGG CAGCCTGGAG AAGTGGCAAG ACGATCTGAG 1500

CACAGGGGGC TCCTCGTCCA CCTCCAGCAC GTGTACCAAA GCATGATGGA AGGACTCTCA 1560
CTTGGGCACA AGTCACCTCC AAATGAGGAC AACAGATACC AAAAGAAAAA AAAGAAAAA 1620
GACACCGGAT TCCTAGCTGG GGCCCTTCAC TGGTG

5 Seq ID NO: 476 Protein sequence
Protein Accession #: NP_004843.1

1 11 21 31 41 51
10 MNPELTMESL GTLHGARGGG SGGGGGGGGG GGGGGPGHEQ ELLASPSPH ARRGPGRSLR 60
GPPPPPTAHQ ELGTAATAAA AASRSAMVTS MASILDGGDY RPELSIPLEH AMSMCDSSP 120
PGMGMSNTYT TLTPQLPLPP ISTVSDKPHH PHPHRHPPHH HHHHHQRLSG NVSGSFTLMR 180
DERGLPAMNN LYSPLYKEMPG MSQSLSPPLAA TPLGNLGLGL HNAQQSLPNY GPPGHDKMLS 240
15 PNFDARHTAM LTRGEQHLRS GLGTPPAAMM SHLNLGLHHPG HTQSHGFVLA PSRERPPSSS 300
SGSQVATSGQ LEEINTKEVA QRITAEIKRY SIPOAIFAQR VLCRSQGTLS DLLRNPKPWS 360
KLKSGRETFR RMWKWLQEPF FORMSALRLA ACKRKEQEPN KDRNNSQKKS RLVTDLQRR 420
TLFAIFKENK RPSKEMQITI SSQLGLELTT VSNFFMNARR RSLEKWQDDL STGSSSTSS 480
TCTRA

20 Seq ID NO: 477 DNA sequence
Nucleic Acid Accession #: NM_013271.1
Coding sequence: 27..809

25 1 11 21 31 41 51
TCCGGAGCCA GGCTCGCTGG GGCAGCATGG CGGGGTGGCC GCTGCTCTGG GGGCGCGGG 60
CGGGGGCGGT CGGCCTTTTG GTGCTGTGTC TGCTGGCCT GTTTCGGCCG CCCCCGCGC 120
TCTGCGCGCG GCGGTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGGCTG 180
AGACTGGCGC TCCTGCGCGC TTCCGGCGGT CAGTGCCCCG AGGTGAGGCG GCGGGGCGG 240
30 TGCAGGAGCT GCGCGCGGCG CTGGCGCATC TGCTGGAGGC CGAACGTGAG GAGCGGGCGC 300
GGGCGGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGGCT CCTGGCGCAG CTGCTGCGCG 360
TCTGGGGCGC CCCCCGCAAC TCTGATCCGG CTCTGGGCTT GGACGACGAC CCGAOGCGC 420
CTGCAGCGCA GCTCGCTCGC GCTCTGCTCC GCGCCCGGCT TGACCTGCGC GCGCTAGCAG 480
35 CCCAGCTTGT CCGCGCGGCC GTCCCGCGCG CGGCGCTCCG ACCCGCGGCC CCGGTCTACG 540
ACGACGCGCC CGCGGGCCCG GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600
CGGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGGCGG AAGCGCGGAC TCGGAGGGGG 660
TGGCAGCGCC GCGCGCGCTC CGCGGTGCGC CGAACACGGA TGTGGGCTCT GAGCTGCCCC 720
CTGAGGGCGT GCTGGGGGCG CTGCTGCGTG TGAACGCGCT AGAGACCCCG GCGCCCGAGG 780
TGCCCTGCAG CGCCCTCTTG CCACCTGAG CACTGCCCGG ATCCCGTGCA CCTGGGGACC 840
40 CAGAAGTGCC CCGCGCATCC CGCCACGAG ACTTCTCCCG GCCAGCAGT CCAGAGCAAC 900
TTACCCCGGC CAGCCAGCCC TCTCACCGGA GGATCCCTAC CCCTGCGGCC ACAATAACAT 960
GATCTGAGC

45 Seq ID NO: 478 Protein sequence
Protein Accession #: NP_037403.1

1 11 21 31 41 51
50 MAGSPILLWGP RAGGVGLLV LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR 60
RSVPRGEAAG AVQELARALA HLLAERQER ARAEAQEAED QQARVLAQLL RVWGAPRNSD 120
PALGLDDDFD APAQLARAL LRLRLDPAAL AAQLVPAPVP AALRPRPPV YDDGAPGPA 180
EAGDETDFD DPELLRLYL RILAGSADSE GVAAPRRLRR AADHDVGSSEL PPEGVLGALL 240
RVKRLTEPAP QVPARRLLPP

55 Seq ID NO: 479 DNA sequence
Nucleic Acid Accession #: NM_002214
Coding sequence: 681..2990

60 1 11 21 31 41 51
CCCAGAGCGC CTCCCGCTG TTGCTGGCAT CCGGAGCTTC CTCCTTGCC AGCCAGGACG 60
CTGCCGACTT GTCTTTGCC GCTGCTCCGC AGACGGGGCT GCAAGCTGC AACTAATGGT 120
GTTGGCCTCC CTGCCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT 180
65 TCCCTCGAC CTCGCGGGG TAOCCTCCCA CAGATCCAGC ATCACCCAGT GAATGTACAT 240
TAGGGTGGTT TCCCGCCAG CTTGGGCTT TGTGGGGTT TGATTGTGTT TGGCTCTTCG 300
CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAG CTCTTTTCTT 360
TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTGGCC GCGGGGCCCT 420
TGGCCGTGCA AGGAGGTGCT TCTCGCGGAG ACCCGGGGAC CCGCGTGGC GAGCGGGAG 480
70 GGCCGTAGGG GCCTGAGAT GCGAGGCGT GCGGGGGGCC GCTTACCTGC ACCGCTTGCT 540
CGAGCGCGG GGTCCGCTC GCTAGGCTCG CGGAAACGT CCTAGCGACA CTGCGCGCG 600
GGCCCCGAGG TCGCCCGGGA GCGCGAGCCC GCGTCCGAA GGCAGCCAGG CGCGGGGCGC 660
GGGGCGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTITACC GCTGCAATTG 720
CTGTGCTGCA AAACGACCGG CGAGGTCCCG CTGCTTCTC CTGGGCGAGC TGGGTGTTTT 780
75 CACTTGTCTT TGGACTGGGC CAGGTGAAG ACAATAGATG TGCACTTTCA AATGACGAT 840
CCTGTGCCAG GTGCTTGGC CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA 900
TTTCAGGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTT CAATTTAATA AGCAAAGGCT 960
GCTCAGTTGA TTCAATAGAA TACCATCTG TGCACTTTAT AATACCCACT GAAATGAAA 1020
TTAATAACCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCGGAAGCTA 1080
80 ATTTTATGCT GAAAGTTTCT CCTCTGAAGA AATATCTGT GGATCTTTAT TATCTTGTG 1140
ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATATAA TTCGTTGGA AACGATTTAT 1200
CTAGAAAAAT GGCATTTTTT TCCCGTGACT TTGCTCTTGG ATTTGGCTCA TACGTTGATA 1260
AAACAGTTTC ACCATACATT AGCATCCACC CGGAAAGGAT TCATAATCAA TGCACTGACT 1320
ACAAATTAGA CTGATGCTCT CCGCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGACAA 1380
TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGAACACATA GATACACCAG 1440

5	AAGAGGTTT	TGACGCCATG	CTTCAGGCAG	CTGTCTGTGA	AAGTCATATC	GGATGGCGAA	1500
	AAGAGGCTAA	AAGATTGCTG	CTGGTGATGA	CAGATCAGAC	GTCTCATCTC	GCTCTTGATA	1560
	GCAAAATTGC	AGGCATAGTG	GTGCCCAATG	ACGGAAACTG	TCATCTGAAA	AACCAACGCT	1620
	ACGTCAAATC	GACAAACCATG	GAACACCCCT	CACTAGGCCA	ACTTTCAGAG	AAATTAATAG	1680
	ACRACAACT	TAATGTATC	TTTGACGTTT	AAGGAAACA	ATTTCATTGG	TATAAGGATC	1740
	TTCTACCCCT	CTTGCCAGGC	ACCATTGCTG	GTGAAATAGA	ATCAAAGGCT	GCAAACTCA	1800
	ATAATTGGT	AGTGGAAAGC	TATCAGAAGC	TCATTTCAGA	AGTGAAAGTT	CAGGTGGAAA	1860
	ACCAAGGTACA	AGGCATCTAT	TTTAACATTA	CGCCATCTG	TCCAGATGGG	TCCAGAAAGC	1920
10	CAGGCATGGA	AGGATGCAGA	AACGTGACGA	GCAATGATGA	AGTTCTTTTC	AATGTAACAG	1980
	TTACAATGAA	AAAATGTGAT	GTACAGGAG	GAAAAAATA	TGCAATAATC	AAACCTATTG	2040
	GTTTTAAATGA	AACCGCTAAA	ATTTCATATC	ACAGAAACTG	CAGCTGTGAG	TGTGAGGACA	2100
	ACAGAGGACC	TAAAGGAAAG	TGTGTAGATG	AACTTTTCT	AGATTCCAAG	TGTTTCCAGT	2160
	GTGATGAGAA	TAAATGTCTAT	TTTGATGAAG	ATCAGTTTTC	TTCTGAGAGT	TGCAAGTCAC	2220
15	ACAAGGATCA	GCCTGTTTGC	AGTGGTCGAG	GAGTTTGTGT	TTGTGGGAAA	TGTTTATGTC	2280
	ACAAAATTA	GCTTGGAAAA	GTGTATGGAA	AATACTGTGA	AAAGGATGAC	TTTTCTTGTG	2340
	CATATCACC	TGGAATCTG	TGTGCTGGGC	ATGGAGAGTG	TGAAGCAGGC	AGATGCCAAT	2400
	GCTTCAGTG	CTGGGAAGGT	GATCGATGCC	AGTGCCCTTC	AGCAGCAGCT	CAGCACTGTG	2460
	TCAATTCAAA	GGGCCAAGTG	TGCAGTGGAA	GAGGCACGTG	TGTGTGTGGA	AGGTGTGAGT	2520
20	GCAACCATCC	CAGGAGCATC	GGCCGCTTCT	GTGAACACTG	CCCCACCTGT	TATACAGCCT	2580
	GCAAGGAAA	CTGGAATTGT	ATGCAATGCC	TTCAACCTCA	CAATTGTGCT	CAGGCTATAC	2640
	TTGATCAGTG	CAAAACCTCA	TGTGCTCTCA	TGGAACAACA	GCATTATGTC	GACCAAACTT	2700
	CAGAATCTTT	CTCCAGCCCA	AGCTACTTGA	GAATATTTT	CTCATTTTTC	ATAGTTACAT	2760
	TCTTGATTGG	GTTCCTTAAA	GTCTGATCA	TTAGACAGGT	GATACTACAA	TGGAATAGTA	2820
25	ATAAAATTA	GTCTCTATCA	GATTACAGAG	TGTCAGCCTC	AAAAAGGAT	AGTTGATTTC	2880
	TGCAAGTGT	TTGCACAAGA	GCAGTCACCT	ACCGACGTGA	GAGCCTGAA	GAAATAAAAA	2940
	TGGATATCAG	CAAAATTAAT	GCTCATGAAA	CTTTCAGGTG	CAACTTCTAA	AAAAAGATT	3000
	TTAAACACT	AATGGGAAC	TGGAATTGTT	AATAATTGCT	CCTAAGATT	ATAATTTTAA	3060
	AAGTCACAG	AGGAGACAAA	TTGCTCACGG	TCATGCCAGT	TGCTGGTGT	ACACTCGAAC	3120
30	GAAGACTGAC	AAGTATCCTC	ATCATGATGT	GACTCACATA	GCTGCTGACT	TTTTCAGAGA	3180
	AAAATGTGT	TTACTACTGT	TTGAGACTAG	TGTGTTGTA	GCATTTACT	GTAATATATA	3240
	ACTTATTAG	ATCAGCATAG	AATGTAGATC	CTCTGAAGAG	CACTGATTAC	ACTTTACAGG	3300
	TACCTGTTAT	CCCTACGCTT	CCCAGAGAGA	ACAATGCTGT	GAGAGAGTTT	AGCATTGTGT	3360
	CACTACAAGG	GTACAGTAAT	CCCTGCACTG	GACATGTGAG	GAAAAAATA	ATCTGGCAAG	3420
35	TATATTCTAA	GGTTGCCAAA	CACCTCAACA	GTGTTGGTGT	GAATAGACAA	GAACAGCTAG	3480
	ATGAATAAAT	GATTCTGTTT	TCACCTCTTC	AAGAGGTGAA	CAGATACAA	CTTAATCTTA	3540
	AAAGATTATT	GCTTTTAAA	GTGTGTAGTT	TTATGCATGT	GTGTTTATGG	TTTGCTTATT	3600
	TTTGCAAGAT	GGATACTAAT	TCCAGCATTC	TCTCTCTTTT	GCCTTTATGT	TTTGTTTTCT	3660
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40	TACTGCCATA	AAAACTAAT	AATACAATGT	CACCTTATCA	GAATACTAGT	TTTAAAGCT	3780
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Seq ID NO: 480 Protein sequence
Protein Accession #: NP_002205

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	LGPECGMCVQ	EDFISGGSRS	ERCDIVSNLI	SKGCSVDSIE	YPSVHVIIPT	ENEINTQVTP	120
50	GEVSIQLRPG	AEANFMLKVH	PLKKYFVDLY	YLVDSASME	NNIEKLNSVG	NDLSRKMAPP	180
	SRDFRLGPGS	YVDKTVSPYI	SIHPERIHNQ	CSDYNLDMP	PHGYIHVLSL	TENITEFEKA	240
	VHRQKISGNI	DTPEGGFDAM	LQAAVCESHI	GWRKEAKRLI	LVMTDQTSHL	ALDSKLAGIV	300
	VPNDRGNCHLK	NNVYVKSTTM	BHPSLGLQSE	KLIDNNINVI	FAVQKQKPHW	YKDLPLLP	360
	TIAGSIESKA	ANLNNLVBEA	YQKLISEVKV	QVENQVQGIY	FNITAI CPDG	SRKPFMEGCR	420
55	NVTSNDEVLF	NVVTVMKKCD	VTGGRNYALI	KPIGFNETAK	IHLHRNCSQ	CEDNRGPKGK	480
	CVDETFLDK	CPQCEKDKCH	FDEDQFSSSE	CKSHKDQFVC	SGRGVCVCGK	CSCHKIKLGK	540
	VYGYKCEKDD	FSCPYHHGNL	CAGHGCECRG	RCQCFSGWEG	DRCQCPASAA	QHCVNSKGVQ	600
	CSGRGTCVCG	RCBCTDPRSI	GRFCEHCPTC	YTACKENMNC	MQCLHPHNL	QAILDQCKTS	660
	CALMBQHYHV	DQTSBCEFPSP	SYLRIFPIIF	IVTFLIGLLK	VLIIRQVILQ	WNSNKKSSS	720
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Seq ID NO: 481 DNA sequence
Nucleic Acid Accession #: NM_003318.1
Coding sequence: 1..2574

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	AACCCAGAGG	ACTGGTTGAG	TTTGTGTCTC	AAACTAGAGA	AAAACAGTGT	TCOOGCTAAGT	240
	GATGCTCTTT	TAAATAAATT	GATTGGTGTG	TACAGTCAAG	CAATTGAAGC	GCTTCCCCCA	300
	GATAAATATG	GCCAAATATG	GAGTTTGTCT	AGAATTCAAG	TGAGATTGTC	TGAATTAATA	360
	GCTATTCAAG	AGCCAGATGA	TGCACGTGAC	TACTTTCAAA	TGGCCAGAGC	AAACTGCAAG	420
75	AAATTTGCTT	TTGTTCATAT	ATCTTTTGCA	CAATTTGAAC	TGTCACAAGG	TAATGTCAAA	480
	AAAAGTAAAC	AACCTCTTCA	AAAAGCTGTA	GAACTGGGAG	CAGTACCACT	AGAAATGCTG	540
	GAAATFGCC	TGCGGAATT	AAACCTOCAG	AAAAAGCAGC	TGCTTTTACA	GGAGGAAAG	600
	AAGAAATTTAT	CAGCATCTAC	GGTATTAACT	GCCCAAGAA	CATTTTCOGG	TTCACTTGGG	660
	CATTTACAGA	ATAGGAACAA	CAGTTGTGAT	TCCAGAGGAC	AGACTACTAA	AGCCAGGTTT	720
80	TTATATGGAG	AGAACTATGC	ACCACAAGAT	GCAGAAATAG	GTTACOGGAA	TTCAATTGAGA	780
	CAAACTAACA	AAACTAAACA	GTCATGCCCA	TTTGAAGAG	TCCAGTTTAA	CCTTCTAAAT	840
	AGCCAGATT	GTGATGTGAA	GACAGATGAT	TCAGTTGTAC	CTTGTTTTAT	GAAAGACAA	900
	ACCTCTAGAT	CAGAAATGCC	AGATTGTGTT	GTGCTCTGGT	CTAAACCAAG	TGGAATGAT	960
	TCCTGTGAAT	TAAGAAATTT	AAAGTCTGTT	CAAAATAGTC	ATTTCAAGGA	ACCTCTGGTG	1020
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Seq ID NO: 482 Protein sequence
Protein Accession #: NP_003309.1

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AIQEPDDARD YQMARANCK KFAPVHISFA QFELSQQNVK KSKQLLQKAV ERGAVPLEML 180
EIALRNINLQ KQLLSEEEK KNLSASTVLT AQESFSGSLG HLQNRNNSCD SRGQTTKARF 240
LYGENMPPQD AEIGYRNSLR QTNKTKQSCP FGRVPVNLIN SPDCDVKTDD SVVPCPFMKRQ 300
TSRSECRDLV VPGSKPSSND SCELRLNLSKV QNSHFKEPLV SDEKSSSELI TDSITLKNKT 360
ESSLLAKLEE TKEYQEPBVP ESNQKQWQSK RKSECIQNPQ AASSNHWQIP ELARKVMTBQ 420
KHTEFEQPVF SVSKQSPPI S TSXWDFPKSI CKTPSSNTLD DYMSCFRTFV VKNDFFPACQ 480
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QVLNEKKQIY AIKYVNLBEE DNQTLDSYRN EIAVNLKLQO HSDKIRLYD YEITDQYIYM 600
VMECGNIDLN SWLKKKKSID PWERKSYWKN MLEAVHTIHQ HGIIVHSDLP ANFLIVDGM 660
KLIDFGIANQ MQPDTTSVVK DSQVGTVNYM PPEAIKDMSS SRENGKSKSK ISPKSDVWSL 720
GCILYMYTNG KTFPQQIINQ ISKLHAIIDP NHEIEFPDIP EKDLQDVLCR CLKRDPKQRI 780
SIEPELLAHFY VQIQTEFPVQ MAKGTTEEMK YVLGQLVLGN SPNSILKAAR TLYEHYSGGE 840
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Seq ID NO: 483 DNA sequence
Nucleic Acid Accession #: NM_003667.1
Coding sequence: 1..2651

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CCTTCCACCC TCAGGCTCTT CACCTCCTAC CTAGACCTCA GTATGAACAA CATCAGTCAG 240
CTGCTCCGAA ATCCCTCGCC CAGTCTCGCC TTCTGAGAG AGTTACGCTT TGCGGGAAAC 300
GCTCTGACAT ACATTCGCCA GGGAGCATTC ACTGGCCTTT ACAGTCTTAA AGTTCTTATG 360
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CAATCCCTCG GTCTGGATGC TAACCAATC AGCTATGTGC CCCCAGCTG TTTCACTGGC 480
CTGCATTCCT TGAGGACACCT GTGGCTGGAT GACAATGCGT TAACAGAAAT CCCCCTCCAG 540
GCTTTTAGAA GTTTATCGGC ATGCAAGCC ATGACCTTGG CCTGAACAA AATACACCAC 600
ATACCAAGAT ATGCTTTGG AAACCTCTCC AGCTTGGTAG TTCTACATCT CCATAACAAT 660
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Seq ID NO: 484 Protein sequence

Protein Accession #: NP_003658.1

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AFRSLSALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLLELD 240
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TGTALESST LTGAQISSLP QTVCNQLFNL QVLDLSYNLL EDLPFSFSVQK KLQKIDLRHN 360
EIYEIKVDTF QQLLSLRSLN LAWNKIAIHH PNAFSTLPSL IKLDLSSNLL SSFPTGLRHG 420
LTHLKLTVGNH ALQSLISEN FPELKVIEHP YAYQCCAFGV CENAYKISNQ WNKGDNSMD 480
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ARHGAWWENG VGCHVIGFLS IFASESSVFL LTLAALERGF SVKYSAPET KAPFSSSLKVI 660
ILLCALLALT MAAYPLLGS KYGASPLCLP LPFGEPTMG YMVALLILNS LCFIMMTIAY 720
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Coding sequence: 73..3117

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AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACAAG GAAGCTACAA GTGCTTTTGC 600
CTCAGTGCCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
ATAAATGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
TCAGGACTCG GCGTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTCT 780
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ATCCCTGAAA ATTCTGTGAA GGAAGTCCCT AGAGCACCTG GTACCATCAA AGACAGAAATC 1080
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GAAGCAGAAC GTGGCAAGGG CAATAACCGC GAAATGCGAG TGGATGGCGT CTTGCTTGT 1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
TTGACTTGT ATGTCAGTTC CCGGTTTTT TTGATATGTC ATCATAGGAC CTCTGGCATT 1980
TTAGAATTAC TAGCTGAAAA ATTGTATGT ACCAACAGAA ATATTATGT AAGATGCCTT 2040

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5 TCTTGATATA GATATGCCAA TATTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
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10 Seq ID NO: 494 Protein sequence
 Protein Accession #: NP_056322

1 11 21 31 41 51
 15 MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRNSKGV 60
 CEATCEPGCK FGECVGPNC RCFPGYTGT CSQDVNECGM KRPQCQRVCV NTHGSYKCF 120
 LSGHMLMPPA TCVNSTRCAM INCQYSCEDT EEGPQCLCP SGLRLAPNGR DCLDIDECAS 180
 GKVICPYNRR CVNTFGSYTC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTNQ 240
 GSPKCKCKQG YKGNGLRCSA IPENSVEVL RAPGTIKDRI KLLLAHKNSM KKKAKIKNVT 300
 20 PEPTRTPTPK VNLQPFNYEB IVSRGGNSHG GKKGNEEKMK BGLEDEKREE KALKNDIEER 360
 SLRGDVFFPK VNEAGFGLI LVQRKALTSK LEHKDLNISV DCSFNHIGCD WKQDREDDFD 420
 WNPADRDNAI GFYMAVPALA GHKIDIGRLK LLLPDLPQPS NFCLLFYDYL AGDKVGLKRV 480
 FVKNSNNALA WEKTTSEDEK WTKGKIQLYQ GTDATKSIIF EAERGGKGTG EIAVDGVLLV 540
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25 Seq ID NO: 495 DNA sequence
 Nucleic Acid Accession #: NM_003506.1
 Coding sequence: 259..2379

30 1 11 21 31 41 51
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 35 ATCTTTGGAT GGGGATCTTC TGAGGATGCA AAGAGTGATT CATCCAGGCC ATGTGGTAAA 240
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 CTCTCAAGAG GGCACAGTCT CTTCACCTGT GAACCAATTA CTGTCCCGAC ATGTATGAAA 360
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 GCGGTGGAAG TGGAGCATTT TCTTCTCTC GCNAATCTGG AATGTTCACC AACATTGAA 480
 40 ACTTTCTCT GCAAGCATT TGTACCAACC TGATAGAAC AAATTCATGT GGTCCACCT 540
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 65 ATTACTAGCC ATGATTACCT AGGACAGAA ACTTTGACAG AAATCCAAAC CTCACCAAGAA 2040
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AACCACTTAC AGTTGCTTAT ATTTTGTGTT TTAACITTTG TTTCTTAACA TTTAGAATAT 3300
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Seq ID NO: 496 Protein sequence
Protein Accession #: NP_003497.1

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FLPLANLECS	ENIETFLCKA	FVPTCIEQIH	VVPPCRKLCE	KVYSDCKKLI	DTFGIRWPBE	120
LECDRLQYCD	ETVPVTFDPH	TEFLGPQKKT	EQVQRDIGFW	CPRLKTSGG	QGYKFLGIDQ	180
CAPPCPNMYF	KSELEFPAKS	PIGTVSIFCL	CATLFTFLTP	LIDVRRFRYP	ERPIIYYSVC	240
YSIVLSMYPF	GFLLDGSTAC	NKADEKLELG	DTVVLGSSQNK	ACTVLFMLLY	PFTMAGTVWW	300
VILTITWFLA	AGRKWSCEAI	EQKAVWFHAV	AWGTPGFLT	MLLALNKVEG	DNISGVCFVG	360
LYDLASRYF	VLLPLCLCVF	VGLSLLLAGI	ISLNHVRQVI	QHDGRNQEKI	KKFMIRIGVP	420
SGLYLVPLAT	LLGCYVYBQV	NRITWEITWV	SDHCRQYHIP	CPYQAKAKAR	PBLALFMIKY	480
LMTLIIVGISA	VFWVSGSKTC	TEWAGFPKRN	RKRDPISER	RVLQESCEFF	LKHNSKVKHK	540
KKHYPSSHK	LKVISKSMGT	STGATANHGT	SAVAITSHDY	LQGETLLEIQ	TSPETSMREV	600
KADGASTPLR	REQDCGEPAS	PAASISRLSG	EQVDGKGQAG	SVSESARSEG	RISPKSDITD	660
TGLAQNNLQ	VPSSSEFSSL	KGSTSLLVHP	VSGVRKEQGG	GCHSDT		

Seq ID NO: 497 DNA sequence
Nucleic Acid Accession #: NM_005046
Coding sequence: 16..777

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TGTGCAAGAG	GCTCCACCCC	ATGGCAGGTG	GCCCTGCTCA	GTGGCAATCA	GCTCCACTGC	180
GGAGGCGTCC	TGGTCAATGA	GCGCTGGGTG	CTCACTGCGG	CCCCTGCAA	GATGAATGAG	240
TACACCGTGC	ACCTGGGCAG	TGATACGCTG	GGCGACAGGA	GAGCTCAGAG	GATCAAGGCC	300
TCGAAGTCAT	TCGCGCACCC	CGGCTACTCC	ACACAGACCC	ATGTTAATGA	CCTCATGCTC	360
GTGAAGCTCA	ATAGCCAGGC	CAGGCTGTCA	TCCATGGTGA	AGAAAGTCAG	GCTGCCCTCC	420
CGCTGCGAAC	CCCCTGGAAC	CACCTGTACT	GTCTCCGGCT	GGGCACTAC	CACGAGCCCA	480
GATGTGACCT	TTCCCTCTGA	CCTCATGTGC	GTGGATGTCA	AGCTCATCTC	CCCCCAGGAC	540
TGCACGAAGG	TTTACAAGGA	CTTACTGGAA	AATTCCATGC	TGTGCGCTGG	CATCCCGAC	600
TCCAAGAAAA	ACGCTGCAAA	TGGTGACTCA	GGGGGACCGT	TGGTGTGCAG	AGGTACCCCTG	660
CAAGGTCTGG	TGTCTCTGGG	AACCTTCCCT	TGCGGCCAAC	CCAATGACCC	AGGAGTCTAC	720
ACTCAAGTGT	GCAAGTTCAC	CAAGTGGATA	AATGACACCA	TGAAAAGCA	TCGCTAACGC	780
CACACTGAGT	TAATTAAGTC	TGTGCTTCCA	ACAGAAAATG	CACAGGAGTG	AGGAGCCCGA	840
TGACCTATGA	AGTCAAATTT	GACITTAOCT	TTCTCTCAAG	ATATATTATA	ACCTCATGGC	900
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Seq ID NO: 498 Protein sequence
Protein Accession #: NP_005037

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MARSLLLPLQ	ILLLSLALET	AGEEAQGDKI	IDGAPCARGS	HPWQVALLSG	NQLHCGGVLV	60
NERWVLPAAH	CKMNEYTVHL	GSDTLGDRRA	QRIKASKSFR	HPGYSTQTHV	NDLMLVKLNS	120
QARLSSMVKK	VRLPSRCEPP	GTICTVSGWG	TTTSPDVTFP	SDLMCVDVIL	ISPQDCTKVY	180
KDLLENSMLC	AGIPDSKINA	CNGDSGGPLV	CRGTLQGLVS	WGTFPCGQPN	DPGVYTVQVK	240
FTKWNIDTMK	KHR					

Seq ID NO: 499 DNA sequence
Nucleic Acid Accession #: NM_007196
Coding sequence: 182..962

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GATTCCACAGT	TAAAGGGCTC	CAGAAATGCTG	TACACAGGAG	AGAACTGAAG	TACTGGGGCC	120
TCCTCCACTG	GGTCCGAATC	AGTAGGTGAC	CCCGCCCTGT	GATTCTGGAA	GACCTCACCA	180
TGGGAGCGCC	CGACCTCGT	GCGGCCAAGA	CGTGGATGTT	CCTGCTCTTG	CTGGGGGGAG	240
CCTGGGCAGG	ACACTCCAGG	GCACAGGAGG	ACAAGGTGCT	GGGGGGTCAT	GAGTGCCAAC	300
CCCATTGCGA	GCTTGGCAG	GCGGCTTGT	TCCAGGGCCA	GCAACTACTC	TGTGGCGGTG	360
TCCTTGATGG	TGGCAACTGG	GTCCTTACAG	CTGCCCCTG	TAAAAACCG	AAATACACAG	420
TACGCTGGG	AGACCAAGC	CTACAGAATA	AAGATGGCCC	AGAGCAAGAA	ATACTGTGG	480
TTCACTGCAT	CCCACACCCC	TGCTACACCA	GCAGCGATGT	GGAGGACCAC	AACCATGATC	540
TGATGCTTCT	TCAACTGCGT	GACCAGGCAT	CCCTGGGGTC	CAAAGTGAAG	CCCATCAGCC	600
TGGCAGAAGT	TTGCAACCCG	CCTGGCCAGA	AGTGACCGT	CTCAGGCTGG	GGCACTGTCA	660
CCAGTCCCCG	AGAGAAATTT	CCTGACACTC	TCAACTGTGC	AGAAAGTAAA	ATCTTTCCCC	720
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GCAGCAAAGG	GGCTGACAGG	TGCCAGGGCG	ATTCTGGAGG	CCCCCTGGTG	TGTGATGGTG	840
CATCCAGGAG	CATCACATCC	TGGGGCTCAG	ACCCCTGTGG	GAGGTCCGAC	AAACCTGGCG	900
TCTATACCAA	GACTGCGCG	TACCTGGACT	GGATCAAGAA	GATCATAGGC	AGCAAGGGCT	960
GATTCTAGGA	TAAGCACTAG	ATCTCCCTTA	ATAAACTCAC	AACCTCTC		

Seq ID NO: 500 Protein sequence
Protein Accession #: NP_009127

1 11 21 31 41 51

5 MGRPRPRAAK TWMFLLLGG AMAGHSRAQE DKVLGGHECQ PHSQPWQAAL FQQQQLLCGG 60
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LMLQLLRDQA SLGSKVKPIS LADHCTQPGQ KCTVSGWGTV TSPRENFPDT LNCAEVKIPP 180
QKCEDAYPG QITDGMVCAG SSRGADTCQG DSGGPLVCDG ALQGITSWGS DPCGRSDKPG 240
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Seq ID NO: 501 DNA sequence
Nucleic Acid Accession #: NM_006103
Coding sequence: 29..406

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20 CGCAATGGC TGTGGGAAGG TGTCTGTGT CACTCCCAAT TTCTGAGGTC CAGCCACCAC 420
CAGGCTGAGC AGTGAGGAGA GAAAGTTTCT GCCTGGCCCT GCATCTGTTT CCAGCCACC 480
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25 Seq ID NO: 502 Protein sequence
Protein Accession #: NP_006094

30 1 11 21 31 41 51
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CCSAGCATFC LLCPNDKEGS CPQVNIFFPQ LGLCRDQCQV DSQCPGQMKC CRNGCGKVSC 120
VTPNF

35 Seq ID NO: 503 DNA sequence
Nucleic Acid Accession #: NM_002407
Coding sequence: 65..352

40 1 11 21 31 41 51
CCTCCACAGC AACTTCCTTG ATCCCTGCCA CGCAGACTG AACACAGACA GCAGCCGCCT 60
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TTCTGGCTGC AAATCCTCTGG AGGACATGGT TGAAAAGACC ATCAATTCCG ACATATCTAT 180
ACCTGAATAC AAAGAGCTTC TTCAGAGATT CATAGACAGT GATGCGCTG CAGAGGCTAT 240
GGGGAATTC AAGCAGTGT TCCTCAACCA GTCACATAGA ACTCTGAAA ACTTTGGA 300
45 GATGATGCAT ACAGTGATAG ACAGCATTG GTGTAATATG AAGAGTAATT AACCTTACCC 360
AAGGCGTTTG GCTCAGAGGG CTACAGACTA TGGCCAGAAC TCATCTGTGT ATTGCTAGAA 420
ACCACTTTTC TTCTTGTGT TGTCTTTTA TGTGAAACT GCTAGACAC TGTGAAACC 480
TCAATTCAT TTCCATTCA ATAATAACT GCAAAATC

50 Seq ID NO: 504 Protein sequence
Protein Accession #: NP_002398

55 1 11 21 31 41 51
MKLLMVLMLA ALLLHCYADS GCKLLEDMEV KTINSDISIP EYKELLQEFI DSDAAABAMG 60
KFKQCFINQS HRTLKNFGLM MHTVYDSIWC NMKSN

60 Seq ID NO: 505 DNA sequence
Nucleic Acid Accession #: NM_014791.1
Coding sequence: 171..2126

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AAAACACACT AGGGAGTGAT TTGCCCGGGA TCAAAACGGA GATTGAGGCC TTGAAGAACC 360
70 TGAGACATCA GCATATATGT CAACTCTACC ATGTGCTAGA GACAGCCAAC AAAATATTCA 420
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75 ATCTACAGC ATGCTGTGGG AGTCTGGCIT ATGCAGCACC TGAGTTAATA CAAGGCAAT 720
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CTACAACTAG ATTAGTGAAT CCAGATCAAC TGTGAATGA AATAATGTCT ATTCTTCCA 1920
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GATATTATTT TGTGTATGAA TCTAAATCAA GCCATCTGT CATTATGTTA CTGTCTTTT 2340
TAAATCATGT GTTTTGTATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG 2400
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Seq ID NO: 506 Protein sequence

Protein Accession #: NP_055606.1

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1 11 21 31 41 51
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LQNLRHQHTC QLYRVLETAN KIFMVLBYCP GGBELFDYIIS QDRLESEETR VVFRQIVSAV 120
AYVHSQYAH RDLKPEMLLP DEYHKLKID FGLCAKPKGN KDYLHQTCCG SLAYAAPELI 180
GKGSYLGSEA DVVSMGILLY VLMCGFLPFD DDNMALYKK IMRGYDVPK WLSFSSILL 240
QQMLQVDPK RISMKNLLNH PHIMQDYNYP VEWQSKNFI HLDDDCVTEL SVHHRNRRQT 300
MEDLISLWQY DHLTATYLL LAKKARGKPV RLRLSSPFCG QASATPFPTDI KSNWNSLEDV 360
TASDKNVVAG LIDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTFANKL 420
KNKENVYTPK SAVKNEEYFM FPEPKTPVNK NQHKREILT PNRYTPPSKA RNQCLKETPI 480
KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV 540
LTRSKRRGSA RDGPRRLKLH YNVTTTRLVN PDQLLNEIMS ILPKHVDVF QKGYTLKQCT 600
QSDPGKVTMQ FELEVQQLQK PDVVGIRQR LKGDWVYKR LVEDILSSCK V

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Seq ID NO: 507 DNA sequence

Nucleic Acid Accession #: NM_000582

Coding sequence: 88..990

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CTTTACAAACA AATACCCAGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG 240
CAGAATCTCC TAGCCCCACA GACCCCTTCCA AGTAAGTCCA ACGAAAGCCA TGACCATG 300
GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATGTACTCG 360
AACGATCTCG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420
TCTGATGAAT CTGATGAAC GGTCACTGAT TTTCCCAAGG ACCTGCCAGC AACCGAAGTT 480
TTCCTCCAG TTGTCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540
GGACTGAGGT CAAAATCTAA GAAGTTTCGC AGACCTGACA TCCAGTACCC TGATGCTACA 600
GACGAGGACA TCACTCACA CATGGAAGC GAGGAGTTGA ATGGTGATA CAAGGCCATC 660
CCCGTTGCC AGGACCTGAA CGGCGCTTCT GATTGGGACA GCGGTGGGAA GGACAGTTAT 720
GAAACGAGTC AGCTGATGTA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCCAGATTA 780
TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCATTCG ATGTGATTGA TAGTCAGGAA 840
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CTCAGTTTAT TGGTTGAATG TGTATCTATT TGAGTCTGGA AATAACTAAT GTGTTTGATA 1140
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TATCTTTTGT TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAATT TGGTGGTGTG 1440
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Seq ID NO: 508 Protein sequence

Protein Accession #: NP_000573

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1 11 21 31 41 51
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PSKSNESHMH MDDMDDDDDD DEVDSDSID SDDSDVDVT DSDHQSDSH HSDESDELVT 120
DFPTDLPAPE VFTPVVFTVD TYDGRGDSVV YGLRSKSKKF RRPDIQYFDA TDEDITSHME 180
SEELNGAYRA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240
NEHSDVIDSQ ELSKVSREPH SHEPHSHEDM LVVDPKSKEB DKHLKFRISH ELDSASSEVN

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Seq ID NO: 509 DNA sequence
Nucleic Acid Accession #: AB051390.1
Coding sequence: 34..2457

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	TCCGACGAGA	CCCTGGACAA	AGTGCCCAAG	TCAGAGGGCT	ACTGCAGCCG	TATCCTGCGC	180
10	GCCCAGGGCA	CGCGCGCGA	GGGCTACACC	GAGTTCAGCC	TCCGCGTGGA	GGGCGACCCC	240
	GACTTCTACA	AGCGGGGAAC	CAGCTACCGC	GTAACACTTT	CAGCTGCTCC	TCCCTCCTAC	300
	TTCAGAGGAT	TCACATTAAT	TGCCCTCAGA	GAGAACAGAG	AGGGTGATAA	GGAGAAGAC	360
	CATGCTGGGA	CCCTCCAGAT	CATAGACGAA	GAAGAACTC	AGTTTATGAG	CAATTGCCCT	420
	GTTCAGTCA	CTGAAAGCAC	TCCAOGGAGG	AGGACCGGA	TCCAGGTGTT	TTGGATAGCA	480
15	CCACCAGCGG	GAACAGGCTG	CGTGATTCTG	AAGGCCAGCA	TCGTACAAAA	ACGCATTATT	540
	TATTTTCAAG	ATGAGGGCTC	TCTGACCAAG	AAACTTTTGT	AACAAGATTG	CACATTTGAT	600
	GGGGTGACTG	ACAAACCCAT	CTTAGACTGC	TGTGCTGCG	GAAGTGCCTG	GTACAGACTC	660
	ACATTTTATG	GGAATTGCTC	CGAGAAGACA	CACCCAAAGG	ATTACCTCTG	TCGGGCCAAC	720
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	GAAGAAATTC	GACCAACAGG	TGATGAGGTC	CTCACCGTCA	TCAAAGCCAA	AGCCCAATGG	900
	CCAGCTCGGC	AGCCTCTCAA	CGTGAGAGCA	GCACCTTCAG	CTGAATTTTC	CGTGGACAGA	960
	ACGCGCATT	TAATGTCTTT	CCTGACCATG	ATGGGCCCTA	GTCCCGACTG	GAACTAGGC	1020
	TTATCTGCAG	AGATCTCTGT	CACCAAGGAA	TGTGGCTGGG	TCCAGAGGTT	GGTGCAAGAC	1080
25	CTGATTCCTT	GGGACGCTGG	CACGACAGC	GGGGTGACCT	ATGAGTCACC	CAACAAACCC	1140
	ACCATTCCTC	AGGAGAAATC	CCGGCCCTCG	ACCAAGCCTG	ACCATCTCTA	GAGTCTCTTC	1200
	TATGACCTGC	AGGGTGGGTC	CATCACTCAA	GTAGCCAGAG	TTGTCTATCG	GAGAATCGCA	1260
	CGGAAGGGTG	AACAATGCAA	TATTGTACCT	GACAAATGTC	ATGATATTGT	AGCTGACCTG	1320
	GCTCCAGAGG	AGAAAGATGA	AGATGACACC	CCTGAAACCT	GCATCTACTC	CAACTGGTCC	1380
30	CCATGGTCCG	CTGTCAGCTC	CTCCACCTGT	GACAAAGGCA	AGAGGATGCG	ACAGCGCATG	1440
	CTGAAGCAGC	AGCTGGACCT	CAGCGTCCCT	TGCCCTGACA	CCAGGACTTC	CCAGCCCTGC	1500
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	TGGTCCGCTT	GCAGCATCTC	CTGCGGCATG	GGCATGAGGT	CCCGGGAGAG	GTATGTGAAG	1620
	CAGTTCGCGG	AGGAOAGGCT	CGTGTGCAG	CTGCCCACTG	AGGAAACGGA	GAAGTGCACG	1680
35	GTCAACAGAG	AGTGCTCTCC	CAGCAGCTGC	CTGATGACCG	AGTGGGGCGA	GTGGGACGAG	1740
	TGCAGCGCCA	CCTGCGGCAT	GGGCATGAAG	AAGCGGCACC	GCATGATCAA	GATGAACCCC	1800
	GCAGATGGCT	CCATGTGCAA	AGCGAGGACA	TCACAGGCAG	AGAAATGCAT	GATGCCAGAG	1860
	TGCCACACCA	TCCCATGCTT	GCTGTCCCCA	TGGTCCGAGT	GGAGTGACTC	CAGCGTGACC	1920
	TGCGGGAGGG	GCATGCGAAC	CCGACAGCGG	ATGCTCAAGT	CTCTGGCAGA	ACTTGGAGAC	1980
40	TGCAATGAGG	ATCTGGAGCA	GGTGAGAGAG	TGCATGCTCC	CTGAATGCCC	CATTGACTGT	2040
	GAGCTCACCG	AGTGGTCCCA	GTGGTCGGA	TGTAACAAGT	CATGTGGGAA	AGGCCACGTG	2100
	ATTGGAACCC	GGATGATCCA	AATGGAGCCT	CAGTTTGGAG	GTGCACCCCTG	CCCAGAGACT	2160
	GTGCAGCGAA	AAAAGTGCCG	CATCCGAAAA	TGCCCTCGAA	ATCCATCCAT	CCAAAAGCTA	2220
	CGCTGAGGAG	AGGCCCGAGA	GAGCCCGCGG	AGTGAGCAGC	TGAAGGAAGA	GTCTGAAGGG	2280
45	GAGCAGTTCC	CAGGTTGTAG	GATGCGCCCA	TGGACGGCCT	GGTCAGAAATG	CACCAAACTG	2340
	TGCGGAGGGT	GAATTGAGGA	ACGTTACATG	ACTGTAAAGA	AGAGATTCAA	AAGCTCCACG	2400
	TTTACCAGCT	GCAAGACAAA	GAAGGAGATC	AGAGCATGCA	ATGTTTATCC	TTGTTAGCAA	2460
	GGGTACGAGT	TCCCAAGGCT	TGCACCTAG	ATTCCAGAGT	CACCAATGCG	TGGATTATTT	2520
	GCTTGTTTAA	GACAATTTAA	ATTGTGTACG	CTAGTTTTC	TTTGTGAGT	GTGGTTGCCC	2580
50	CAGTATCTTT	GTGATGCGCA	GAGACATCCT	TTCTGAATAC	TTCTTGATGG	GTACAGGCTG	2640
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	GCATTGATGT	TGGGTGGCTT	TTGTCTTTTC	ACTGAGAAAT	TGGGAATACA	TTTGTCTCAC	3060
	CCCTGATATT	GCTTCTGAT	GCCCCCCCAA	CAAAAATAAA	TAAATAAATT	ATGGCTGCTT	3120
	TATTTAAATA	TAAGGTAGCT	AGTTTTTACA	CCTGAGATAA	ATAATAAGCT	TAGAGTGAT	3180
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	CTGAACCTTT	TGGTACTAAA	TCCCTATTGG	AACCAAGACA	AAGGAAGCAA	AATTGGTCTC	3300
	TTTAGAGACC	AATTGTGCTA	AATTTTAAAA	TCTTCTTACA	CACATCTAGA	CGTTCAAGTT	3360
	TGCAAAATCAG	TTTTTAGCAA	GAAAACATTT	TTGCTATACA	AACATTTTGC	TAAGTCTGCC	3420
	CAAGGCCCCC	CCAATGCATT	CCTTCAACAA	AATACAATCT	CTGTACTTTA	AAGTTATTTT	3480
65	AGTCATGAAA	TTTTATATGC	AGAGAGAAAA	AGTTACGAG	ACAGAAAACA	AATCTAAGGG	3540
	AAAGGAATAT	TATGGGATTA	AGCTGAGCAA	GCAATTCTGG	TGGAAAGTCA	AACCTGTCTG	3600
	TGCTCCACAC	CAGGCTGTGT	GTCTCCACAG	ACATGCATAG	GAATGGCCAC	AGGTTTACAC	3660
	TGCTTCCCA	GCAATTATAA	GCACCCAGA	TTGAGGGAGA	CTGACCAACA	AGGGATAGTG	3720
	TAAAAGGACA	TTTTCTCAGT	TGGGTCCATC	AGCAGTTTTT	CTTCTGCTAT	TTATTGTTGA	3780
70	AAACTATTGT	TTTATTTCTT	CTTTTATAGG	CCTTATTACT	GCTTAATCCA	AATGTGTACC	3840
	ATTGGTGAGA	CACATACAA	GCTCTGAATA	CACATGCAAT	TTGTATTAAA	CACATCAGAA	3900
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	TCAATAAAAA	CTCACTGGGT	CTTTTATGTC	TTTAAGCTAA	GTAAGTGTTC	AGAAGGTTCT	4020
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75	TTCTTGGAGG	GACCAATTAT	ACATCTCTGA	ACTACCTTTG	TATCCAAAT	GTTTTAAATC	4140
	CTTAAATGAA	TGCTTTCTCT	CCAAAAAAG	CACAATATAA	AGAAACACAA	GATTTAATTA	4200
	TTTTTCTACT	TGGGGGGAAA	AAAGTCTCTA	TGTAGAAGCA	CCCACTTTTG	CAATGTTGTT	4260
	CTAAGCTATC	TATCTAACTC	TCAGCCCATG	ATAAAGTTCC	TTAAGCTGGT	GATTCTTAAT	4320
	CAAGGACAAA	CCACCTTAGT	GTCTCATGTT	TGTATTTGGT	CCCACTTTGG	TACATTTTAA	4380
	AATCTGATTT	TTGGAGACTT	AAAACCAAGT	TAATGGCTAA	GAATGGGTAA	CATGACTCTT	4440
80	GTGGATGAT	TATTTTGTG	TTGCAATGGG	GAATTTATAA	GAAGCATCAA	GTCTCTTTCT	4500
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Seq ID NO: 510 Protein sequence
Protein Accession #: BAB18461.1

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ETQFMNSNCPV AVTESTPRRR TRIQVFWIAP PAGTGCVILK ASIVQKRIIY PQDEGSLTKK 180
LCEQDSTFDG VTDKPIIDCC ACGTAKYRLT FYGNWSEKTH PKDYPRRANH WSAIIGGSHS 240
10 KNYVLNEYGG YASBGVKQVA ELGSPVKMEE EIRQOSDEVL TVIKAKAQWP AWQPLNVRAA 300
PSAEFSDVDT RHLMSFLTMQ GPSPDMNVGL SAEDLCTKEC GWVQKVQDL IPMDAGTDSG 360
VTYESPNKPT IPQEKIRPLT SLDHPQSPFY DPEGGSITQV ARVVIERIAR KGEQCNIVPD 420
NVDDIVADLA PERKDEDDTP ETCIYSNWSF WSACSSSTCD KGKRMQRML KAQLDLSVPC 480
PDTQDFQPCM GPGCSDSDGS TCTMSEWITW SPCSIOSGMS MRSRERYVKQ FPEDGSVCTL 540
15 PTEETEKCTV NEBCSPSSCL MTENGWDEC SATCGMGMKK RHRMIKNMFA DGSMDKAETS 600
QAEKOMPEC HTIPCLLSPW SEWSDCSVTC GKMRTRQRM LKSLAELGDC NEDLEQVEKC 660
MLPECPIDCE LTEMNQWSEC NKSCGKGHVI RTRMIQMEPQ FGGAPCPETV QRKRCRIRKC 720
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Seq ID NO: 511 DNA sequence
Nucleic Acid Accession #: NM_003108.1
Coding sequence: 76..1401

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30 CGGGAGGCGC TGGACACGGA GGAGGGCGAA TTCATGGCTT GCAGCCCGGT GGCCCTGGAC 180
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ATCCCGTTCA TCCGGGAGGC GGAGCGGCTG CGCTCAAGC ACATGGCCGA CTACCCCGAC 420
35 TACAAGTACC GGCCCGGAAA AAAGCCCAA ATGGACCCCT CGGCCAAGCC CAGCGCCAGC 480
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45 GAGGTGCGGG CCGGCGCGAC CTGCGGCGCC GGGGCGGGCA GCGGCTCTTA CTACAGCTTC 1020
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55 ATATTGATAA GATGTCGTGA CGCAAGGAAA TTGGAAGAAA TGATGAAAAT TTTGGTGGAG 1620
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AAAATGTGTT TTTGTAATTA CTATTTCTTT TTCTGAAAT TCGTGTATGC AACAAAGGCA 1800
GAGGGGGCGG CGCGGCGGAG GGGAGGTAGG ACCCGCTCCG GAAGGCGCTG TTTGAAGCTT 1860
60 GTCGCTCTTT GAAGTCTGGA AGACGCTCTG AGAGGACCCCT TTTGGCAGCA CAACCTGTAC 1920
TCTAGGAGT TGGTGAGAT ATTTTTTTTT CTTAAGAGAA CTTAAGAAC TGGTGATTTT 1980
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Seq ID NO: 512 Protein sequence
Protein Accession #: NP_003099.1

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KIERRKIMEQ SPDMHNAEIS KRLGKRWKML KDSEKIPFIR EAERLRLLKH ADYPDYKYRP 120
70 RKXPKMDPSA KPSASQSPER SAAGGGGSSA GGGAGGAKTS KGSKKCKGKL KAPAAAGAKA 180
GAGKAAQSGD YGGAGDDYVL GSLRVSGSGG GGAGKTVKVC FLDEDDDDDD DDELQLQLIK 240
QEPDEDEDEP PHQQLQPPG QQPQLLLRRY NVAKVPASPT LSSSAESPEG ASLYDEVVRAG 300
ATSGAGGGSR LYYSFKNITK QHPPLAQPA LSPASSRSVS TSSSSSSGSS SGSSGEDADD 360
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Seq ID NO: 513 DNA sequence
Nucleic Acid Accession #: CAT Cluster

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Seq ID NO: 514 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
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 TACAGGATTC TCTGGGTTGT ATTCCAGAA GTCTGGAGGT CATTTGGATA TTTGTGGGCC 180
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Seq ID NO: 515 DNA sequence
 Nucleic Acid Accession #: NM_012427
 Coding sequence: 43..924

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 AGGCCCAACC AGCTCTACTG CGGGGCGGTG TTGGTGATC CACAGTGGCT GCTCACGGCC 360
 GGGCACTGCA GGAAGAAAGT TTTGAGATC CGTCTCGGCC ACTACTCCCT GTCACCAAGT 420
 TATGAATCTG GGCAGCAGAT GTTCCAGGGG GTCAAAATCCA TCCCCACCC TGGCTACTCC 480
 CACCCCTGCC ACTCTAAAGA CCTCATGCTC ATCAAACTGA ACAGAAGAAT TCGTCCCACT 540
 AAGATGTCA GACCCATCAA CGTCTCTCT CATTTGCTCT CTGCTGGGAC AAAGTGTCTG 600
 GTGTCTGCTG GGGGACAAAC CAAGAGCCCC CAAGTGCACT TCCCTAAGGT CCTCCAGTGC 660
 TTGAATATCA GGTGTCTAAG TCAGAAAAGG TGCGAGGATG CTTACCCGAG ACAGATAGAT 720
 GACACCATGT TCTGCGCCGG TGACAAAAGCA GGTAGAGACT CCGTCCAGGG TGATTCTGGG 780
 GGGCCTGTGG TCTGCAATGG CTCCCTGCAG GGACTCGTGT CCTGGGGAGA TTACCTCTGT 840
 GCGCGGCCCA ACAGACCGGG TGTCTACAG AACCTCTGCA AGTTCAACAA GTGGATCCAG 900
 GAAACCATCC AGGCCAATCT CTGAGTCATC CCAGGACTCA GCACACCGGC ATCCCCACCT 960
 GCTGACGGGA CAGCCCTGAC ACTCCTTTCA GACCCCTCAT CTTCCCCAGA GATGTTGAGA 1020
 ATGTTTCTCT CTCCAGCCCC TGACCCCATG TCTCCTGGAC TCAGGGCTCTG CTTCCCCAC 1080
 ATTGGGCTGA CGTGTCTCT CTAGTTGAAC CCTGGGAACA ATTTCCAAAA CTGTCCAGGG 1140
 CGGGGGTGGC GTCTCAATCT CCCTGGGGCA CTTTCATCCT CAAGCTCAGG GCCCATCCCT 1200
 TCTCTGAGC TCTGACCCAA ATTTAGTCCC AGAAATAAAC TGAGAAGTGG AAAAAAATAA

Seq ID NO: 516 Protein sequence
 Protein Accession #: NP_036559

1 11 21 31 41 51
 MATARPPWMV VLCAITALL LGVTEHVLN NDVSCDHPSN TVPSGNSQDL GAGAGEDARS 60
 DDSSSRILNG SDQDMHTQFW QAALLLRPNQ LYCGAVLVHP QWLLTAHCR KKVPRVRLGH 120
 YLSLSPVYEG QQMPQGVKSI PHPGYSHPGH SNDLMLIKLN RRIRPTKQVR PINVSSHCPFS 180
 AGTKALVSWG GTTKSPQVHP PKVLQCLNIS VLSQKRCEDA YPRQIDDTMF CAGDKAGRDS 240
 CQDSDGGPVV CNGSLQLGLVS WGDYPCARPN RGVYTNLCK FTKWIQETIQ ANS

Seq ID NO: 517 DNA sequence
Nucleic Acid Accession #: NM_001719
Coding sequence: 123..1418

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5      1      11      21      31      41      51
|      |      |      |      |      |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACGGACGGCC GGGACGGCCG CCTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GSCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCGCACAGC CTTCGTGGCG CTCTGGGCAC 180
10    CCCTGTTCTT GCTGCGCTCC GCGCTGGCGG ACTTCAGCCT GGACACAGAG GTGCACTCGA 240
GCTTCATCCA CGCGCGCTTC CGCAGCCAGG AGCGCGCGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACTTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTCT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGCGG 420
GCCAGGGCTT CTCTACCCC TACAAGGCGG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
15    GCCTGCAAGA TAGCAATTC CTACCGAAG CGACATGGT CATGAGCTTC GTCAACCTCG 540
TTGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
TTTCCAGAGT CCCAGAAGGG GAAGCTGTCA CGGCAGCGGA ATTCCGATC TACAAGGACT 660
ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CGGTACCCTC TGGGCTCGG 780
20    AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACAGCAA CCACTGGGTG GTCAATCGCG 840
GGCACACCTT GGGCTTCGAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960
TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGAGGC AAACAGCGCA 1020
GCCAGAACCG CTCCTAACCG CCCAAGAACC AGGAAGCCCT CGGATGGCG AACGTGGCAG 1080
25    AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG OGCTGAAGG CTACGCGGCC TACTACTGTG 1200
AGGGGAGAGT TGCCCTTCCCT CTGAACCTCT ACATGAAGGC CACCAACACG GCATCGTGC 1260
AGACGCTGGT CCACCTCATC AACCCGGAAG CGGTGCCCAA GCCTGCTGT GCGCCACGCG 1320
AGCTCAATGC CATCTCGCTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
30    ACAGAAACAT GGTGGTCCGG GCGTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440
TTGGGGCCAA GTTTTTCCTG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCCTTTTG TGAGACCTTC CCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
35    TCCTACAAGC TGTGCAGGCA AAACCTAGCA GGAAGAAAAA ACAACGCATA AAGAAAAATG 1680
GCCGGGAGTG GGTATGGGCT GGGAAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
TTATGAGCGC CTACAGCCA GGCACCCAG CCGTGGGAGG AAGGGGCGGT GGCAAGGGGT 1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCGGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAAACG AATGAATG
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Seq ID NO: 518 Protein sequence
Protein Accession #: NP_001710

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45      1      11      21      31      41      51
|      |      |      |      |      |
MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRLRSQ RREMQRILS 60
ILGLPHRPRP HLQGGKNSAP MFMLDLYNAM AVEEGGGPGG QGFSPYKAV PSTQGPPLAS 120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREPRPDL SKIPEGEAVT AAEFRYKDY 180
IRERFDNETP RISVTVQLQE HLGRESDLFL LDSRTLWASE EGWLVPDITA TSNHWVNP 240
HNLGLQLSVE TLGGGQINPK LAGLIGRHGP QNKQPPMVAE PKATEVHFRS IRSTGSKQRS 300
50    QNRSKTPKQ EALRMANVAE NSSSDQRQAC KRHELYVSPR DLGWDWIIA PEGYAAYYCE 360
GECAFPLNSY MNATNHAIQV TLVHFNPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
RNMVVRACGC H
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Seq ID NO: 519 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 264..782

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60      1      11      21      31      41      51
|      |      |      |      |      |
CCCTGCTCCA GTCAACCCCG GAAGCTGACT GGTCCAAGCA CAGCTGAAGC ATGAGGAAAC 60
TCATCGCGGG ACTAATTTTC CTTAAATTT AGACTTGCAC AGTAAGGACT TCAACTGACC 120
TTCTTCAGAC TGAGAACTGT TTCCAGTATA TACATCAAGT CACTGAGATC TCCAGCACCC 180
TGCCGGTGGC ACTACTGAGA GACGAGGTGC CAGGGTGGTT CCTGAAAGTG CCTGAGCCCC 240
65    AACTTATCAG CAGGAGCTC ATCATGCTGA CAGAAGTCAT GGAGGTCTGG CATGGCTTAG 300
TGATCGCGGT GGTGTCCCTC TTCTGTCAGG CCTGCTTCTC CACCGCCATC AACTACCTGC 360
TCAGCAGGCA CATGGCCAC AAGAGTGAAC AGATACTGAA AGCGGCCAGT CTCCAGGTTT 420
CCAGGCCAGC CCTTGGCCAC CATCATCCAC CTGCTGTCAA AGAGATGAAG GAGACTCAGA 480
CAGAGAGAGA CATCCCAATG TCTGATTCCC TTACAGGCA TGACAGCGAC ACACCTCAG 540
70    ATAGCTTGA TAGCTCTGCG AGTTCGCTC CTGCTGCCA GGCCACAGAG GATGTGGATT 600
ACACACAAGT GCTCTTTTCT GACCTGGAG AACTAAAAAA TGACTCCCG CTGGAATATG 660
AGAACATAAA GGAATATACA GATTATGTCA ATGTCAATCC AGAAAGACAC AAGCCAGTT 720
TCTGTATTCT TGTCAACCTT GCTCTGTCTG AGCCAGCGGA ATATGATCAA GTGGCCATGT 780
GAATTCCAAA TAATTTTAAAT GGGGTCCAGT TCTCTATGGA TTCTTACATT TAAATTTTAG 840
75    GGAATGCCA TTTTTCCTCC TTAACAAGG CATGGGCTC ACAAGTCTAT GGAGACAGGC 900
CAAAAAGAT GTGAGAAGA AACTGATAA ATACACAGAG GTCCCTAAGA CCCATGGACT 960
CCTGGTCTGT ACCCAAAAAA GCTGTTGGTT CCTCAAAAAC AAAACAAGG CTTGGCTGGG 1020
AAAACAGGCC AATGCCCGG CAAGAAAGGT TGAGATCAGA TGTTAGGAAG AACTTTCAGG 1080
TAAAGTATGA GAATATGGA GTCCATCAGC AGAGATAGTA GTGAAGTCTC TCCCAGGGA 1140
80    AAATTTTAAA AAGGTTGAAT CAGCTGTGT AGAGTTCTAT TTGGCAATCT CATGGTTAAA 1200
TGACTTCCCT TTGAGCTCTT TAATTATTGG CAATAAACAA CTCTTTTAAA AGTTTATAAT 1260
AAAAATAGCA CACCAACA
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Seq ID NO: 520 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
 5 MLTEVMEVWH GLVIAVVSLE LQACFLTAIN YLLSRHMAHK SEQILKAASL QVPRPSPGH 60
 HPPAVKEMKE TQTRRDIPMS DSLYRHSDT PSDSLDSSCS SPPACQATED VDYTQVVFSD 120
 PGEKNDSP DYENIKIITD YVNVNPERHK PSFWYFVNPA LSEPARYDQV AM

Seq ID NO: 521 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 107..328

1 11 21 31 41 51
 15 CTGCTCTGTC TGAGCCAGCG GAATATGATC AAGTGGCCAT GTGAATTOCA AATATTTT 60
 ATGGGGTCCA GTTCTCTATG GATTCTTACA TTTAATTGT AGGGAATGC CATTTTTCCC 120
 CCTTAAACAA GGCATGGGGC TCACAAGTCT ATGGAGACAG GCCAAAAGA ATGTGGAGAA 180
 GAAACTGAT AAATACACAG AGGTCTCTCA GACCCATGGA CTCTGTGTCT GTACCCAAA 240
 AAGCTGTTCG TTCTCAAAA ACAAAAACAA GGCTTGGCTG GGAACACAGG CCAATGCCCC 300
 GGCAAGAAAG GTTGAGATCA GATGTTAGGA AGAACTTTCA GGTAAAGTAT GAGAAGTATG 360
 20 GAGTCCATCA GCAGAGATAG TAGTGAAGTC TCTCCCAGG GAAATTTTAA AAAAGGTTGA 420
 ATCAGCTGTT GTAGAGTTCT ATTTGGCAAT CTCATGGTAA AATGACTTCC CTTTGAGCTC 480
 TTTAATTATT GGCAATAAAC AACTTCTTAA AAAGTTTAA ATAAATAGC AACCACCACC 540
 A

Seq ID NO: 522 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51
 30 MPFFPLKQGM GLTSLWRQAK KNVEKKTDKY TEVLKTHGLL VCTQKSCSFL KNKNKAWLGK 60
 QANAPARKVE IRC

Seq ID NO: 523 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 211..1895

1 11 21 31 41 51
 40 GGATCTGAGG GGGGCCAGT CACTTCTCTC ACGTCTCTGT GCTGGGCGGG AGGAGCGSAT 60
 GGGGCTTGGG AGGCAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTTT TTGGGTGGGA 120
 GAGGAATTAT CTGATAAAAT TCCTGGGTTA ATATTTTAA AAACGGAGAG TTTTAAAAA 180
 TGATTTTTTT CCTCGAAAA TGACCTTTT ATGCTTCGAA GCAGTTTGTC AACCAGCATA 240
 GTGCTTTTTC TTTTCTCTTC TTTTCTACG ATAAATGAAA GCATTTCTTC AAGAAAAAGG 300
 45 CACAGGTTC TGAACAGCT GGATTCGTAT GGCACCATTA CTATAGAGGA GCAGATTGTC 360
 CTGTGTGTA AGCGAAAGT ACAATGTGAA CTCACATCA CAGCTCAACT CCAGGAGGGA 420
 GAAGGTAATT GTTCCCTGTA ATGGGATGGA CTCATTGTGT GGCCGAGAGG AACAGTGGGG 480
 AAAATATCGG CTGTTCATG CCTCCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540
 TTCCGACACT GTAACCCCA TGAACATGG GATTTTATGC ACAGCTTAAA TAAACATGG 600
 50 GCCAATTATT CAGACTGCTT TCGCTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA 660
 TTCTTTGAAC GCCTCTATGT AATGTATACC GTTGGCTACT CCATCTCTTT TGGTTCCTTG 720
 GCTGTGGCTA TTCTCATCTT TGGTACTTTC AGAGGATGTC ATTGCACTAG GAACTATATC 780
 CACATGCACT TATTTGTGTC TTTCTGCTG AGAGCTACAA GCATCTTTGT CAAAGACAGA 840
 GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900
 55 CAAAATTCOA TTGAGGCAAC TTCTGTGGAC AAATCACAAT ATATCGGGTG CAAGATTGCT 960
 GTTGTGATGT TTATTTACTT OCTGGCTACA AATTATTTAT GGAATCTGGT GGAAGGTCTC 1020
 TACCTGCATA ATCTCATCTT TGTGGCTTTC TTTTGGGACA CCAATAACCT GTGGGGCTTC 1080
 ATCTTGATAG GCTGGGGGTT TCCAGCAGCA TTTGTGCGAG CATGGGCTGT GGCACGAGCA 1140
 ACTCTGCGTG ATGCGAGGTG CTGGGAACCT AGTGTGCGAG ACATCAAGTG GATTATATCA 1200
 60 GCACCGATCT TAGCAGCTAT TGGGCTGAAT TTTATCTGT TTCTGAATAC GGTTAGAGTT 1260
 CTAGCTACCA AATCTGGGA GACCAATGCA GTTGGGCATG ACACAAGGAA GCAATACAGG 1320
 AAACGGCCA AATCGACACT GGTCTGTGTC CTAGTCTTTG GAGTGCAATTA CATGTGTTT 1380
 GTATGCTGTC CTCATCTCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440
 TTCTTCAACT CCTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500
 65 GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAATC TCTCGTGA CTGGAAGAG 1560
 ACACCGCAT GTGGCAGCCG CAGATGCGGC TCAGTGTCTA CCACCGTGAC GCACAGCACC 1620
 AGCAGCCAGT CACAGGTGGC GGCCAGCACA CGCATGTGTC TTATCTCTGG CAAAGCTGCC 1680
 AAGATCGCCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC 1740
 TCAGAGCAGG ACTGCTGCC ACACCTTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800
 70 CAGGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCCTA TGAATCTAA CACAGACACT 1860
 GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 524 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51
 75 MLRSSLSSTI VLFLFSSFSF INESISSRKR HRFLEQLDSD GTITIEBQIV LVLKAKVQCE 60
 LNITATLQEG EGNCFPEWDG LICNFRGTVG KISAVPCPPY IYDFNHRGVA FRHCNPNGTW 120
 DFMHSLNKTW ANYSDCLRFL QPDISIGKQE FFERLYVMYT VGYSSISFSL AVAILIIGYF 180
 80 RRLHCTNRYI EMLHLSFVFLM RATSIFVKDR VVHARIGVKE LESLIMQDDP QNSIATSVD 240
 KSYIIGCKIA VVMPIYFLAT NYWILVEGL YLEHLIFVAF PSDTKYLWGF ILIGWGFPA 300
 PVAANAVARA TLADARCWEL SAGDIKWIYQ APILAAIGLN FILPLNTRV LATKIWNENA 360
 VGHDTKRYR KLAKSTLVLV LVFGVHYIVF VCLPHSPTGL GWEIRMHCEL FPNFQGFV 420
 SIIYCYNGE VQAEVKMWS RKNLSVDWKR TPCCGSRRCG SVLTTVTHST SSQSQAAS 480

RMVLISGKAA KIASRQPDSDH ITPGYVWSN SEQDCLPHSF HEETKEDSGR QGDDILMEKP 540
SRPMESNPDT BGCQGETEDV L

Seq ID NO: 525 DNA sequence
Nucleic Acid Accession #: NM_005048
Coding sequence: 143..1795

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1      11      21      31      41      51
|      |      |      |      |      |
10  GGCCGGTGGC CCGGGCCCGA CCACCCAGC TCGCGTGTGT TACTGGCCAC AAGTTTGCTC 60
    TGGGCCAGCC AAGTTGGCAA CTGGGAAGCT TCTCCCGGCG TCTGGAGGAG GGTCCCTGCT 120
    TCTTCTTACA GCCGTTCCGG GCATGGCCGG GCTGGGGGGG TCGTCTCCAG TCTGGGGTTG 180
    GCTAATGTCT GGCAGCTGCC TCCTGGCCAG AGCCAGCTG GATTCTGATG GCACCAATTAC 240
    TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300
15  AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTTCCTGAA TGGGATGGAC TCATTGTGTG 360
    GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGTC CCTCCTTATA TTTATGACTT 420
    CAACCATATA GAGGTTGTCT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480
    CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTTCTGC AGCCAGATAT 540
    CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600
20  CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCATT GGTACTTCA GAGATTGCA 660
    TTGCATAGG AACTATATCC ACATGCACCT ATTTGTGTCT TTCATGCTGA GAGCTACAAG 720
    CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780
    AATAATGCAG GATGACCCAC AAAATTCCAT TGAGGCAACT TCTGTGACA AATCACAATA 840
    TATCGGGTGC AAGTAAGTCT TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG 900
25  GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTTCT TTTGGGACAC 960
    CAATATACCTG TGGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTTGCAGC 1020
    ATGGGCTGTG GCACGAGCAA CTCTGGCTGA TCGAGGTTGC TGGGAACCTA GTGCTGGAGA 1080
    CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140
    TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1200
30  CACAAGGAAG CAATACAGGA AACTGGCCAA ATGACACTG GTCTGTGCTC TAGTCTTTGG 1260
    AGTGCAATAC ATCGTGTTCG TATGCTCTGC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320
    CCGCATGCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGGT TTCTTTGTGT CTATCATCTA 1380
    CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440
    CTCGCTGGAC TGGAAAAGGA CACCGCCATG TGGCAGCGCG AGATGCGGCT CAGTGCTCAC 1500
35  CACCGTAGAG CACAGCAGCA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560
    TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACCTTACC 1620
    TGGCTATGCT TGGAGTAACT CAGAGCAGGA CTGCCTGCGA CACTCTTTCC ACGAGGAGAC 1680
    CAAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAGCCCTT CCAGGCCTAT 1740
    GGAATCTAAC CCAGACTCTG AAGGATGCCA AGGAGAAACT GAGGATGTTT TCTGAATGGA 1800
    CATTTGTGGC TGACTTTTAT GGGCTGTGTC AATGGCTGCT TGTGTGAGAG GGCTTGGCTG 1860
    ATACTCCTAT GCTTGAGTTC AAAGGCTGAA AATTCAAGTA AGGTGTACTT TAATAATAGT 1920
    TTTTAGGCTC CATGAATTGG CTCTGTGAAA TACTAACGAC ATGAAATATG AAGTGTCAAT 1980
    GGAGTAGTAT ATTACCTTCT ATTGGCATCA AGTTTTCTCT TAAATTAATG TATGATATT 2040
    GCTCTGTGAT TGTTCATTTT TTTCTGCTAC TTTTGGGTAG AAAAAGAGAT CAATTGCTTG 2100
    GCTGTAGCTT TCTCTCATAT ATATCACCTT AAATATAATG AAGATCTTTT AGTGTGTATC 2160
    ATTTTCTCTT TAGAACTAGT TATCTCTTCT TTTCTTACTT TAATGTACTT CTATCACTGC 2220
    ATTTATTTTG CCTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280
    GATCTAAGAA CAAGTACTTG CTGGAAAAAT AGTTGGCTCG ACATTGTATA AATAATGCAT 2340
    TTATAACAAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAAG AATATTTTAC 2400
50  ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC 2460
    TTCTTTGTAA ACCATGTCAT GTGAAAGAT TTCCTCAGTT AGTGAGCTTG TGTCTGCAAA 2520
    TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTCTCTTG 2580
    TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAAAAATTT GTTTTAAAAA 2640
    T

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Seq ID NO: 526 Protein sequence
Protein Accession #: NP_005039

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1      11      21      31      41      51
|      |      |      |      |      |
60  MAGLGASLHV GGNLMLGSLC LARAQLSDG TITIEEQIVL VLKAKVQCEL NITAOQEBGE 60
    GNCFFPEWDGL ICNPRGTGK ISAVPCPPYI YDFNHRGVAF RHCNPNGTWD FMHSLNKTWA 120
    NYSDCLRLPQ PDISIGKQEP FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYIH 180
    MHLFVFMRLR ATSIIFVKDRV VHAHIVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKLAV 240
    VMFIYFLATN YYNWLVEGLY LHNLIIVAFV SDTKYLNQPI LIGWGFPAAF VAAWAVARAT 300
    LADARCWELS AGDIKNIYQA PILAAIGLNP ILPLNTVRVL ATKIWEINAV GHDTRKQYRK 360
    LAKSTLVVLV VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFGGFVVS IYCYCNGEV 420
    QAEVKMWSR WNLVDWKRT PPGSRRCGS VLTVTHTSTS SQSQVAASR MVLISGKAAK 480
    IASRQPDSDH ITPGYVWSN SEQDCLPHSF HEETKEDSGR QGDDILMEKP 540
    SRPMESNPDT BGCQGETEDV L

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Seq ID NO: 527 DNA sequence
Nucleic Acid Accession #: XM_036683
Coding sequence: 38..3655

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1      11      21      31      41      51
|      |      |      |      |      |
75  GCTTTGCCCA GTAGTTGGAA AGTGAACCTG ACTCGTGATG GTTCTCCTGT CACTTTGGTT 60
    GATAGCAGCC GCTCTGTTAG AGGTTAGGAC TTCAGTGATG GGACAAGCTG GTAATGAAGA 120
    AATGGTGCAA ATAGATTTAC CAATAAAGAG ATATAGAGAG TATGAGCTGG TGAATCCAGT 180
    CAGCACAAAAT ATAGAAGGAC GCTATCTCTC CCATCTCTT TCTGCGAGTC ACAAAAGAG 240
    GTCAGCGAGG GACGTGTCTT CCAACCTGTA GCAGTTGTTC TTAAACATCA CGGCATTTGG 300
    AAAAGATTTT CATCTGGGAC TAAAGCCCAA CACTCAACTA GTAGCTCCTG GGGCTGTGT 360
    GGAGTGGCAT GAGACATCTC TGGTGCCTGG GAATATAACC GATCCCATTA ACAACCATCA 420

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	ACCAGGAAGT	GCTAOGTATA	GAATCOGGAA	AACAGAGCCT	TTGCAGACTA	ACTGTGCTTA	480
	TGTTGGTGAC	ATCGTGGACA	TTCCAGGAAC	CTCTGTTGCC	ATCAGCAACT	GTGATGGTCT	540
	GGCTGGGAAT	ATAAAAAGTG	ATAATGAAGA	GTATTTTCATT	GAACCCCTGG	AAAGAGGTAA	600
5	ACAGATGGAG	GAAGAAAAAG	GAAGGATTCA	TGTTGTCTAC	AAGAGATCAG	CTGTAGAACA	660
	GGCTCCCAT	GACATGTCCA	AAGACTTCCA	CTACAGAGAG	TGGACCTGG	AAGGCCTTGA	720
	TGATCTAGGT	ACTGTTTATG	GCAACATCCA	CCAGCAGCTG	AATGAAACAA	TGAGACGCG	780
	CAGACAGCG	GGAGAAAACG	ATTACAATAT	OGAGGTACTG	CTGGGAGTGG	ATGACTCTGT	840
	GGTCCGTTTC	CATGGCAAAG	AGCAGCTCCA	AACTACCTC	CTGACCTTAA	TGAACATTGT	900
10	GAATGAAAT	TACCATGATG	AGTCCCTCGG	AGTGATATA	AATGTGGTCC	TGGTGCAT	960
	GATAATGCTG	GGATATGCAA	AGTCCATCAG	CCTCATAGAA	AGGGGAAACC	CATCCAGAAG	1020
	CTGGGAGAT	GTGTGTGCT	GGGCGTCCA	ACAGCAAAGA	TCTGATCTCA	ACCACTCTGA	1080
	ACACCATGAC	CATGCAATTT	TTTTAACCCAG	GCAAGACTTT	GGACCTGCTG	GAATGCAAGG	1140
	ATATGCTCCA	GTCAACGGCA	TGTGTCTACC	AGTGAGAAAT	TGTACCTTGA	ATCATGAGGA	1200
15	TGGTTTTC	TCTGCTTTTG	TAGTAGCCCA	TGAAACGGGC	CATGTGTTGG	GAATGGAGCA	1260
	TGATGGACAA	GGCAACAGGT	GTGGTGTGTA	GACTGCTATG	GGAAGTGTCA	TGGCTCCCTT	1320
	GGTACAAGCA	GCATTCCATC	GTTACCACTG	GTCCCGATGC	AGTGGTCAAG	AACGTGAAAG	1380
	ATATATCCAT	GTCTATGACT	GTCTCCTTGA	TGACCTTTT	GATCATGATT	GGCCTAAACT	1440
	CCCAAGACTT	CCTGGAATCA	ATTATTTCTAT	GGATGAGCAA	TGTGTTTGG	ATTTTGGTGT	1500
20	TGGCTATAAA	AGGTATGACG	CGTTCCGAAC	CTTTGACCCA	TGTAAACAGC	TGTGGTGTAG	1560
	CCATCCTGAT	AATCCCTACT	TTTGTAAGAC	TAAAAGGGA	CCTCCACTTG	ATGGGACTGA	1620
	ATGTGCTGCT	GGAAAAATGT	GCTATAAGGG	TCATTGCAATG	TGGAAGAAATG	CTAATCAGCA	1680
	AAAAACAGAT	GGCAATTGGG	GGTCATGGAG	TAAATTTGGC	TCTGTCTC	GGACATGTGG	1740
	AACTGGTGT	CGTTTCAGAA	CACGCCAGTG	CAATAATCCC	ATGCCCATCA	ATGGTGGTCA	1800
25	GGATTGTCT	GGGTGTTAAT	TTGAGTACCA	GCTTTGTAA	ACAGAAAGAT	GCCAAACAA	1860
	CTTTGAGGAC	TTCAAGACAC	AGCAGTGCTA	GCAGOGAAAC	TCCCACTTTG	AATACCAGAA	1920
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30	CTGTGATAAA	GAAATTTGGT	CTAATAAGGT	TGAGGATAAG	TGTGGTGTCT	GTGGAGGAGA	2160
	TAATTTCCAC	TGCCGAACCG	TGAAGGGGAC	ATTTACCAGA	ACTCCAGGA	AGCTTGGGTA	2220
	CCTTAAGATG	TTTGATATAC	CCCTGGGGC	TAGACATGTG	TTAATCCAAG	AAGACGAGGC	2280
	TTCTCCTCAT	ATTCTTGCTA	TTAAGAACCA	GGCTACAGGC	CATTATATTT	TAAATGGCAA	2340
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	CTGGGTAGCA	GAAGAAATGG	AACACTGCAC	CAAAACCTGT	GGAAGTTCTG	GCTATCAGCT	2820
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Seq ID NO: 528 Protein sequence
Protein Accession #: XP_036683

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LNETMRRRH AGENDYNIEV LLGVDDSVVR FHGKEHVQNY LLTLMNIVNE IYHDESLGVH 300
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Seq ID NO: 529 DNA sequence
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Coding sequence: 246..980

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Seq ID NO: 530 Protein sequence
Protein Accession #: NP_002765

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LIQPLFLERD CSANFTSCHL LGWGTADGD PFDTIQAYI HLVSRECEH AYPGQITQNM 180
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Seq ID NO: 531 DNA sequence
Nucleic Acid Accession #: NM_012152
Coding sequence: 43..1104

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Seq ID NO: 532 Protein sequence

Protein Accession #: NP_036284

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LVIIVERHMS	IMRMVHSNL	TKKRVTLIL	LWVAIAPMG	AVPTLGNWCL	CNISACSSLA
PIYSRSLVFP	WTVSNLMAFL	IMVVVLYRIY	VYVKRKTINV	SPHTSGSISR	RRTPMKLMKT
VMTVLGAFVV	CNTPLGLVLL	LDGLNCRQCG	VQHVKKRWFL	LALLNSVNP	IYSYKDEDM
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Seq ID NO: 533 DNA sequence

Nucleic Acid Accession #: NM_002821

Coding sequence: 150..3362

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Seq ID NO: 534 Protein sequence

Protein Accession #: NP_002812

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| | | | |
MGAARGSPAR PRRLPLLVL LPLLLGGTQT AIVFIKQPS QDALQRRAL LRCEVEAPGP 60
VHVYLLDGA PQDTERREFA QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE EARSANASFN 120
IKWIEAGPVV LKHPASEAEI PQQTQVTLRC HIDGHPRTY QWFRDGTPLS DQSNHTVSS 180
KERNLTLRPA GPEHGLYSC CAHSAPQAC SSQNFLLSTA DESFARVULA PQDVVVARVE 240
EAMFHCQFSA QPPPSLQWLF EDETPIITNRS RPHLLRRATV FANGSLLLTQ VRPNAGIYR 300
CIGQQQRGPP ILEATLHLA EIEDMPLFEP RVPTAGSEER VTCLPPLKLP EPSVWWEHAG 360
VRLPTHGRVY QKGHELVLAN IAESDAGVYT CHAANLAGQR RQDVNITVAT VPSHLKKPQD 420
SQLLEGKFGY LDCLTQATPK PTVVWYRNQM LISEDSRFEV FKNGTLRINS VEVDGTWYR 480
CMSSTPAGSI EAQARQVLE KLKFTPPPQP QQCMFEDKEA TVPCSATGRE KPTIKWERAD 540
GSSLEFWTD NAGTLHFARV TRDDAGNYTC IASNGPOGQI RAHVQLTVAV FITFKVEPER 600
TTVYQGHATL LQCEAQGDPK PLIQWKGKDR ILDPKLGPR MHIFQNGSLV IHDVAPEDSG 660
RYTCIAGNSC NIKHTEAPLY VVDKFPVEES BPGSPPPFYK MIQTIGLSVG AAVAYIIAVL 720
GLMPYCKKRC KAKRLQKQPE GEPEMEBCLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN 780
KRHSTDKMHI FPRSLQPIIT TLGKSEFGEV FLAKAQGLEE GVAETLVLVK SLQTKDEQQQ 840
LDFRRELMF GKLNHANVVR LLGLCREAEP HYMWLEYVDL GDLKQFLRIS KSKDEKLKSK 900
PLSTKQKVAL CTQVALGMEH LSNRPFVHKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY 960
YHFRQAWPL RHMSPEALIE GDFSTKSDVN AFGVLMWEVF THGEMPHGGQ ADDEVLLADLQ 1020
AGKARLPQPE GCPSLYLRLM QRCWALSPKD RPSFSEIASA LGDSTVDSKP

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Seq ID NO: 535 DNA sequence

Nucleic Acid Accession #: NM_013952

Coding sequence: 161..1357

55
60
65
70
75
80

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1 11 21 31 41 51
| | | | |
TTCAGAAGGA GGAGAGACAC CGGGCCCAGG GCACCCCTGC GGGCGGGGCG ACCCAAGCAG 60
TGAGGGCCTG CAGCCGGCCG GCCAGGGCAG CGGCAGGCGC GGCCCGGACC TACGGGAGGA 120
AGCCCCGAGC CCTCGGCGGG CTGCGAGCGA CTCCCGGGCG ATGCCTCACA ACTCCATCAG 180
ATCTGCCCAT GGAGGCTGGA ACCAGCTGGG AGGGGCCCTT GTGAATGGCA GACCTCTGCC 240
GGAAGTGTCT CGCCAGCGCA TCGTAGACCT GGCCCAACCG GGTGTAAGGC CCTGCGACAT 300
CTCTCGCCAG CTCGCGGTCA GCCATGGCTG CGTCAGCAAG ATCCTTGGCA GGTACTACGA 360
GACTGGCAGC ATCCGGCCTG GAGTGATAGG GGGCTCCAAG CCAAGGTGG CCACCCCCAA 420
GGTGGTGGAG AAGATTGGGG ACTACAAAGC CCAGAACCTT ACCATGTTTG CTGGGAGAT 480
CCGAGACCGG CTCTGCTG AGGGCGTCTG TGACAATGAC ACTGTGCCCA GTGTCAGCTC 540
CATTAAATAGA ATCATCGGA CCAAGATGCA GCAACCATTC AACCTCCCTA TGGACAGCTG 600
CGTGGCCACC AAGTCCCTGA GTCCCGGACA CAOGCTGATC CCGAGCTCAG CTGTAACTCC 660
CCGGAGTCA CCCCAGTGG ATTCCCTGGG CTCCAACCTC TCCATCAATG GGCCTCTGGG 720
CATGCTCAG CTTGGCAGCG ACAAGAGGAA AATGGATGAC AGTGATCAGG ATAGCTGCGG 780
ACTAAGCAAT GACTCACAGA GCAGCAGCAG CGGACCCCGA AAGCACCTTC GCACGGATGC 840
CTTCAGCCAG CACCACTCG AGCCGCTGTA GTGCCATTT GAGCGGCAGC ACTACCCAGA 900
GGCCTATGCC TCCCCAGACC ACACCAAAGG CGAGCAGGGC CTCTACCCGC TGCCCTTGCT 960
CAACAGCACC CTGGAGCAGG GGAAGGCCAC CCTGACCCCT TCCACACGC CACTGGGGCG 1020
CAACCTCTCG ACTACACAGA CCTACCCCGT GGTGGCAGCT CGGCCCTTTT GGATCTGCA 1080
CAAGTCTGGT CCGGGGTCCC GCCCTTCAAT GCCTTTCCCC ATGCTGCTCT CGTGTAGGG 1140
CAGTTCACGG GCCAGGCCCT CCTCTCAGGG CGAGAGATGG TGGGGCCAC GCTGCCCGGA 1200
TACCCACCCC ACATCCCCAC CAGCGGACAG GGCAGCTATG CCTCTCTG CTGCGAGGC 1260
ATGGTGGCAG GAAGTGAATA CTCTGGCAAT GCCTATGGCC ACACCCCTTA CTCCTCTTAC 1320
AGCGAGGCCCT GGGGCTTCCC CAACTCCAGC TTGCTGAGTT CCCCATATTA TTACAGTTCC 1380
ACATCAAGGC CGAGTGACCC GCCCACCCTT GCCAGGCCCT TTGACCATCT GTAGTTGCCA 1440
TGGGGACAGT G

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Seq ID NO: 536 Protein sequence
Protein Accession #: NP_039246

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5      1      11      21      31      41      51
|      |      |      |      |      |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND 120
TVPSVSSINR IIRTKVQQPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
SINGLLGIAQ PGSDKRRMDD SDQDSCLRSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF 240
10 ERQHYPEAYA SPSHTKGEQG LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYFVVAA 300
PPFWICSKSA PGSRPSMPPF MLPPCTGSSR ARPSQGERW WGPCRCDTHP TSPPADRAAM 360
PPLPSQAWWQ EVNTLAMPMA TPPTPTPTARP GASPTPAC

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Seq ID NO: 537 DNA sequence
Nucleic Acid Accession #: NM_003466.1
Coding sequence: 11..1363

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20      1      11      21      31      41      51
|      |      |      |      |      |
GAATTCGGCG ATGCCTCACA ACTCCATCAG ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG 60
AGGGGCTTTT GTGAATGGCA GACCTCTGCC GGAAGTGGTC CGCCAGCGCA TCGTAGACCT 120
GGCCACCCAG GGTGTAAGGC CCTGCGACAT CTCTCGCCAG CTCGCGTCA GCCATGGTTG 180
CCTCAGCAAG ATCCTTGGCA GGTACTACGA GACTGGCAGC ATCCGGCCTG GAGTGATAGG 240
GGGCTCCAAG CCCAAGGTGG CCACCCCAAA GGTGGTGGAG AAGATTGGGG ACTACAAACG 300
25 CCAGAACCCT ACCATGTTTG CCTGGAGAT CCGAGACCGG CTCCTGGCTG AGGGCGTCTG 360
TGACAATGAC ACTGTGCCCA GTGTGAGCTC CATTAAATAGA ATCATCCGGA CCAAAGTGCA 420
GCAACCATTT AACCTCCCTA TGGACAGCTG CGTGGCCACC AAGTCCCTGA GTCCCGGACA 480
CAGCGTATGC CCGAGCTCAG CTGTAACCTC CCGGAGTCA CCCCAGTGG ATTCCCTGGG 540
CTCCACCTAC TCCATCAATG GGCTCCTGGG CATGCTCAG CTGGCAGCG ACAAGAGGAA 600
30 AATGGATGAC AGTGATCAGG ATAGCTGCCG ACTAAGCATT GACTCACAGA GCAGCAGCAG 660
CGGACCCCGA AAGCACCTTC GCACGGATGC CTTCAGCCAG CACCACCTCG AGCCGCTCGA 720
GTGCCCATTT GAGCGGCGAG ACTACCCAGA GGCTATGCTC TCCCCAGCC ACAACAAAGG 780
CGAGCAGGGC CTCTACCGCG TGCCCTTGCT CAACAGCACC CTGGACGAG GGAAGGCCAC 840
CCTGACCCCT TCCACACGCG CACTGGGGCG CAACCTCTCG ACTCACAGA CCTACCCCGT 900
35 GGTGGCAGAT CCTCACTCAC CCTTCGCCAT AAAGCAGGAA ACCCCGAGG TGTCCAGTTC 960
TAGCTCCACC CCTTCTCTCT TATCTAGCTC CGCTTTTGTG GATCTGCAGC AAGTCGGCTC 1020
CGGGTCCCGC CCCTTCAATG CCTTCCCA TGCTGCTCC GTGTACGGGC AGTTCAAGGG 1080
CCAGGCCCTC CTCTCAGGGC GAGAGATGGT GGGGCCACG CTGCCCGGAT ACCCACCCCA 1140
CATCCCCACC AGCGGACAGG GCAGCTATGC CTCTCTGCC ATCGCAGGCA TGGTGGCAGG 1200
40 AAGTGAATAC TGTGCAATG CCTATGGCCA CACCCCTTAC TCCTCTTACA GCGAGGCCGT 1260
GGCTTCCCCC AACTCCAGCT TGCTGAGTTC CCCATATTAT TACAGTTCCA CATCAAGGCC 1320
GAGTGACCG CCCACCATG CCACGGCCTT TGACCATCTG TAGTTGAAGC TT

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Seq ID NO: 538 Protein sequence
Protein Accession #: NP_003457

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50      1      11      21      31      41      51
|      |      |      |      |      |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND 120
TVPSVSSINR IIRTKVQQPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
SINGLLGIAQ PGSDKRRMDD SDQDSCLRSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF 240
ERQHYPEAYA SPSHTKGEQG LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYFVVAD 300
PHSPFAIKQE TPEVSSSSST PSSLSSSAFL DLQVVGSGVF PFNAFPHAAS VYGFQFTQAL 360
55 LSGREMGPT LPGYPPHPT SGQGSYASSA IAGMVAGSEY SGNAYGHTPY SSYSEAWRFP 420
NSSLLSSPHY YSSTRPSAP PTTATAPDHL

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Seq ID NO: 539 DNA sequence
Nucleic Acid Accession #: NM_006799
Coding sequence: 19..963

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65      1      11      21      31      41      51
|      |      |      |      |      |
GCGCGGGGAG AGGAGGCCAT GGGGCGGCGC GGGGCGCTGC TGCTGGGCT GCTGCTGGCT 60
CGGGCTGGAC TCAGGAAGCC GGAGTGCAG GAGGCGGCGC CGTTATCAGG ACCATGCGGC 120
CGACGGGTCA TCACGTCGCG CATGCTGGGT GGAGAGGACG CGSAACTCGG GCGTGGCCG 180
TGGCAGGGGA GCCTGCGCCT GTGGGATTCC CACGTATGCG GAGTGAGCCT GCTCAGCCAC 240
CGCTGGGCAC TCACGCGCGC GCACTGCTTT GAAACCTATA GTGACCTTAG TGATCCCTCC 300
GGGTGGATGG TCCAGTTTGG CCAGCTGACT TCCTATGCAT CCTTCTGAG CTTGAGGCC 360
70 TACTACACCC GTTACTTCGT ATCGAATATC TATCTGAGCC CTGCTAGCT GGGGAATTCA 420
CCCTATGACA TTGCTTGGT GAAGCTGTCT GCACCTGTCA CCTACACTAA ACACATCCAG 480
CCCATCTGTC TCCAGGCCTC CACATTTGAG TTTGAGAACC GGACAGACTG CTGGGTGACT 540
GGCTGGGGT ACATCAAGA GGAATGAGGA CTGCCATCTC OCCACACCT CCAGGAAGTT 600
CAGGTGCGCA TCATAACAA CTCTATGTGC AACCACTCT TCCTCAAGTA CAGTTTCCGC 660
75 AAGGACATCT TTGGAGACAT GGTTTGTGCT GGCATGCCC AAGGCGGGA GGTATGCTGC 720
TTGCGTGACT CAGGTGGACC CTGCGCTGT AACAGAATG GACTGTGTA TCAGATTGGA 780
GTGCTGAGCT GGGGAGTGGG CTGTGTCGG CCAATCGCG CCGGTGTCTA CACCAATATC 840
AGCCACCTG TTGAGTGGAT CCAGAAGCTG ATGGCCAGCA GTGGCATGTC CCAGCCAGAG 900
CCCTCTGGC CGCTACTCTT TTTCCCTCT CTCTGGGCTC TCCACTCCT GGGGCGGCTC 960
80 TGAGCCTACC TGAGCCCATG CAGCCTGGG CCACTGCCAA GTCAGGCCCT GGTCTCTCTC 1020
TGCTTGTGTT GGTAATAAAC ACATTCCAGT TGATGCTTG CAGGGCATTC TTCARAA

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Seq ID NO: 540 Protein sequence
Protein Accession #: NP_006790

1 11 21 31 41 51
5 MGARGALLLA LLLARAGLRK PESQEAAPLS GPCGRRVITS RIVGGEDAEL GRWPMQGSRLR 60
LMDSHVCGVS LLSHRNALTA AHCFETYSDL SDPSGWMVQF GQLTSMPSFW SLQAYYTRYF 120
VSNLYLSPRY LGNSPYDIAL VKLSAPVYTT KHIQPICLQA STPEFENRTD CWVTGWGYIK 180
EDEALSPHPT LQEVQVAIIN NSMCNHLFLK YSFRKIDIFGD MVCAGNAQGG KDACEFGDSGG 240
PLACNKNGLW YQIGVVSNGV CGGRPNRPGV YTNISHHFEW IQKLAQSGM SQPDPSWPLL 300
10 PFPLWALFL LGPV

Seq ID NO: 541 DNA sequence
Nucleic Acid Accession #: NM_014344
Coding sequence: 131..1444

1 11 21 31 41 51
15 GCGGCGCGGA TGGGGCCGAA GCGCCCGAAG CCGCGGAGCC CACAAACTGC CGGGCCCGCC 60
TCGCGCGCGG GACCCGGGTG CCTGGGCTCG GCTTGAAGCG GCGGCGCGCG ACCGGCACAG 120
CCGCGGGAGC ATGGGCAGGA GATGCGGGG CCGCGCGGCC ACCGCGGGGC TCTGGCTGCT 180
20 GCGCTGTGGC TCGCTGTGGG CGCTGTGGGG AGGGCTCCTG CCGCGCGGGA CCGAGCTGCC 240
CGCCTCCCGG CCGCCCGAAG ACCGACTCCC ACGGCGCCCG GCGCGGAGCG GCGGCCCGCG 300
GCGCGCGCCT CGCTTCCCTC TGCCCCCGCC CTTGGCGTGG GACGCCCGCG GCGGCTCCCT 360
GAAAACTTTC CGGGCGCTGC TCACCTCTGC GCGCGCGCGG GACGCCCGCG CCGGCGAGTC 420
CCGAGGAGAG CCGAGGTGGC ACGTGTGAGC CAGGCAGCCC CCGCGGAGG AGAGCGCGCG 480
25 GGTGCACGGG GCGCTCTTCT GGAGCGCGCG CTTGGAGGAG CAGGTGCCCC CGGGCTTTTC 540
GGAGGCCGAG GCGGCGCGGT GGCTGGAGGC GGCTCGCGCG GCGCGGATGG TGGCCCTGGA 600
GCGCGGGGTG TGCGGGCGCA GCTCCAACCG ACTGGCCCGT TTTGCCGACG GCACCGCGCG 660
CTGCGTGCAG TACGGCATCA ACCCGGAGCA GATTGAGGCG GAGGCCCTGT CTTACTATCT 720
GGCGCGCGCT GTGGGCTTCC AGCGCCACGT GCGCGCGCTG GCACTGGCTC GGTGGAGGCG 780
30 TCGGGCGCGG CAGTGGGCGC AGGTGCAGGA GGAGCTGCGC GCTGCGCACT GGACCGAGGG 840
CAGCGTGGTG AGCCTGACAC GCTGGCTGCC CAACCTCACG GACGTGGTGG TGCCCGCGCC 900
CTGCGCGTGC GAGGACCGCG GTCTGCGCCC CCTCGGGAT GCGGGGGGTG AGCTGGCCAA 960
CCTCAGCCAG CCGGAGCTGG TGGACCTAGT ACAATGGACC GACTTAATCC TTTTGGACTA 1020
CCTGACGCGC AACTTTCAGC GGCTGTAAAG CAACCTCTTC AGCCTGCAGT GGGACCGCGG 1080
35 CGTCATGCAG CGTGCCACCA GCAACTGCA CCGCGGTCCG GCGCGGGCGC TGGTCTTTCT 1140
GGACAATGAG GCGGGCTTGG TGCAAGGCTA CCGGGTAGCA GGCAATGTGG ACAAGTATAA 1200
CGAGCGCGCT TTGCAATGCA TGTGCGTGT TCGGAGGCGG ACCGCGCGCG GGTCTCTGGA 1260
GCTGCACCGC GGACAGGAGC CCGCGGGCGG GCTGCTGCGC CTCTACCGCG GOCACGAGCC 1320
40 TCGCTTCCCC GAGCTGGCGG CCCTTGCAGA CCCCCACGCT CAGCTGCTAC AGCGCGCGCT 1380
CGACTTCTCT GCCAAGCACA TTTTGCACGT TAAGGCCAAG TACGGCGCGC GGTCTGGGAC 1440
TTAGTGTGAC CCGGAGGAAA AGAGAGAGAT CTGGGGCTGG GGTATGGATG ATGGGGGGAA 1500
GGGCGGCTCG TCTTGCCTAG CTCAGGAGCC AGCCCGCCAA CGCCACCGCG CAAAGTGTCT 1560
TAAAACTTCT AGCTTTTCAC CCACTGCCCC CTTTCTTTCA ATCCACGCTC GTTTCCTTTC 1620
45 AAAGTTCTGG GAGGACGAAC TCACCGAGGC GAGAAAGTGA ACATTTCTCT CACCCAGCTT 1680
ATAAAAGGAT TCTTTACTGT GCCAGCACGG GGATTGGATC OGAAGAAACT GGCTACTGGG 1740
GTTTGGCCCC CGAGTGGCGG TCCCTGTGGG AGATGCACCC CATTTCTGGG CCCCCCTCAT 1800
TCCCTTTCCG AAAAAGGAAA ACTTGGCTTT GAGCGGTTGA GCTAATTCTG CAATTTTCTA 1860
CCAAACAGAG CGCTGGTGGC CCGGAGCAG GGCTGTGACA TTGGCTGGTG GAGCCCCCTC 1920
50 CTGTGTTCTC CTTTGTGTCC AGCGCGCGGA TGGTGAGATC ACTGTTCCAA GCAGGGGGAC 1980
GGCTCGCGAT AGGACAAAGA GAGCAGGACC TCCAGACTCT GGGGAGCCCT GCAGACCTTG 2040
ACAAATTTGCC TGACTCATTC CTGACCTCTT GTCAATTTGG CTTGAAGGCT ACAAAATCAG 2100
GGTACGCTGT ATGCACTAAG TCAATAATG AATTTCTTCC TCCCTCTGCG AACCGACCAA 2160
AATTTTGACA ACGATGATGT TCACCAGAAG GAAAAAATA TCAGTTTATG GCACCTTTAT 2220
55 TGTGTTTGAT TTTCAATTTT TATTAAGAAA AAATTTTATT TTACAGAATT TACCTTCTCT 2280
GTATATATGT GCATAAAGTG TGGTGTAAT ATACTAAACA AACTTATATT TCAATAAAG 2340
GGAGTTTAAA ATTTAAAAA AAAAAA

Seq ID NO: 542 Protein sequence
Protein Accession #: NP_055159

1 11 21 31 41 51
60 MGRMRGAA TAGLWLLALG SLLALWGGLL PPRTELPASR PPEDRLPRRP ARSGPAPAP 60
RFPLPPPLAW DARGGSLKTF RALLTLAAGA DGPPRQSRSE PRWHVSARQP RPESAABVHG 120
65 GVFWERGLEE QVPPGFSEAQ AAAMLEAARG ARMVALERGG CGRSSNRLAR FADGTRACVR 180
YGINPEQIQG EALSYYLALR LGLQRHVPL ALARVEARGA QMAQVQEELR AAHWTEGSSV 240
SLTRWLPNLT DUVVPAPWRS EDGRLRPLRD AGGELANLSQ AELVDLVQWT DLILFDYLT 300
NFDRLVSNLF SLQWDPVRVQ RATSNLHRGP GGALVFLDNE AGLVHGYRVA GMDKYNELP 360
70 LQSVCFRER TARRVLELHR GDAAAARLLR LYRREHPRFP ELAALADPHA QLLQRRDLFL 420
AKHILECKAK YGRRSGT

Seq ID NO: 543 DNA sequence
Nucleic Acid Accession #: XM_007652.4
Coding sequence: 1..1290

1 11 21 31 41 51
75 ATGGCGCGCT CTGGCGCGTG GAAGCGCCTC AAATCTATGC TAAGGAAGGA TGATGCGCGG 60
CTGTTTTTAA ATACACCCAG CGCCTTGGAC TTCTGGGATG AGGCGGGGGA CGAGGGGCTT 120
80 TCTCGGTTCA ACACACTTGG AGTTGTGGTG GCCGATGAGC GTTCCGAAGC CCGGAAAGG 180
CCTGTATACG GGGCGGACCC GACCTCCAG GCGGACGATG ATTCTTACT GGACCAAGAC 240
TTACCTTTGA CCAACAGTCA GCTGAGTTTG AAGGTGGACT CCTGTGACAA CTGCAGCAA 300
CAGAGAGAG TACTGAAGCA GAGAAAGGTG AAAGCCAGGT TGACCATTCG TGCGGTTCTG 360
TACTTGCTTT TATGATTGG AGAATCTGTA GGTGGATACA TTGCAATAG CTTAGCAATC 420

5 ATGACAGATG CACTTCATAT GTTAACTGAC CTAAGCGCCA TCATACTCAC CCTGCTTGCT 480
 TTGTGCTAT CATCAAAATC ACCAACCAAA AGATTCACTT TTGGATTTC TCGCTTAGAG 540
 GTTTTGTGAC CTATGATTAG TGTGCTGTTG GTGTATATAC TTATGGGATT CCTCTTATAT 600
 GAAGCTGTGC AAAGAATCAT CCATATGAAC TATGAAATAA ATGGAGATAT AATGCTCATC 660
 ACCGCGCTG TTGGAGTTGC AGTTAATGTA ATAATGGGCT TTCTGTTGAA CCAGTCTGGT 720
 CACGCTCACT CCCATTCCCA CTCCTGCCT TCAATTTCCC CTACCAGAGG TTCTGGGTGT 780
 GAACGTAAAC ATGGGCAGGA TAGCCTGGCA GTGAGAGCTG CATTGTGACA TGCTTTGGGA 840
 GATTTGGTAC AGAGTGTGTG TGTGCTAATA GCTGCATACA TCATACGATT CAAGCCAGAA 900
 10 TACAAGATTG CTGATCCCAT CTGTACATAC GTATTTTCAT TACTTGTGGC TTTTACAACA 960
 TTTGCAATCA TATGGGATAC AGTAGTTATA ATACTAGAAG GTGTGCCAAG CCATTTGAAT 1020
 GTAGACTATA TCAAGAAGC CTGTGATGAA ATAGAAGATG TATATTCACT CGAAGATTTA 1080
 AATATCTGGT CTCTCACTTC AGGAAAATCT ACTGCCATAG TTCACATACA GCTAATTCCT 1140
 GGAAGTTCAT CTAAATGGGA GGAAGTACAG TCCAAAGCAA ACCATTATT ATTGAACACA 1200
 15 TTTGGCATGT ATAGATGTAC TATTCAGCTT CAGAGTTACA GGCAAGAAGT GGACAGAACT 1260
 TGTGCAAAAT GTGAGAGTTC TAGTCCCTGA

Seq ID NO: 544 Protein sequence
 Protein Accession #: XP_007652.1

20 1 11 21 31 41 51
 MAGSGAWKRL KSMRLKDDAP LFLNDTSAPD FSDEAGDEGL SRFNKLRRVVV ADDGSEAPER 60
 PVNGAHPFLQ ADDSLLDQD LPLTNSQLSL KVDSCDNCCK QREILKQKRV KARLTIAAVL 120
 YLLFMIGELV GGYIANSGLAI MTDALHMLTD LSAIILTLA LMLSSKSPK RFTFGPHRLE 180
 25 VLSAMISVLL VYILMGPLYL EAVQRTIEMV YEINGDIMLI TAAVGVAVNV IMGFLNQSG 240
 KRHSHSLSLP SNSPTRGSGC ERNHQDLSLA VRAAFVHALG DLVQSVGVLI AAYIRFKPE 300
 YKIADPTCY VPSLLVAFPT PRIIWDTVVI ILEGVPSHLN VDYIKELMK IEDVSVEDL 360
 NIWSLTSGKS TAIVHIQLIP GSSSKWEEVQ SKANHELLNT FGMRYCTIQL QSYRQEVDR 420
 CANQSSSP

Seq ID NO: 545 DNA sequence
 Nucleic Acid Accession #: AB037765.1
 Coding sequence: 1..2478

35 1 11 21 31 41 51
 ATGTTTTCCG GCTTCAATGT CTTTAGAGTT GGGATCTCTT TTGTCATAAT GTGCATTTT 60
 TACATGCCAA CAGTAACTC TTTACCAGAA CTGAGTCCTC AGAAATATTT TAGTACATTG 120
 40 CAACCAGGAA AAGCCTCTTT AGCTTATTTT TGTCAGCTG ATTCCCAAG AACATCTGTA 180
 TTTCTTGAAG AACTGAATGA GGCTGTAGA CCTCTGAGG ACTATGGAAT TTCAGTTGCC 240
 AAGGTTAATT GTGTCAAAGA AGAAATATCA AGATACTGTG GAAAAGAAA GGATTTGATG 300
 AAAGCATATT TATTCAAGG CAACATATTG CTCAGAGAA TCCCTACTGA CACCTGTGTT 360
 GATGTGAATG CCATTGTGCG CCATGTTCTC TTTGCTCTTC TTTTATGTA AGTGAATAT 420
 ATTACCAACC TGAAGAGCCT TCAGAACATA GAAATGCTC TGAAGGAAA AGCAATATT 480
 45 ATATTCTCAT ATGTAAAGAG CATTGGAATA CCAGAGCACA GAGCAGTCAT GGAAGCGCT 540
 TTTGTGTATG GGACTACATA CCAATTGTTC TTAACCAAG AAATTGCCCT TTTGAAAAGT 600
 ATTGGCTCTG AGGATGTGGA ATATGCACAT CTCTACTTTT TTCAATGTAA ACTAGTCTTG 660
 GACTTGACCC AGCAATGTAG AAGAACAATA ATGGAACAGC CATTGACTAC ACTGAACATT 720
 50 CACCTGTTTA TTAAGACAAT GAAAGCACTC CTGTTGACTG AAGTTGCTGA AGATCCTCAA 780
 CAAGTTTCAA TATCTCATCT CCAACTGGGC TTACCACTGG TTTTATTGTT TATGCCAACG 840
 GCTACTTATG AAGCTGATAG AAGAAGTCGA GAATGGGTG CTGGCGTCT TCTGGGAAA 900
 GCAGAGTTTC TACTCTTGT AAGGACTCTT TTGGAAGTGA ACATTCTCTA AGATGCTAAT 960
 GTGGTCTTCA AAGAGCAGA AGAGGGAGTT CCAGTGGAA TTTTGGTATT ACATGATGTT 1020
 GATTTAATAA TATCTCATGT GGAATAAAT ATGCACATTG AGGAATACA AGAAGATGAA 1080
 55 GACAATGACA TGAAGAGTCC AGATATAGAT GTTCAGGATG ATGAAGTGGC AGAACTGTT 1140
 TTCAAGATA GGAAGAGAAA ATTACCTTTG GAACCTACAG TGAACCTAAC AGAAGAAA 1200
 TTTAATGCAA CAGTATGTC TTCTGACAG ATAGTACTCT TCTATGCTGG TTGGCAAGCA 1260
 GTATCCATGG CATTTTGTCA ATCCTATATT GATGTGGCAG TTAACCTGAA AGGCACATCT 1320
 60 ACTATGCTTC TTAAGTAAT AAAGTGTGCA GATTGCTCTG ATGTATGTAC TAAGCAAAAT 1380
 GTTACTGAA TTTCTATCAT AAAGATGTAC AAGAAAGGCG AGAACCCAGT ATCTATGCT 1440
 GGAATGTAG GAACCGAAGA TCTCTTAAAT TTTATCCAGC TCAACAGGAT TTCATATCCA 1500
 GTGAATATAA CATGATCCA AGAAGCAGAA GAATATTTAA GTGGGGAATT ATATAAGAC 1560
 CTCATCTTGT ATTCTAGTGT GTCAATATTG GGACTATTTA GTCCAACCAT GAAACAGCA 1620
 65 AAAGAAGATT TTAGTGAAGC AGGAACTAC CTAAAGGAT ATGTATCAC TGAATTTAT 1680
 TCTGAAGAAG ATGTTTTGCT ACTGTCAACC AAATATGCTG CAAGTCTTCC AGCCCTGCTG 1740
 CTGCGCAGAC ACACAGAAGG CAAATAGAG AGCATCCAC TAGCTAGCAC ACATGCACAA 1800
 GACATAGTTC AAATAATAAC AGATGCACTA CTGGAATGT TTTGGGAAAT CACTGTGGAA 1860
 70 AATCTTCCCA GTTATTTTCA ACTTCAGAAA CCATTATTGA TTTTGTTCAG TGATGGCACT 1920
 GTAAATCCTC AGTATAAAAA AGCAATATTG AACTGTTAA AGCAGAAATA CTTGGATTCA 1980
 TTTACTTCCAT GCTGGTTTAA TCTAAAGAA ACTCCAGTGG GGAGAGGAAT CTTGAGGGA 2040
 TATTTGATC CTCTGCTCTC CTCTCTCTCT CTGTGTTTGG TGAATCTGCA TTCAGGTGGC 2100
 CAAGTATTGG CATTTCTCTC AGACAGGCT ATAATTGAAG AAAACCTTGT ATTGTGGCTG 2160
 AAGAAATTTG AAGCAGGACT AGAAAATCAT ATCACAATT TACCTGTCTA AGAATGGAAA 2220
 75 CCTCTCTCTC CAGCTTATGA TTTTCTAAGT ATGATAGATG CCGCAACATC TCAACGTGGC 2280
 ACTAGGAAG TTCCCAAGTG TATGAAAGAA ACAGATGTGC AGGAGAATGA TAAGGAACAA 2340
 CATGAAGATA AATCGGCAGT CAGAAAAGAA CCGATTGAAA CTCTGAGAAT AAAGCATTGG 2400
 AATAGAAGTA ATTGGTTTAA AGAAGCAGAA AAATCATTTA GACGTGATAA AGAGTTAGGA 2460
 TGCTCAAAAG TGAACATA

Seq ID NO: 546 Protein sequence
 Protein Accession #: BAA92582.1

1 11 21 31 41 51
 | | | | |

5 MFSGFNVRV GISFVIMCIP YMPTVNSLFE LSPQKYFSTL QPGKASLAYF CQADSPTSIV 60
 FLEELNEAVR PIQDYGISVA KVMCVKEEIS RYCGKEKDIM KAYLFKGNIL LRBFPTDTLP 120
 DVNAIVAHVL FALLFSEVKY ITNLEDLQNI ENALKGKANI IPSYVRAIGI PEHRAVMEAA 180
 FVYGTYYQFV LTTRIALLES IGSEDVEYAH LYFFHCKLVL DLTOQCRRTL MEQPLTTINI 240
 HLPKTKMKAP LLTEVAEDPQ QVSTVHLQLG LPLVPIVSQQ ATYEADRRTA ESWAVRLLGK 300
 AGVLLLLRDS LEVNIPODAN VVFKRAEBSV PVEFLVLHDV DLIISHVENN MHIEIQEDE 360
 DNDMEGPDID VQDDEVAETV FRDRKRKLPL ELTVELTSET FNATVMASDS IVLFYAGWQA 420
 VSMAPLQSYI DVAVKLKQTS TMLLTRINCA DNSDVCTKQN VTEFPIIKMY KKGPNVSYA 480
 GMLGTEDLLK PIQLNRISYP VNITSIQEAE EYLSGELYKD LILYSSVSVL GLFSPTMKTA 540
 10 KEDFSEAGNY LKGVYITGIY SBEDVLLST KYAASLPALL LARHTGKIE SIFLASTHAQ 600
 DIVQIITDAL LEMFPEITVE NLPSYFRLQK PLLILFSDGT VNPQYKAIL TLVKQKYLDS 660
 FTPCWLNLKN TPVGRGILRA YFDPLPPLFL LVLVNLHSGG QVFAPPSDQA IIEENLVNL 720
 KKLEAGLENH ITILPAQEWK PPLPAYDFLS MIDAATSQRG TRKVPKCKE TDQVENDKEQ 780
 15 HEDKSAVRKE PIETLRKHW NRSNWFKEAE KSFRDRKELG CSKVN

Seq ID NO: 547 DNA sequence
 Nucleic Acid Accession #: NM_033102.1
 Coding sequence: 1..1662

20 1 11 21 31 41 51
 ATGGTCCAGA GGCTGTGGGT GAGCCGCGCTG CTGCGGCACC GGAAAGCCCA GCTCTGCTG 60
 GTCAACCTGC TAACCTTTGG CCTGGAGGTG TGTTTGGCCG CAGGCATCAC CTATGTGCG 120
 CCTCTGCTGC TGGAACTGGG GGTAGAGGAG AAGTTCATGA CCAATGGTCT GGCATTTGGT 180
 25 CCAGTGTGCG GCCTGGTCTG TGTCCCGCTC CTAGGCTCAG CCAAGTGACCA CTGGCGTGA 240
 GCCTATGGCC GCCGCGCGCC CTTCATCTGG GCACTGTCTT TGGGCATCTT GCTGAGCCTC 300
 TTTCTCATCC CAAGGGCGCG CTGGCTAGCA GGGCTGCTGT GCCCGGATCC CAGGCCCTG 360
 GAGCTGGCAC TGCTCATCTT GGGCGTGGG CTGCTGGACT TCTGTGGCCA GGTGTGCTTC 420
 ACTCCACTGG AGGCCCTGCT CTCTGACCTC TTCGGGACCC CGGACCACTG TCGCCAGGCC 480
 30 TACTCTGTCT ATGCCTTCAT GATCAGTCTT GGGGGCTGCC TGGGCTACCT CCTGCCCTGC 540
 ATTGACTGGG ACACCAAGTC CCTGGCCCCC TACCTGGGCA CCCAGGAGGA GTGCCTCTTT 600
 GGCCCTGCTA CCTCATCTTT CCTCACCTGC GTAGCAGCCA CACTGTCTGT GGCTGAGGAG 660
 GCAGCGCTGG GCCCACCGA GCCAGCAGAA GGGCTGTGG CCCCTCTCTT GTGCCCCAC 720
 TGCTGTCCAT GCCGGGCCCG CTGGGCTTTC CGGAACCTGG CGGCCCTGCT TCCCGGCTG 780
 35 CACCACTGCT GTGCGCGCAT GCCCGCACCC CTGCGCCGCG TCTTCGTGGC TGAGCTGTGC 840
 AGCTGGATGG CACTCATGAC CTTCACGCTG TTTTACACGG ATTTCTGTGG CGAGGGGCTG 900
 TACCAGGGCG TGCCAGAGC TGAGCGGGCG ACCGAGGCCC GGAGACACTA TGATGAAGGC 960
 GTTCGGATGG GCAGCTGGG GCTGTCTCTG CAGTGCSCCA TCTCCCTGGT CTCTCTCTG 1020
 40 GTCATGGACC GGCTGGTGA CGGATTCGGC ACTCGAGCAG TCTATTGGC CAGTGTGGCA 1080
 GCTTTCTACT TGGCTGCCGG TGCCACATGC CTGTCCACA GTGTGGCGGT GGTGACAGCT 1140
 TCAGCGGCC TCACCGGGTT CACCTTCTCA GCCCTGCAGA TCCTGCCCTA CACACTGGCC 1200
 TCCCTCTACC ACCGGGAGAA GCAGGTGTTT CTGCCAAAT ACCGAGGGA CACTGGAGGT 1260
 GCTAGCAGTG AGGACAGCCT GATGACCAGC TTCTGCGCAG GCCCTAAGCC TGGAGCTCCC 1320
 45 TTCCCTAATG GACAGTGGG TGCTGGAGG AGTGGCCTGC TCCCACTCC ACCCGGCTC 1380
 TGCGGGGCT CTGCGCTGTA GTCTCCGTA CGTGTGTGG TGGGTGAGCC CACCGAGGCC 1440
 AGGGTGGTTC CGGGCGGGG CATCTGCCTG GACCTCGCCA TCCTGGATAG TGCCTCTCTG 1500
 CTGTCCAGG TGGCCCATC CTTGTTATG GGCTCCATTG TCCAGCTCAG CCAGTCTGTC 1560
 ACTGCCTATA TGGTGTCTGC CGCAGGCGCT GGTCTGTGCG CCATTACTT TGCTACACAG 1620
 50 GTAGTATTGG ACAAGAGCGA CTGGGCCAAA TACTCAGCGT GA

Seq ID NO: 548 Protein sequence
 Protein Accession #: NP_149093.1

55 1 11 21 31 41 51
 MVQLRWVSL LRHRKAQLLL VMLTFGLEV CLAAGITYVP PLLLEVGVVE KFMIMVLGIG 60
 FVLGLVCVPL LGSASDHWRG RYGRRRPFIW ALSLGILLSL FLIPRAGWLA GLLCPDPRPL 120
 ELALLILGVG LLDPCQVQCP TPLEALLSDI FRDPDHCRQA YSVYAFMISL GGCLGYLLPA 180
 60 IDWDSALAP YLGTQEECLF GLLTLIFLTC VAATLLVAEE AALGPTFPAS GLSAPSLSPH 240
 CCPCLRALP RNLGALLPRL HQLCRMPRT LRLFLVAELC SWMALMTFTL FYTFVVEGL 300
 YQGVPRAEFG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFQ TRAVYLASVA 360
 AFPVARGATC LSHSVAVVTA SAALTGTFPS ALQILPYTLA SLYHREKQVF LPKYRGDTGG 420
 ASSEDSLMTS FLPGPKPGAP FPNGHVAGG SGLLPFPFAL CGASACDVSV RVVVEPTEA 480
 65 RVVPGRIGLC DLAILDSAFI LSQVAPSLFM GSIVQLSQSV TAYMVAAGL GLVRIYFATQ 540
 VVFDKSDLAK YSA

Seq ID NO: 549 DNA sequence
 Nucleic Acid Accession #: E05 sequence
 Coding sequence: 1..1389

70 1 11 21 31 41 51
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC COGCGCAGA GAGATTAGA TGACAGAGAA 60
 ACCCTTGTTT CTGAACATGA GTATAAGAG AAAACCTGTC AGTCTGTGTC TCTTTTAAAT 120
 75 GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTATTCAAT GAAGCAAGCT 180
 GGGTTTCTCT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTTACGGA CTTTCCCTT 240
 GTTTTATTGA TAAAGGAGG GGCCTCTCTT GGAAACAGATA CCTACCAATC TTTGGTCAAT 300
 AAAACTTTCG GCTTTCCAGG GTATCTGCTC CTCTCTGTTT TTCAGTTTGT GTATCTTTT 360
 80 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAGT TTTTCAAGA 420
 ATCCAGGAGG TTGATCTCTA AAACGTGTTT ATTTGGTCGC ACTTCATTAT TGGACTTTCC 480
 ACAGTTACCT TTAATCTGTC TTTATCTGTC TACCGAAATA TAGCAAGCT TGGAAAGGTC 540
 TCCTCATCT CTACAGGTTT AACAACTCTG ATTCTTGAA TTGTAATGGC AAGGGCAATT 600
 TCACTGGTTC CACACATACC AAAAACAGAA GACGCTGGG TATTGCAAA GCCCAATGCC 660
 ATCAAGCGG TCGGGGTTAT GTCCTTTTGA TTTATTTGCC ACCATAACTC CTCTCTAGTT 720

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TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780
GTGATTTCTG TATTTATCTG TATATTCITT GCTACATGTG GATACTTGAC ATTACTTGGC 840
TTCACCCAAG GGGACTTATT TGAAAATTAC TGCAGAAATG ATGACCTGGT AACATTGGGA 900
AGATTTTGGT ATGGTGTGAC TGTCATTTTG ACATACCCTA TGGAAATGCTT TGTGACAAGA 960
GAGGTAAATG CCAATGTGTT TTTTGGTGGG AATCTTTTCAT CGGTTTTCCTA CATTTGTGTA 1020
ACAGTAGTGG TCATCACTGT AGCCACGCTT GTGTCAATGC TGATTGATTG CCTCGGGATA 1080
GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATCAT TCCATCAGCC 1140
TGTTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200
ATGCTTCCCA TTTGGTCTGT GGTGATGGTT TTTGGATTGG TCATGGCTAT TACAAATACT 1260
CAAGACTGCA CCAATGGGCA GGAATGTTC TACTGCTTTC CTGACAAATT CTCTCTCACA 1320
AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACTTT CTACTTTAAA TATTAGTATC 1380
TTTCAATGA

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Seq ID NO: 550 Protein sequence
Protein Accession #: Eos sequence

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1 11 21 31 41 51
| | | | |
MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIIGSGI IGLPYSMKQA 60
GFPLGILLFL WVSYYTDFSL VLLIKGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYPP 120
IAMISYNIIA GDTLSKVFOR IPGVDPENVF IGRHFIIGLS TVTFTLPLSL YRNIAKLKGV 180
SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVFAKPNQ IQAVGVMSPA FICHHSNPLV 240
YSSLEETVA KWSRLHMSI VISVFICIFF ATCGYLTFTG FTQGDLPENY CRNDDLVTFG 300
RFCYGVTVIL TYMBCFVTR EVIANVFFGG NLSSVFHIVV TVMVTIVATL VSLLDCLGI 360
VLELNGVICA TPLIFIPSA CYLKLSEPR THSKIMSCV MLPIGAVMV FGFVMAITNT 420
QDCTHQEMF YCFPDNFSLT NTSSEHVQQT TQLSTLNISI FQ

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Seq ID NO: 551 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1284

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1 11 21 31 41 51
| | | | |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGAGGA GAGGATTGCC TTATTCAATG 60
AAGCAAGCTG GGTTCCTTTT GGAATATATG CTTTATTCCT GGTTCCTATA TGTACAGAC 120
TTTCCCTTGG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACAGCTCT 180
TTGGTCAATA AAATCTTCGG CTTTCAGGG TATCTGCTCC TCTCTGTTCT TCAGTTTTTG 240
TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGTACTTTT GAGCAAAAGT 300
TTTCAAGAAA TCCCAGGAGT TGATCCTGAA AACGTGTTTA TTGGTCGCCA CTTCAATTAT 360
GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCCTTGT ACOGAAATAT AGCAAAGCTT 420
GGAAAGGTCT CCCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGGAAAT TGTAATGGCA 480
AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAAG 540
CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTATTGGCCA CCATAACTCC 600
TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660
ATGTCATCAT TGATTTCTGT ATTTATCTGT ATATTCTTGT CTACATGTGG ATACTTGACA 720
TTTACTGGCT TCACCAAGG GGAATTATTT GAAATTAATG GCAGAAATGA TGACCTGGTA 780
ACATTGTGAA GATTTTGTGA TGGTGTCACT GTCAATTGGA CATACCTCAT GGAATGCTTT 840
GTGACAAAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTCATC GGTTTTCCAC 900
ATTGTTGTAA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCATTGCT GATTGATTGC 960
CTCGGAGTAG TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCTCTCAT TTTTATCATT 1020
CCATCGACCT GTTATCTGAA ACTGTCTGAA GAAACCAAGG CACACTCCGA TAAGATTATG 1080
TCTTGTGTC TACTTCCCAT TGGTGTCTGT GTGATGGTTT TTGATTGGT CATGGCTATT 1140
ACAAATCTC AAGACTGCAC CCATGGGCAG GAAATGTCT ACTGCTTTC TGACAAATTC 1200
TCTCTCACA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260
ATTAGTATCT TTCAACTCGA GTAA

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Seq ID NO: 552 Protein sequence
Protein Accession #: Eos sequence

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1 11 21 31 41 51
| | | | |
MGYQRQEPVI PPQRGLPYSM KQAGFPLGIL LLEFWVSYYTD FSLVLLIKGG ALSGTDYQS 60
LVNKTGFPFG YLLSVLQFL YPFIAMISYN IAGDTLSKV PQRIPGVDP E NVFGRHFII 120
GLSTVTFTLP LSLYRNIAKL GKVSLLSTGL TTLILGIVMA RAISLGP HIP KTEDAWVPAK 180
FNAIQAVGVN SFAPICHENS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT 240
FTGFTQGLDF ENYCRNDDL VTFGRFCYGV T VILTYMBCF VTREIVANV FFGNLSSVFH 300
IVVTVMVITV ATLVSLLDIC LGIVLELNGV LCATPLIPII PSACYLKLSE EPRTHSKIM 360
SCVMLPIGAV VMVFGFVMAI TMTQDCTHQQ EMFYCFPDNF SLNTSSEHV QQTTLSTLN 420
ISIFQLE

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Seq ID NO: 553 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1203

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1 11 21 31 41 51
| | | | |
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGAGT TTTCCCTTGT TTTATTGATA 60
AAAGGAGGGG CCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACTTTCCGC 120
TTTCCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTPTTTGT ATCCTTTTAT AGCAATGATA 180
AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAGTTT TCAAGAAGAT CCAAGGAGTT 240
GATCCTGAAA AGGTGTTTAT TGGTCCGCAC TTCAATTATG GACTTTCCAC AGTTACCTTT 300
ACTCTGCCTT TATCCTTGTA CGAAATATA GCAAGCTTGG GAAAGGTCTC CCTCATCTCT 360
ACAGGTTTAA CAACTCTGAT TCTTGGAAAT GTAATGGCAA GGGCAATTTT ACTGGGTCCA 420
CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAGC CCAATGCCAT TCAAGCGGTC 480

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GGGTTATGT CTTTGCATT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA 540
GAAGAACCCA CAGTAGCTAA GTGGTCCCGC CTATCCATA TGTCATCGT GATTTCTGTA 600
TTTATCTGTA TATCTTTGCG TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG 660
GACTTATTTG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTTGGAGG ATTTTGTATT 720
GGTGTCACTG TCATTTTGAC ATACCCATG GAATGCTTTG TGACAAGAGA GGTAAATGCC 780
AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTCCACA TTGTTGTAAC AGTGATGGTC 840
ATCACTGTAG CCACGCTTGT GTCAATTGCTG ATTGATTGCC TOGGGATAGT TCTAGAACTC 900
AATGGTGTGC TCTGTGCAAC TCCCCTCATT TTTATCATTC CATCAGCCTG TTATCTGAAA 960
CTGTCTGAAG AACCAAGGAC ACACCTCGAT AAGATTATGT CTGTGTGTCAT GCTTCCCAT 1020
GGTGTCTGGG TGATGGTTTT TGGATTGCTG ATGGCTATTA CAAATACTCA AGACTGCACC 1080
CATGGGCAAG AAATGTTCTA CTGCTTTCCT GACAATTCT CTCTCACAAA TACCTCAGAG 1140
TCTCATGTTC AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCACTCGAG 1200
TAA

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Seq ID NO: 554 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51

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MGYQRQBPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFFG FPGYLLLSVL QFLYPFIAMI 60
SYNIIAGDTL SKVQRIPIGV DPENVFIGRH FIIGLSTVTF TPLSLYRNI AKLGKVLIS 120
TGLTTLILGI VMARAIISLGP HIPKTEDAWV FAKPNAIQAV GVMSPAFICH HNSFLVYSSL 180
EPTVAKWSR LIHMSIVISV FICIFFATCG YLFTGTGFTQG DLFENYCRND DLVTFGRFCY 240
GVTILTYPM ECFVTREVI NVPFGNLS VPHIVVTMV ITVATLVSL IDCLGIVLEL 300
NGVLCAPLI FIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360
HGQEMFYCFP DNFSLTNTSE SHVQTTQLS TLNISIFQLE

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Seq ID NO: 555 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1140

1 11 21 31 41 51

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ATGGGCTACC AGAGGCAGGA GCGTGTCTC CCGCCGCGAG TCAATAAAAC TTTGGGCTTT 60
CCAGGGATAC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTTATAGC AATGATAAGT 120
TACATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180
CTGAAAACG TGTTTATGCG TGCCCACTTC ATTATGGAC TTCCACAGT TACCTTTACT 240
CTGCCCTTAT CCTGTACCG AAATATAGCA AAGCTTGGAA AGGTCCTCCCT CATCTCTACA 300
GGTTTAAACA CTCTGATTCT TGGAAATGTA ATGGCAAGGG CAATTTCAT GGGTCCACAC 360
ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATTCA AGCGGTCCGG 420
GTTATGTCTT TTGCAATTTT TTGCCACCAT AACTCTCTCT TAGTTTACAG TTCTCTAGAA 480
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATT 540
ATCTGTATAT TCTTGTCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660
GTCACTGTCA TTTTGACATA CCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
GTGTTTTTTG GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC 780
ACTGTAGCGA CCGTGTGTCT ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840
GGTGTGCTCT GTGCAACTCC CCTCATTTT ATCATTCAT CAGCCTGTTA TCTGAAACTG 900
TCTGAAGAAC CAAGGACACA CTCOGATAAG ATTATGTCTT GTGTCATGCT TCCCATTGGT 960
GCTGTGGTGA TGGTTTTTGG ATTCGTATG GCTATTACAA ATACTCAAGA CTCGACCCAT 1020
GGGAGGAAA TGTCTACTG CTTTCTGAC AATTCTCTCT TCACAATAC CTCAGAGTCT 1080
CATGTTTACG AGACACACA ACTTCTACT TTAAATATTA GTATCTTTCA ACTCGAGTAA

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Seq ID NO: 556 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51

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MGYQRQBPVI PPQVNKTFFG PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPIGV 60
PENVPFGRHF IIGLSTVTF TPLSLYRNI AKLGKVLIS GLTTLILGIV MARAIISLGP 120
IPKTEDAWV FAKPNAIQAV GVMSPAFICH NSFLVYSSLE EPTVAKWSR LIHMSIVISV 180
ICIFFATCGY LFTGTGTGQD LFNENYCRND LVTFGRFCY VTIILTYPM ECFVTREVI 240
VFPFGNLSV FHVIVVTMV ITVATLVSLI DCLGIVLELN GVLCATPLIF IIPSACYLKL 300
SEEPRTSDK IMSCVMLPI AVVMVFGFV AITNTQDCTE GQEMFYCFPD NFSLINTSES 360
HVQTTQLST LNISIFQLE

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Seq ID NO: 557 DNA sequence

Nucleic Acid Accession #: XM_057188.1

Coding sequence: 769..4269

1 11 21 31 41 51

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ATGGGATGCG CTCTCCCTCT CACTCTGGGC TTCTGTCCCA CTCTTATCTT AGTGTCACTC 60
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CTGCCCTTCC CCAATTCTT TGGTTTTTGC ATCCCCCTCT GCGCCCTGCC TCAGTCAAGT 180
CTCCCCCTGG TGCTCTCTCT CCCCCGCCCC GGACCTCTGC ACCCCCCAGG TCGTGTCCC 240
TCTGTCCCTT TATCGGGGCC TGGGACCGCG CCTCTCCCGG CCTCCCGCTT TGGCGTCTCC 300
AAGACTCCCC GCGCCCCAGA CCTCGCCCCG CCGCAGGCTA GCGTGGAAAG TGGAGGATCC 360
GGTTTCTCTT GGGCGGGTCT GGAAGCAGAG CCGCGGAGG GAGCGCGGG GCGCTGGGCT 420
GCAGGAGGTT GCGCGGCGCG CGGCAGCATG GTGGTCCGG AGAAGGAGCA GAGCTGGATC 480
CCCAAGATCT TCAAGAAGAA GACCTGCACG AGGTTCTATG TTGACTCCAC AGATCGGGG 540
GATGGGGTCT CGCTCTATTG CCCAGGCTGT TCTCAAACCT CTGGGCTCAA GCAGTCTCT 600
TGCTTGACCT TCCCAAAGTG CTTGGATTGT GCGCAGCGCT CCTTGAAGTT TTGCTCAGAA 660
GAGCAACTT TCTGGGAAGT AGCTGCAGGT GTTGAAGTA GCTGCAGGG AACTAGGGGA 720

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TTCAAGGATG GAGCTGAAAT GGGTGAACGG ACAAGTCCG TAAACTGAAT GGAGGATGCC 780
 TTCGGGGCAG CCGTGGTGAC CGTGTGGGAC AGCGATGCAC ACACCCAGGA GAAGCCCAACC 840
 GATGCCCTAG GAGAGCTGGA CTTACCGGG GCGGCGCGCA AGCAGACGAA TTTCCTCCGG 900
 CTCTCTGACC GAACGGATCC AGCTGCAGTT TATAGTCTGG TCACACGCAC ATGGGGCTTC 960
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 TTGGCGCGTG ACCCGGAGGA CCGGGTCCAG TTCCCTCGG ACTACAACTA CTGCGCCTTC 1320
 TTCTCGGTGG ACGAGCGCAC ACACGGCTGC CTGGGGGGGG AGAACCGCTT CCGCTTGGCG 1380
 CTGGAGTCTT ACATCTTACA GCAGAAGACG GCGGTGGGAG GAGCTGGAAT TGACATCCCT 1440
 GTCTGTCTCC TCTGTATTGA TGGTGTATGAG AAGATGTTGA CCGCAATAGA GAACGCCACC 1500
 CAGGCTCAGC TCCCATGTCT CCTCGTGGCT GGCTCAGGGG GAGCTGCGGA CTGCTGGCG 1560
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 AGGATTATGA CCCGGAAGGA GCTCCTGACA GTCTATTCTT CTGAGGATGG GTCTGAGGAA 1740
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 TACCTTGGATG ACCTGAGTGT GGCTGTGGCT TGGAAACCGG TGGACATGTG CCAGAGTGAA 1860
 CTCTTTCCGG GGGACATCCA ATGGCGGTCC TTCCATCTCG AAGCTTCCCT CATGGAAGCC 1920
 CTGCTGAATG ACGGCTGGA GTTCTGTGCG TTGCTCATTT CCCACGGCCT CAGCTTGGCC 1980
 CACTTCTGTA CCCGATGGG CCTGGCCCAA CTCTACAGCG CCGCGCCCTC CAACTCGCTC 2040
 ATCCGCAACC TTTTGGACCA GCGCTCCAC AGCGCAGGCA CCAAAGCCCC AGCCCTAAAA 2100
 GGGGAGCTCG CGGAGCTCGG GCGCCCTGAC GTGGGGCATG TGCTGAGGAT GCTGCTGGGG 2160
 AAGATGTGGG CGCGAGGTA CCGCTCCGGG GCGCGCTGGG ACCCTCACCC AGGCCAGGGC 2220
 TTCCGGGAGA GCATGTATCT GCTCTCGGAC AAGGCCACCT CGCGCTCTC GCTGGATGCT 2280
 GGCTCTGGCG AGGCCCTCTG GAGCGACCTG CTCTTTGGG CACTGTGCTG GAACAGGGCA 2340
 CAGATGGCCA TGTACTTCTG GGAGATGGGT TCCAAATGAG TTCTCTCAGC TCTTGGGGCC 2400
 TGTTTGCTCG TCCGGGTGAT GGCACGCGTG GAGCTGACG CTGAGGAGGC AGCAGCGAGG 2460
 AAAGACCTGG CGTTCAAGTT TGAGGGGATG GCGTTGACC TCTTTGGCGA GTGCTATGCG 2520
 AGCAGTGAGG TGAGGGCTGC CCGCTCTCTC CTCGCTCGCT GCGCGCTCTG GGGGGATGCC 2580
 ACTTGCCTCC AGCTGGGCTG GCAAGCTGAC GCGCGTGCTT TCTTTGCCCA GGATGGGGTA 2640
 CAGTCTCTCG TGACACAGAA GTGGTGGGGA GATATGGCCA GCACTACACC CATCTGGGCC 2700
 CTGGTTCTCG CCTTCTTTTG CCTCCACTC ATCTACACCC GCGCTATCAC CTTGAGGAAA 2760
 TCAGAAGAGG AGCCACACG GGAGGAGCTA GAGTTTGACA TGGATAGTGT CATTAAATGG 2820
 GAAGGGCGTG TCGGGAGCGG GAGCCAGACC GAGAAGACG CGCTGGGGGT CCGCGCCAG 2880
 TCGGGCGGTG CCGGTGTCTG CCGGGGCGCG TCGGGGGGGC GCGGTGCTCT ACGCGCTGG 2940
 TTCCACTTCT GGGGCGCGCC GGTGACCATC TTCTATGGGA AGTGGTCTG CTACCTGTCT 3000
 TTCTGTCTCG TTTCTGTGCG GGTGTGCTC GTGGATTCC AGCGCGCGCC CCGCGCTCC 3060
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 CTGAGCGGAG GCGGGGCGAG CCTCGCCAGC GGGGGGCCCG GCGCTGGCCA TGCTCTACTG 3180
 AGCCAGCGCC TGCGGCTCTA CCTCGCCGAC AGCTGGAACC AGTGGGACTT AGTGGCTCTC 3240
 ACCTGCTTCC TCCTGGGCGT GGGCTGCGCG CTGACCCCGG GTTGTATCCA CTTGGGCGCC 3300
 ACTGTCTCTT GCATCGACTT CATGTTTTC ACGGTGCGGC TGCTTCACAT CTTCAAGGTC 3360
 AACAAACAGG TGGGGGCCAA GATCGTCATC GTGAGCAAGA TGATGAAGGA CGTGTCTTTC 3420
 TTCTCTTCTT TCCTCGGCGT GTGGCTGGTA GCCTATGGCG TGGCCACGGA GGGGCTCCTG 3480
 AGGCCACGCG CAGTGTGCTT CCAAGTATC CTGCGCGCGG TCTTCTACCG TCCCTACCTG 3540
 CAGATCTTCC GGCAGATTCC CCAGGAGGAC ATGGAAGTGG CCTTCATGGA GCACAGCAAC 3600
 TGCTCGTCCG AGCCCGGCTT CTGGGCACAC CTCTCTGGGG CCCAGCGGGG CACCTGCGTC 3660
 TCCAGATGAG CCAACTGGCT GGTGGTGTCT CTCTCGTCA TCTTCTGCTC CGTGGCCAAC 3720
 ATCTGTCTCG TCAACTGTCT CATTGCCATG TTCAGTTACA CATTGCGCAA AGTACAGGGC 3780
 AACAGCTGAG TCTACTGGAA GCGGCGAGGT TACCGCTCA TCGGGGAATT CCACTCTCGG 3840
 CCGCGCTGCG CCGCGCCCTT TATCGTCATC TCCACTTGC GCGCTCTGCT CAGGCAATTG 3900
 TGCAGGCGAC CCGGAGCGCC CCAGCGGTCC TCCCGGGCCC TCGAGCATTT CCGGGTTTAC 3960
 TTTTCTAAGG AAGCGGAGCG GAAGCTGCTA ACGTGGGAAT CGGTGCATAA GGAGAACTTT 4020
 CTGCTGCGAC CGGCTAGGGA CAGCGGGAG AGCGACTCCG AGCGTCTGAA GCGCAGCTCC 4080
 CAGAAGTGG ACTTGGCACT GAAACAGCTG GGACACATCC GCGAGTACGA ACAGCGCTG 4140
 AAAGTGTGAG AGCGGGAGGT CCAGCAGTGT AGCCGCGTCC TGGGTGGGT GGGCGAGGCC 4200
 CTGAGCGCTG CTGCTGTGCT GCGCCAGGT GGGCGCGCAC CCGCTGACCT GCGTGGGTCC 4260
 AAAGACTGAG CCGCTGTGGC GCACTTCAAG GAGAAGCCCC CACAGGGGAT TTTGCTCTTA 4320
 GAGTAAGCTT CATCTGGGCC TCGGCCCCCG CACCTGGTGG CTTGTCTCTT GAGGTGAGCC 4380
 CCATGTCCAT CTGGGCCACT GTGAGGACCA CTTTGGGAG TGTCATCTTT ACAAACCACA 4440
 GCATGCCCGT TCTCTCCAG AACCACTCCC AGCCTGGGAG GATCAAGGCC TGGATCCCGG 4500
 GCGTTATACC ATCTGGAGGC TGCAGGCTCC TTGGGGTAAC AGGGAACACA GACCCCTCAC 4560
 CACTCACAGA TTCTTCACAC TGGGGAATAA AAGCATTTC AGAGGAAAAA AAAAAAAA 4620
 AAAAAAAAAA AAAAAAAAAA A

Seq ID NO: 558 Protein sequence
 Protein Accession #: XP_057188.1

70
 75
 80

1 11 21 31 41 51
 MEDAFGAIV TVVDSAHHT EKPTDAYGEL DFTGAGRKHS NFLRLSDRTD PAAVYSLVTR 60
 TWGFRAPNLV VSVLGGSGGP VLQTLWLDLL RRLVRAAQS TGAWIVTGGL HTGIGRHVGV 120
 AVRHDQMAST GGTKVVMGV APWGVVRNRD TLINPKGSFP ARYRMWDPE DGVQFPLDYN 180
 YSAFFLVDDG THGCLGGENR FRLRLSEYIS QKKTGVGGTG IDIPVLLLLL DGDEKMLTRI 240
 ENATQAQLPC LLVAGSGGAA DCLAEFTLED LAPSGGARQ GEARDRIRRF FPGDLEVLQ 300
 AQVERIMTRK ELLTVYSSD GSEEFETIVL KALVKACGSS EASAYLDEL R LAVAMNRVDI 360
 AQSELFRGDI QWRSHFLEAS LMDALLNDRP EFRVLLISHG LSLGHFLTPM RLALYLSAAP 420
 SNLIRNLID QASHSAGTKA PALKGAAREL RPPDVGHVLR MLLGKMCAPR YPSGGANDPH 480
 PGQGGESMY LLSDKATSPL SLDAGLGQAP WSDLLWALL LNRAQMAMF WEMGSNAVSS 540
 ALGACILLRV MARLEPDAEE AARRKDLAFK FEGMGVLDLF ECRYSSEVRA ARLLLRRCPL 600
 WGDATCLQLA MQADARAPFA QDGVQSLLTQ KMWGDMASTT PINALVLAF CPFLIYTLI 660
 TFRKSEEP RELEFDMD VINGEGPVGT ADPAEKTPLG VPRQSGRPGC CGRCGGRRC 720

5 LRRWFHFWGA PVTIFMGNV SYLLFLLLF S RVLVDFQPA PPGSLELLLY FWAFTLLCEE 780
LRQGLSGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY 840
HLGRTVLICID FMVPTVRLH IPTVNRQLQP KIVIVSKMK DVFFLFPLG VMLVAYGVT 900
EGLLRPRDS PPSILRRVY RPYLQIFQI PQEDMDVALM EHSNCSSEPO FWAHPGGAQA 960
GTCVSOYANW LVVLLLVIFL LVANILLVNL LIAMFSYTFG KVQGNSDLYN KAQRYELIRE 1020
FHSRFPALAP FIVISHLRL LRQLCRRPRS PQSSPALEH FRVYLSKBAE RKLLTWESVH 1080
KENFLARAR DKRESOSERL KRTSQKVDLA LKQLGHIREY EQRLKVLERE VQCSRVLGW 1140
VAELSRSL LPPGPPPPD LPSKD

10 Seq ID NO: 559 DNA sequence
Nucleic Acid Accession #: NM_006853.1
Coding sequence: 26..874

15 1 11 21 31 41 51
AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTGAGG TGGCTGGGG ACTGGAAGTC 60
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CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC 180
CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCAG CCCTGGCAGG CAGCCCTGTT 240
20 CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCAGATGGC TCCTGACAGC 300
AGCCACTGC CTCAGAGCCC GCTACATAGT TCACCTGGGG CAGCACAAAC TCAGAAGGA 360
GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCCACCCCG GCTTCAACAA 420
CAGCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT 480
CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCCTCA CGCTGTGTCA CTGCTGGCAC 540
25 CAGCTGCCTC ATTTCCGGCT GGGGCAGCAC GTCCAGCCCC CAGTTACGCC TGCTTCAAC 600
CTTGCGATGC GCCAACATCA CCATCATGGA GCACCAAGG TGTGAGAAGC CCTACCCCGG 660
CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAAGAA GGGGGCAAGG ACTCTGCCA 720
GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CAGTCTCTT CAAGGCATTA TCTCTGGGG 780
30 CCAGGATCCG TGTGCGATCA CCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAATATATG 840
GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900
ACCTCCATT TCCACTTGGT GTTTGGTTCC TGTCACTCT GTTAATAAGA AACCTAAGC 960
CAAGACCTTC TACGAACATT CTTTGGGCTC CTGGAGTAC AGGAGATGCT GTCACTTAAT 1020
AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT 1080
35 GACTCTGGGA ATGACAACAC CTGGTTTGT CTCTGTGTGA TCCCCAGCCC CAAAGACAGC 1140
TCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

Seq ID NO: 560 Protein sequence
Protein Accession #: NP_006844.1

40 1 11 21 31 41 51
MRILQLILLA LATGLVGGET RIIKGFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA 60
ARCLKPRYIV HLGQRNLQKE EGCEQTRTAT ESFPHGPFNN SLPNKDHRND IMLVKMASPV 120
SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIE HQKCEWAYPV 180
45 NITDTMVCAS VQEGGKDSQ GDSGGPLVCN QSLQGIISWG QDPCAIRKP GVTYTKVCKV 240
DWIQETMKNN

50 Seq ID NO: 561 DNA sequence
Nucleic Acid Accession #: AY046419.1
Coding sequence: 1..1743

55 1 11 21 31 41 51
ATGTTTACCT TCCTGTCATC TGTCAGTCT GCTGTCACTG GCCCTCTGGT GGGTTATGAA 60
CTTGGGATCA TCTCTGGGGC TCTTCTTCAG ATCAAAACCT TATTAGCCCT GAGCTGCCAT 120
GAGCAGGAAA TGGTGTGAG CTCCTCTGTC ATTGAGAGCC TCCTTGCTTC ACTCACCGGA 180
GGGGTCTGTA TAGACAGATA TGAAGAAGG ACAGCAATCA TCTGTGATC CTGCTGCTT 240
60 GGACTCGGAA GCTTAGTCTT GATCCTCAGT TTATCCTACA CGGTCTTAT AGTGGGACGC 300
ATTGCCATAG GGGTTTCCAT CTCCTCTCT TCCATTGCCA CTGTGTGTTA CATGCGAGAG 360
ATTGCTCCTC AACACAGAAG AGGCCCTTCT GTGTCACTGA ATGAGCTGAT GATTGTATC 420
GGCATTCTTT CTGCCTATAT TTCAAATTAC GCATTGCCA ATGTTTCCA TGGCTGGAAG 480
TACATGTTTG GTCTGTGAT TCCTTGCGGA GTTTTGCAAG CAATTGCAAT GTATTTTCTT 540
CCTCCAAGCC CTCGGTTTCT GGTGATGAAA GGACAGAGG GAGCTGCTAG CAAGGTTCTT 600
65 GGAAGGTGAA GAGCACTCTC AGATACAAC TGGGAACTCA CTGTGATCAA ATCTCTCCTG 660
AAAGATGAAT ATCAGTACAG TTTTGGGAT CTGTTTCGTT CAAAAGACAA CATGCGGACC 720
CGAATAATGA TAGGACTAAC ACTAGTATTT TTTGTACAAA TCACTGGCCA ACCAAACATA 780
TTGTTCTATG CATCAACTGT TTTGAAGTCA GTTGGAITTC AAAGCAATGA GGCAGCTAGC 840
CTCGCTCCA CTGGGGTTGG AGTGTGCAAG GTCATTAGCA CCATCCCTGC CACTCTTCTT 900
70 TTGAGACATG TGGGCAAGAA AACATCTCT TGCATTGGCT CCTCTGTGAT GGCAGCTTGG 960
TTGGTGACCA TGGGCATCGT AAATCTCAAC ATCCACATGA ACTTCACCCA TATCTGCAGA 1020
AGCCACAATT CTATCAACCA GTCTCTGAT GAGTCTGTGA TTTATGGACC AGGAAACCTG 1080
TCAACCAACA ACAATACTCT CAGAGACCAC TTCAAAGGGA TTTCTTCCCA TAGCAGAAGC 1140
TCACTCATGC CCCTGAGAAA TGATGTGGAT AAGAGAGGGG AGACGACCTC AGCATCTCTG 1200
75 CTAATATGCT GATTAGGCCA CACTGAATAC CAGATAGTCA CAGACCCCTG GGCAGTCCCA 1260
GCTTTTTTGA AATGGCTGTC CTTAGCCAGC TTGCTTGTAT ATGTGTGCTG TTTTCAATT 1320
GGTCTAGGAC CAATGCCCTG GCTGGTCTC AGCGAGATCT TTCCTGTGTG GATCAGAGGA 1380
CGAGCCATGG CTTTAACTTC TAGCATGAAC TGGGGCATCA ATCTCTCAT CTGCTGACA 1440
80 TTTTGTAGCT TACTGATCT TATTGGCCTG CCATGGGTGT GCTTTATATA TACATCATG 1500
AGTCTAGCAT CCCTGCTTTT TGTGTTATG TTTATACCTG AGACAAAGGG ATGCTCTTTG 1560
GAACAAATAT CAATGGAGCT AGCAAAAGTG AACTATGTGA AAAACAACAT TTGTTTATG 1620
AGTCATCACC AAGAAGAATT AGTGCCAAA CAGCTCAAA AAAGAAAACC CCAGGAGCAG 1680
CTCTGGAGT GTAACAGCT GTGTGTGAGG GGCCATCCA GGCAGCTTC TCCAGAGACC 1740
TAA

Seq ID NO: 562 Protein sequence
Protein Accession #: AAL02327.1

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5      1      11      21      31      41      51
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MFTFLSSVTA AVSGLLVGYE LGIISGALLQ IKTLLALSCH EQEMVSSSLV IGALLASLTG 60
GVLIDRYGRR TAILSSCLL GLGSLVLILS LSYTVLIVGR IAIGVISISLS SIATCVYIAB 120
IAPQHRRLGL VSLNMLMIVI GILSAYISNY AFANVFHGWK YMFGLVPLG VLQAIAMYFL 180
PPSPRFLVMK QGEGAASKVL GRLRALSDTT EELTVIKSSL KDEYQYSFWD LFRSKDNMRT 240
10 RIMIGLTLVF FVQITGQPNL LFYASTVLKS VGFQSNAAAS LASTGVGVVK VISTIPTALL 300
VDHVGSKTFL CIGSSVMAAS LVTMGIVNLN IHMFTHICR SHNSINQSLD ESVIYGPGLN 360
STNNNTLRDH PKGISSSHRS SLMLPLRNDVD KRGETTSASL LNAGLSHTEY QIVTDPGDVP 420
AFLKWLSLAS LLVYVAAPSI GLGPMPLVLV SEIPPGGIRG RAMALTSSMN WGINLLISLT 480
15 FLTVTDLIGL PWVCFIYTIM SLASLLFVVM FIPETKGCSE EQISMELAKV NYVKNNICFM 540
SHHQEELVPK QPQKRKPQEQ LLECNKLCGR GQSRQLSPET

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Seq ID NO: 563 DNA sequence
Nucleic Acid Accession #: XM_059466.1
Coding sequence: 1..894

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20      1      11      21      31      41      51
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ATGGAGCCGC GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCCTGTG CTCCTCGGGG 60
CTGCTCGTCA CGGCCATCTT CACCGACCAC TGGTAAGAGA CCGACCCCGG GCGCCACAAG 120
25 GAGAGCTGCG AGCGCAGCCG CGCGGGCGCC GACCCCGCGG ACCAGAAGAA CCGCCTGATG 180
CGCTGTGCGC ACCTGCGGCT GCGGGACTCG CCCCCTGCGG GCGSCCGGCT GCTCCCGGGC 240
GGCCCGGGCG GCGCGGACCC CGAGTCCTGG CGCTCGCTCC TGGGGCTCGG CCGGCTGGAC 300
GCCGAGTGCG GCGCGCCCTT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGTACTTTC 360
CTGGGAGTGC ACCGGGACAT CGACACCTTC ATCTGAAAG GTATTGCGCA GCGATGCAAG 420
30 GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGCGAA ACATTCCTTT TAATTAAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCATTTAA GAAGAATCAC TGCTGGCTTC 540
CTCGCATGCG CGGTAGCCGT CCTTCTCTGC GGTGTCATTG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGAATCTGTT TCCTCATGAC AGGGATATT 660
TGCACCATTT CCCTCTGTAC TTATGCGGCC AGTATCTGTT ATGATTGAA CCGGCTCCCA 720
35 AAGCTAATTT ATAGCTGCC TGCTGATGTG GAACATGGTT ACAGCTGGTC CATCTTTTGC 780
GCCTGGTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCGGTTT 840
ATTAGCGGGA CCAAGATTGC ACAGCTAAG TCTGGCAGAG ACTCCACGGT ATGA

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Seq ID NO: 564 Protein sequence
Protein Accession #: XP_059466.1

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40      1      11      21      31      41      51
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45 PLSHLPLRDS PPLGRRLLPF GPGRADPESW RSLGLGLGLD AECGRPLFAT YSGLWRKCYF 120
LGIDRIDITL ILKGIAQCT AIKYHFSQPI RLNRNIPNLT KTIQDEWHL LHLRRITAGF 180
LGMVAVALLC GCIVATVSFF WEBSLTQHVA GLLFLMTGIF CTISLCTYAA SISYDLNRLP 240
KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISR7KIAQLK SGRDSTV

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Seq ID NO: 565 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3315

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55      1      11      21      31      41      51
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ACCCGAGACC TGTACTCCAG CGCGTCTCGG AGCAGAGACT TGTCTTACAG TGAAGCGCAC 120
TTGGTGAATT TTATTCAAGC AAATTTTAAG AAACGAGAAT GTGTCTTCTT TACCAAAGAT 180
TCCAAGGCCA CGGAGATGTT GTGCAAGTGT GGCTATGCCC AGAGCCAGCA CATGGAAGGC 240
60 ACCCAGATCA ACCAAAGTGA GAAATGGAAC TACAAGAAAC ACACCAAGGA ATTTCTTACC 300
GAGCGCTTTG GGGATATTCA GTTTGAGACA CTGGGGAAGA AAGGGAAGTA TATACGTCTG 360
TCTCTGCGAC CGACGCGGGA AATCCTTTAC GAGCTGCTGA CCCAGCACTG GCACCTGAAG 420
ACACCCAAAC TGGTCAATTC TGTGACCGGG GCGGCCAAGA ACTTCGCCCT GAAGCGCGGC 480
ATGCGCAAGA TCTTCAGCCG GCTCATCTAC ATCGCGCAGT CCAAGAGTGC TTGGATTCTC 540
65 ACGGGAGGCA CCCATTATGG CCTGATGAAG TACATCGGGG AGGTGCTGAG AGATAACACC 600
ATCAGCAGGA GTTCAGAGGA GAATATTGTG GGCATTGGCA TAGCAGCTTG GGGCATGGTC 660
TCCAACCGGG ACACCTCAT CAGGAATTGC GATGCTGAGG GCTATTTTTT AGCCAGTAC 720
CTTATGGATG ACTTCACAAG AGATCCACTG TATATCCTGG ACAACAACCA CACACATTG 780
CTGCTCGTGG ACAAATGGCTG TCATGGACAT CCCACTGTGG AAGCAAAGCT CCGGAATCCAG 840
70 CTAGAGAAGT ATATCTCTGA GCGCACTATT CAAGATTCCA ACTATGGTGG CAAGATCCCC 900
ATTGTGTGTT TTGCCCAAGG AGGTGGAAGA GAGACTTTGA AAGCCATCAA TACCTCCATC 960
AAAAATAAAA TTCTTGTGTG GGTGGTGGAA GGCTCGGGCC AGATCGCTGA TGTGATCGCT 1020
AGCCTGGTGG AGGTGGAGGA TGCCCTGACA TCTTCTGCGG TCAAGGAGAA GCTGGTGGCG 1080
TTTTTACCCC GCACGCTGTC CCGGCTGCCT GAGGAGGAGA CTGAGAGTTG GATCAAAATG 1140
75 CTCAGAGAAA TTCTCGAATG TTCTCACCTA TTAACAGTTA TTAAATGGA AGAAGCTGGG 1200
GATGAAATTG TGAGCAATGC CATCTCCTAC GCTCTATACA AAGCCTTCAG CACCAAGTGG 1260
CAAGACAAGG ATAACTGGAA TGGGCAGCTG AAGCTTCTGC TGGAGTGGAA CCAGCTGGAC 1320
TTAGCCAATG ATGAGATTTT CACCAATGAC CGCGATGGG AGTCTGCTGA CCTTCAAGAA 1380
GTCAATGTTA CGGCTCTCAT AAAGGACAGA CCAAGTTTGG TCGGCTCTT TCTGGAGAA 1440
80 GGCTTGAACC TACGGAAGTT TCTCACCAT GATGCTCTCA CTGAATCTT TCCCAACCAC 1500
TTCAGCACGC TTGTGTACCG GAATCTGCAG ATCGCCAGA ATTCTATAA TGATGCCCTC 1560
CTCACGTTTG TCTGGAATCT GGTTCGGAAC TTCGGAAGAG GCTTCCGGAA GGAAGACAGA 1620
AATGGCGGGG ACAGATGGGA CATAGAATCT CACGAGTGT CTCTATTAC TCGGCAACCC 1680
CTGCAAGCTC TCTTCATCTG GGCATCTCT CAGAAATAGA AGGAATCTC CAAAGTCATT 1740

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5
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TGGGAGCAGA CCAGGGGCTG CACTCTGGCA GOCCTGGGAG CCAGCAAGCT TCTGAAGACT 1800
CTGGCCAAAG TGAAGAACGA CATCAATGCT GCTGGGGAGT CCGAGGAGCT GGCTAATGAG 1860
TACGAGACCC GGGCTGTTGA GCTGTTCACT GAGTGTACGA GCAGCGATGA AGACTTGGCA 1920
GAACAGCTCG TGGTCTATTCT CTGTGAAGCT TGGGGTGGAA GCAACTGTCT GGAGCTGGCG 1980
GTGGAGGCCA CAGACCAGCA TTTCATCGCC CAGCCTGGGG TCCAGAAATT TCTTTCTAAG 2040
CAATGGTATG GAGAGATTTC CCGAGACACC AAGAACTGGA AGATTATCCT GTGTCTGTTT 2100
ATTATACCTT TGGTGGGCTG TGGCTTTGTA TCATTTAGGA AGAAACCTGT CGACAAGCAC 2160
AAGAAGCTGC TTGGTACTA TGTGGCGTTC TTCACCTCCC CCTTCTGGGT CTCTCTCTGG 2220
AATGTGTCTC TGTACATCGC CTTCCTCCTG CTGTTTGCTT ACGTGTCTCT CATGGATTTC 2280
CATTGCTGTC CACACCCCCC CGAGCTGGTC CTGTACTCGC TGGTCTTTGT CCTCTCTGTG 2340
GATGAAGTGA GACAGTGGTA CGTAAATGGG GTGAATTATT TTACTGACCT GTGGAATGTG 2400
ATGGACACGC TGGGGCTTTT TTACTTCATA GCAGGAATTG TATTTCGGCT CCACTCTTCT 2460
AATAAAGCTC CTTTGTATTCT TGGACGAGTC ATTTTCTGTC TGGACTACAT TATTTTCACT 2520
CTAAGATTGA TCCACATTTT TACTGTAAAG AGAAACTTAG GACCCAAGAT TATAATGCTG 2580
CAGAGGATGC TGATCGATGT GTTCTTCTTC CTGTTCTCTT TTGGGTGTG GATGGTGGCC 2640
TTTGGCGTGG CCAGGCAAGG GATCCTTAGG CAGAATGAGC AGCGCTGGAG GTGGATATTC 2700
CGTTGCGTGA TCTACGAGCC CTACCTGGCC ATGTTGCGCC AGGTGCCAG TGACGTGGAT 2760
GGTACCAAGT ATGACTTTGC CCACTGCAAC TTCACTGGGA ATGAGTCCAA GCCACTGTGT 2820
GTGGAGCTGG ATGAGCAAAA CCTGCCCGG TTCCCGGAGT GGATCACCAT CCCCCTGGTG 2880
TGCATCTACA TGTATCCAC CACATCTCTG CTGGTCAACC TGCTGGTGGC CATGTTTGGC 2940
TACAGGTGGG GCACCGTCCA GGAGAACAAAT GACCAGGTCT GGAAGTTCCA GAGGTACTTC 3000
CTGGTGACAG AGTACTGTCG CCGCCTCAAT ATCCCTTCC CCTTCATCGT CTTCGCTTAC 3060
TTCTACATGG TGGTGAAGAA GTGCTTCAAG TGTGTCTGCA AGGAGAAAAA CATGGAGTCT 3120
TCTGTCTGCT GTTCAAAAAA TGAAGACAAAT GAGACTCTGG CATGGGAGGG TGTCAATGAAG 3180
GAAAACCTACC TTGTCAAGAT CAACACAAA GCCAACGACA CCTCAGAGGA AATGAGGCAT 3240
CGATTTAGAC AACTGGATAC AAAGCTTAAT GATCTCAAGG GTCTTCTGAA AGAGATTGCT 3300
AATAAATCA AATGA

Seq ID NO: 566 Protein sequence

Protein Accession #: Eos sequence

35
40
45
50
55

1 11 21 31 41 51
MSFRAARLSM RNRNRNDTLDL TRTLYSSASR STDLSYSESD LVNFIQANFK KRECVPFTKD 60
SKATENVCKC GYAQSQHMEG TQINQSEKWN YKKHTKEPPT DAFGDIQFET LGKKGKYIRL 120
SCDTDAEILY ELLTQHWHLK TPNLVISVTG GAKNFALKPR MRKIFSRLLY IAQSKGAWIL 180
TGGTHYGLMK YIGEVVRDNT ISRSSEENIV AIGLAANGMV SNRDTLIRNC DAEGYFLAQV 240
LMDDPTRDPL YILDNNHNLH LLVDNGCHGH PTVEAKLRNQ LEKYISERTI QDSNYGGKIP 300
IVCPAQQGGK ETLKAINTSI KKKIPCVVVE GSGQIADVIA SLVEVEDALT SSAVKEKLV 360
FLPRTVSLRP EETESWIKW LKBIELCSHL LTVIKMEAG DEIVSNAISY ALYKAFSTSE 420
QDKDNWNGQL KLLLENQQLD LANDEIFTND RRWESADLQE VMFTALIKDR PKFVRLPLEN 480
GLMLRKPLTH DVLTELFNSH FSTLVYRNLO IAKNSYNDAL LTFVWKLVAN FRRGFRKEDR 540
NGRDEMDELH HDVSPITRHP LQALFIWAIL QMKKELSKVI WEQTRGCTLA ALGASKLLKT 600
LAKVKMDINA AGESEELANE YETRAVELFT ECVSSDEDLA BQLLVYSCEA WGGSNCLELA 660
VEATDGHPIA QPGVQNPLSK QWYGEISRDT KWKIILCLF IIPLVGCGFV SFRKKPVDKH 720
KLLLWYVAVF PTFSPFVVSF NVVFYIAFL LFAFVLLMDF HSPVHPPELV LYSLVFVLFC 780
DEVROKYVNG VNYFTDLNWN MDTLGLFYFI AGIVFRLHSS NKSSLYSGRV IFCLDYIIFT 840
LRLIHIFTVS RNLGPKIIML QRMLIDVFFF LFLFAVMMVA FGVARQGILR QNEQRWRWIF 900
RSVIYEPYLA MFGQVPSVDV GTTYDPAHCT PTGNESKPLC VELDEHNLPR FPEWITIPLV 960
CIYMLSTNXL LVNLLVAMPG YTVGTQENN DQVWKQRYF LVQEYCSRLN IPFPFIVFAY 1020
FYMVVKCKFK CCKCKKNMES SVCCPKNEDN ETLAWEGVMK ENYLVKINTK ANDTSEEMRH 1080
RFRQLDTKLN DLKGLLKEIA NKIK

Seq ID NO: 567 DNA sequence

Nucleic Acid Accession #: NM_006911.1

Coding sequence: 1..558

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65
70

1 11 21 31 41 51
ATGCTCTGCC TGTCTCTGTT CCACCTGCTA GAATTCCTGT TACTACTGAA CCAATTTTCC 60
AGAGCAGTCG CGGCCAAATG GAAGGACGAT GTTATTAAAT TATGCGGCGG OGAATTAGTT 120
CGCGGCGAGA TTGCCATTGT CGGCATGAGC ACCTGGAGCA AAAGGTCTCT GAGCCAGGAA 180
GATGCTCCTC AGACACCTAG AOCAGTGGCA GAAATTGTAC CATCCTTCAT CAACAAAGAT 240
ACAGAAACTA TAATTATCAT GTTGAATTC ATTGCTAATT TGCCACCGGA GCTGAAGGCA 300
GCCCTATCTG ABAGGCAACC ATCATTACCA GAGCTACAGC AGTATGTACC TGCATTAAAG 360
GATTCCAATC TTAGCTTTGA AGAATTAAAG AAACCTATTC GCAATAGGCA AAGTGAAGCC 420
GCAGACAGCA ATCCTTTCAGA ATTAATAATC TTAGGCTTGG ATACTCATT TCACAAAAAG 480
AGACGACCCT ACGTGGCACT GTTTGAGAAA TGTGCTCTAA TTGGTTGTAC CAAAAGGTCT 540
CTTGCTAAAT ATTGCTGA

Seq ID NO: 568 Protein sequence

Protein Accession #: NP_008842.1

75
80

1 11 21 31 41 51
MPRLFLPHLL EFCLLLNQFS RAVAARKWDD VIRKCGRELV RAQIAICGMS TWSKRSLSQE 60
DAPQTPRPVA EIVPSFINKD TETIIIMLEF IANLPPELKA ALSERQPSLP ELQYVPALK 120
DSNLSPFEFK KLIRNRQSEA ADSNPSELKY LGLDTHSQKK RRPYVALFEK CCLIGCTKRS 180
LAKYC

Seq ID NO: 569 DNA sequence

Nucleic Acid Accession #: XM_036453.1

Coding sequence: 1..3978

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5 1 11 21 31 41 51
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ATGCTGCCCG TGTACCAGGA GGTGAAGCCC AACCOCCTGC AGGACGCGAA CCTCTGCTCA 60
CGCGTGTCT TCTGGTGGCT CAATCCCTTG TTTAAATTTG GCCATAAAGC GAGATTAGAG 120
GAAGATGATA TGTATTTCAGT GCTGCCAGAA GACCGCTCAC AGCACCTTGG AGAGGAGTTG 180
CAAGGTTCTT GGTATAAAGA AGTTTTTAAGA GCTGAGAATG ACGCACAGAA GCCTTCTTTA 240
ACAAGAGCAA TCATAAAGTG TTACTGGAAA TCTTATTTAG TTTTGGGAAT TTTTACGTTA 300
ATTGAGGAAA GTGCCAAAGT AATCCAGCCC ATATTTTTTG GAAAAATTAT TAATTATTTT 360
GAAAAATTAT ATCCCATGGA TTCTGTGGCT TTGAACACAG CGTACGCCCTA TGCCACGGTG 420
CTGACTTTTT GCACGCTCAT TTGGGCTATA CTGCATCACT TATATTTTTA TCAOGTTTCA 480
TGTGCTGGGA TGAGGTTTACG AGTAGCCATG TGCCATATGA TTTATCGGAA GGCACCTTCG 540
CTTAGTAACA TGCCCATGGG GAAGACAACC ACAGGCCAGA TAGTCAATCT GCTGTCCAAT 600
GATGTGAACA AGTTTGATCA GGTGACAGTG TTCTTACACT TCCTGTGGGC AGGACCACTG 660
CAGGCGATCG CAGTGACTGC CCTACTCTGG ATGGAGATAG GAATATCGTG CCTTGTCTGG 720
ATGGCAGTTC TAATCATTCT CCTGCCCTTG CAAAGCTGTT TTGGGAAGTT GTTCTCATCA 780
CTGAGGAGTA AACTGCAAC TTTTCCGGAT GCCAGGATCA GGACCATGAA TGAAGTTATA 840
ACTGGTATAA GGATAATAAA AATGTACGCC TGGGAAAAGT CATTTTCAAA TCTTATTACC 900
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75 Seq ID NO: 570 Protein sequence
Protein Accession #: XP_036453.1

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Seq ID NO: 572 Protein sequence

Protein Accession #: AAC27076.1

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Seq ID NO: 574 Protein sequence

Protein Accession #: Eos sequence

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TGGAATGTGT	GAAAAATGAT	TCAGAAACTT	TAAATTTTAA	AAAAGGCTTC	TAGTTAGCTG	1740
CTTAAATCT	ATCTATATAA	TGTAGTATGA	TGTAATGTGG	TCITTTTCTT	AGATTTTGAG	1800
CAGTTAATAC	TAAACATTGA	TTTATTTTCT	AATCATTTAA	ATATTATATCA	ACTTTCCTTA	1860
AAATAAATAG	CCCTTAGTGT	AAAAATATAA	GAACCTTGATA	TATTTTCATT	TCTTATATAG	1920
TATTCATTTT	CCTACCTATA	TTACACAAAA	AAGTATAGAA	AAGATTTAAG	TAATTTTGCC	1980
ATCCTAGGCT	TAAATGCAAT	ATTCCTGGTA	TTATTTACAA	TGCAGAATTT	TTTGAGTAAT	2040
TCTAGCTTTC	AAAAATTAGT	GAAGTTCTTT	TACTGTAAAT	GGTGACAATG	TCACATAATG	2100
AATGCTATTG	AAAAGGTTAA	CAGATACAGC	TCGGAGTTGT	GAGCAGTCTA	CTGCAAGACT	2160
TAAATAGTTC	AGTATAAATT	GTCTTTTTTT	TCTTGTGCTG	ACTAATCTATA	AGCATGATCT	2220
TGTTAATGTA	TTTTTGATGG	GAAGAAAAAG	TACATGTTTA	CAAAGAGGTT	TTATGAAAAG	2280
AATAAAATTT	GACTTCTTGC	TTGTACATAT	AGGAGCAATA	CTATTATATT	ATGTAGTCCG	2340
TTAACACTAC	TTAAAAGTTT	AGGGTTTTCT	CTTGGTTGTA	GAGTGGCCCA	GAATTGCATT	2400
CTGAATGAAT	AAGGTTTAAA	AAAAAATCCC	CAGTGAAAAA	AAA		

Seq ID NO: 576 Protein sequence
Protein Accession #: NP_001864.1

55
60
65

1	11	21	31	41	51	
MAGRGGALL	ALCGALAAAG	WLLGABAEQEP	GAPANGMRRR	RRLQEDGIS	FEYHRYPELR	60
EALVSVNLQC	TAISRYITVG	RSFEGRELLV	IELSDNPGVH	EPGEPEPKYI	GNMHGNEAVG	120
RELLIFLAGY	LCNEYQKQNE	TIVNLIHSTR	IHIMPSLNPD	GPEKAASQPG	BLKDWPFVGRS	180
NAQIDILNRY	FFDLDIRIVV	NEKEGGFNNH	LLKNMKICVD	QNTKLAPETK	AVIHWIMDIP	240
FVLSANLHGG	DLVANYFYDE	TRSGSAHEYS	SSPDDAIFQS	LARAYSSFPN	AMSDFNRPFC	300
RKNDSSFPV	DGTITNGGAWY	SVPGGMQDFN	YLSNCFBIT	VELSCEKPPP	EETLKYTWED	360
NKNSLISYLE	QIHRGVKGFV	RDLQGNPIAN	ATISVEGIDH	DVTSKQGDY	WRLLIPGNYK	420
LTASAPGYLA	ITKKVAVPYS	PAAGVDFELE	SPSERKEEBK	EELMEWKMM	SETLAF	

Seq ID NO: 577 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..933

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1	11	21	31	41	51	
ATGTGACAGCA	ATGGACGGTG	CATCCCGGCG	GCCTGGCAGT	GTGACGGGCT	GCCTGACTGC	60
TTGACACAGA	GTGATGAGAA	GGAGTGCCCG	AAGGCTAAGT	CGAAATGTGG	CCGACCTTTC	120
TTCCCTGTGT	CCAGCGGCAT	CCATTGCATC	ATTGGTGCCT	TCGGGTGCAA	TGGGTTTGGG	180
GACTGTCCCG	ATGGCAGCGA	TGAAGAGAAC	TGCACAGCAA	ACCCCTCTGT	TTGCTCCACC	240
GCCCGCTACC	ACTGCAAGAA	CGGCTCTGT	ATTGACAAGA	GCTTCATCTG	CGATGGACAG	300
AATAACTGTC	AAGACAACAG	TGATGAGGAA	AGCTGTGAAA	GTTCTCAAGA	ACCCGGCAGT	360
GGGCAAGTGT	TTGTGACTTC	AGAGAACCAG	CTTGTGTATT	ACCCAGCATG	CACCTATGCC	420
ATCATCGGCA	GCTCCGTCAT	TTTTGTGCTG	GTGGTGGCCC	TGCTGGCACT	GGTCTTGAC	480
CACCAAGCGA	AGCGGAACAA	CCTCATGACG	CTGCGCGTGC	ACCGGCTGCA	GCACCTGTG	540
CTGCTGTCCC	GCTCGGTGGT	CCTGGACCA	CCCCACCACT	GCAACGTCA	CTACAACTGC	600
AATAATGGCA	TCCAGTATGT	GGCCAGCCAG	GCGGAGCAGA	ATGCGTCCGA	AGTAGGCTCC	660
CACCCCTCCT	ACTCCGAGGC	CTTGTGGGAC	CAGAGGCGCT	CGTGGTATGA	CCTTCTCTCA	720
CGGCCCTACT	CTTCTGACAC	GGAATCTCTG	AAACAGCCCG	ACCTGCCCCC	CTACCGCTCC	780
CGGTCCGAGA	GTGCCAGTCC	TGCCAGCTCC	CAGGCAGCCA	GCAGCCTCCT	GAGCGTGGAA	840
GACACCAAGC	ACAGCCCGGG	GCAGCCTGCG	CCCCAGGAGG	GCACTGCTGA	GCCAGGGGAC	900

TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA

Seq ID NO: 578 Protein sequence
 Protein Accession #: Eos sequence

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 30
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1	11	21	31	41	51	
MCSNGRCIPG	AWQCDGLPDC	FDKSDKESCP	KAKSKCGPTF	PPCASGIHCI	IGRFRONGPE	60
DCPDGSDEEN	CTANPLLCST	ARYHCKNGLC	IDKSFICDGO	NNQDNDSEDE	SCSSSQEPGS	120
GQVFVTSENQ	LVYVPSITYA	IIGSSVIFVL	VVALLALVLH	HQRJRNLMIT	LPVHRLQHPV	180
LLSRLVLDH	PHHCNVITNV	NNGIQYVASQ	AEQNASEVGS	PPSYSEALLD	QRPAYDLP	240
PPYSSDTESL	NQADLPYRS	RSGSANSASS	QAASSLLSVE	DTSHSPGQPG	PQEGTAEPD	300
SEPSQGTTEE						

Seq ID NO: 579 DNA sequence
 Nucleic Acid Accession #: AF179274.1
 Coding sequence: 1..1125

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 35
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1	11	21	31	41	51	
ATGGTGCTGT	GGGAGTCCCC	GCGGCAGTGC	AGCAGCTGGA	CACTTTGCGA	GGGCTTTTGC	60
TGGCTGCTGC	TGCTGCCCGT	CATGCTACTC	ATCGTAGCCC	GCCCGGTGAA	GCTCGCTGCT	120
TTCCCTACCT	CCTTAAGTGA	CTGCCAAACG	CCCAACGGCT	GGAATTGCTC	TGGTTATGAT	180
GACAGAGAAA	ATGATCTCTT	CCTCTGTGAC	ACCAACACCT	GTAATTTTGA	TGGGGAATGT	240
TTAAGAATTG	GAGACACTGT	GACTTGGGTC	TGTCACTTCA	AGTGCAACAA	TGACTATGTG	300
CCTGTGTGTG	GCTCCAATGG	GGAGAGCTAC	CAGAATGAGT	GTTACCTGCG	ACAGGCTGCA	360
TGCAACACAG	AGAGTGAGAT	ACTTGTGGTG	TCAGAAGGAT	CATGTGCCAC	AGATGCAGGA	420
TCAGATCTGT	GAGATGGAGT	CCATGAAGGC	TCTGGAGAAA	CTAGTCAAAA	GGAGCATCC	480
ACCTGTGATA	TTTGCCAGTT	TGGTGCAGAA	TGTGAAGAG	ATGCCGAGGA	TGCTCGGTGT	540
GTGTGTAATA	TTGACTGTTC	TCAAAACCAAC	TTCAATCCCC	TCTGCGCTTC	TGATGGGAAA	600
TCTTATGATA	ATGCATGCCA	AATCAAGAA	GCATCGTGTC	AGAAACAGGA	GAAAATTGAA	660
GTCAATGCTT	TGGGTGAGTG	TCAAGATAAC	ACAACTACAA	CTACTAAGTC	TGAAGATGGG	720
CATTATGCAA	GAACAGATTA	TGCAGAGAAT	GCTAACAAAT	TAGAAGAAAG	TGCCAGAGAA	780
CACACATAC	CTTGTCGGGA	ACATTACAAT	GGCTTCTGCA	TGCATGGGAA	GTGTGAGCAT	840
TCTATCAATA	TGCAGAGGCC	ATCTTGACAG	TGTGATGCTG	GTTATACCTG	ACAACACTGT	900
GAAAAAAGG	ACTACAGTGT	TCTATACGTT	GTTCCCGGTC	CTGTACGATT	TCAGTATGTC	960
TTAATGCGAG	CTGTGATTGG	AACAATTCAG	ATTGCTGTCA	TCTGTGTGGT	GGTCCTCTGC	1020
ATCACAAGGA	AATGCCCCAG	AAGCAACAGA	ATTCACAGAC	AGAAGCAAAA	TACAGGGCAC	1080
TACAGTTCAG	ACAATACAAAC	AAGAGCGTCC	ACGAGGTAA	TCTGA		

Seq ID NO: 580 Protein sequence
 Protein Accession #: NP_057276.2

45
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1	11	21	31	41	51	
MVLWESPRQC	SSWTLCBFC	WLLLLPVMLL	IVARFVKLAA	FPTSLSDQQT	PTGNWCSGYD	60
DRENDLFLCD	TNTCKFDGEC	LRIGDTVTCV	QQFKCNNDYV	PVCGSNGESY	QNECYLRQAA	120
CRQGSILLVV	SEGSCTADAG	SGSGDGVHEG	SGETSQKETS	TCDICQFGAE	CEDEADVWVC	180
VCMIDCSQTN	FNPLCASDGL	SYDNACQIKE	ASQKQKEKIE	VMSLGRQDN	TTTTTKSEDD	240
HYARTDYAEN	ANKLEESARE	HHIPCPPEHYN	GFCMHGKCEH	SINMQEPSCR	CDAGYTGQHC	300
EKKDYSVLVY	VPGPVRFQVY	LIAAVIGTIQ	IAVICVVVLC	ITRKCPRSNR	IHRQKQNTGH	360
YSSDNTTRAS	TRLI					

Seq ID NO: 581 DNA sequence
 Nucleic Acid Accession #: S78203.1
 Coding sequence: 1..2190

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GAGGTACCAC	CTCGACCACC	TAGCCCTCCA	AAGAAGCCAT	CTCCGACAA	CTGTGGCTCC	120
AACATATCCAC	TGAGCATTTG	CTTCATTGTG	GTGAATGAAT	TCTGCGAGCG	CTTTTCCTAT	180
TATGGAAATGA	AAGCTGTGCT	GATCCTGTAT	TTCTGTATT	TCTGCACTG	GAATGAAGAT	240
ACCTCCACAT	CTATATACCA	TGCCCTCAGC	AGCCTCTGTT	ATTTTACTCC	CATCTCTGGG	300
GCAGCCATTG	CTGACTCGTG	GTTGGGAAAA	TTCAAGACAA	TCATCTATCT	CTCCTTGGTG	360
TATGTGCTTG	GCCATGTGAT	CAAGTCTCTG	GGTGCCTTAC	CAATACTGGG	AGGACAAGTG	420
GTACACACAG	TCCTATCATT	GATCGGCTTG	AGTCTAATAG	CTTTGGGGAC	AGGAGGCATC	480
AAACCCGTGT	TGGCAGCTTT	TGGTGGAGAC	CAGTTTGAAG	AAAAACATGC	AGAGGAACGG	540
ACTAGATACT	TCTCAGTCTT	CTACCTGTCC	ATCAATGCAG	GGAGCTTGAT	TTCTACATTT	600
ATCACACCCA	TGCTGAGAGG	AGATGTGCAA	TGTTTTGGAG	AAGACTGCTA	TGCATTGGCT	660
TTTGGAGTTG	CAGGACTGCT	CATGGTAATT	GCACTTGTGT	TGTTTGCAAT	GGGAAGCAAA	720
ATATACAAAT	AACCAACCCC	TGAAGGAAAC	ATAGTGGCTC	AAGTTTTCAA	ATGTATCTGG	780
TTTGTCTATT	CCAATCGTTT	CAAGAACCGT	TCTGGAGACA	TTCCAAGCG	ACAGCACTGG	840
CTAGACTGGG	CAGCTGAGAA	ATATCCAAG	CAGCTCATT	TGGATGTAAA	GGCACTGACC	900
AGGGTACTAT	TCCTTTATAT	CCCATTGCCC	ATGTTCTGGG	CTCTTTTGGG	TCAGCAGGGT	960
TCACGATGGA	CTTTGCAAGC	CATCAGGATG	AATAGGAATT	TGGGGTTTTT	TGTGCTTCAG	1020
CCGACACAGA	TGCAGGTTCT	AAATCCCTTT	CTGGTTCTTA	TCTTCATCCC	GTGTGTTGAC	1080
TTTGTCTATT	ATCGTCTGGT	CTCCAAGTGT	GGAATTAAC	TCTCATCACT	TAGGAAAAATG	1140
GCTGTTGGTA	TGATCCTAGC	GTGCTTGGCA	TTTGCACTTG	CGGCAGCTGT	AGAGATAAAA	1200
ATAAATGAAA	TGGCCCCAGC	CCAGTCAGGT	CCCCAGGAGG	TTTTCCTACA	AGTCTTGAAT	1260
CTGCGAGATA	ATGAGGTGAA	GGTGACAGTG	GTGGGAAATG	AAACAATTC	TCTGTTGATA	1320
GAGTCCATCA	AATCCTTTCA	GAAAACACCA	CACATTTCCA	AACTGCACCT	GAAAACAAAA	1380
AGCCAGGATT	TTCACTTCCA	OCTGAAATAT	CACAAATTGT	CTCTCTACAC	TGACCATCT	1440
GTGCAGGAGA	AGAACTGGTA	CAGTCTTGTC	ATTGTTGAAG	ATGGGAACAG	TATCTCCAGC	1500

5 ATGATGGTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGGT 1560
 AACACTTTGC ATAAAGATGT CAACATCTCC CTGAGTACAG ATACCTCTCT CAATGTTGGT 1620
 GAAGACTATG GTGTGCTCTG TTATAGAACT GTGCAAGAG GAGATAACCC TGCAGTGAC 1680
 TGTAGAACAG AAGATAAGAA CTTTTCTCTG AATTGGGGTC TTCTAGACTT TGGTGCAGCA 1740
 TATCTGTTTG TTATTACTAA TAACACCAAT CAGGCTCTTC AGGCTCGGAA GATTGAAGAC 1800
 ATCCAGCCA ACAAAATGTC CATTGCGTGG CAGCTACCAC AATATGCCCT GGTTCAGACT 1860
 GGGGAGGTCA TGTCTCTGT CACAGGTCTT GAGTTTCTT ATTCTCAGGC TCCCTCTAGC 1920
 ATGAAATCTG TGCTCCAGGC AGCTTGGCTA TTGACAATTG CAGTTGGGAA TATCATCTGT 1980
 10 CTGTGTTGTG CACAGTTCAG TGGCCTGGTA CAGTGGGCGG AATTCATTTT GTTTCTCTGC 2040
 CTCTGCTGTG TGATCTGCTT GATCTTCTCC ATCATGGGCT ACTACTATGT TCCTGTAAAG 2100
 ACAGAGGATA TGCGGGGTCC AGCAGATAAG CACATTCTCT ACATCCAGGG GAACATGATC 2160
 AACTAGAGA CCAAGAAGAC AAAACTCTGA

15 Seq ID NO: 582 Protein sequence
 Protein Accession #: AAB34388.1

1 11 21 31 41 51
 20 MNPFQKNEBK ETLFSPVSIE EVPPRPSPSP KKPSPITCGS NYPLSIAPIV VNEFCERFSY 60
 YGMKAVLILY FLYPLHWNED TSTSIYHAPS SLCYFTPILG AALADSWLKG FKTIYLSLV 120
 YVLGHVILSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAFQGD QFEKHAEER 180
 TRYFSPVYLS INAGSLISTP ITPMLRGDVQ CPGEDCYALA FGVPGLLMVI ALVVVFAMGSK 240
 IYNKPPPEGN IVAQVFKCIW FAISNRFKNR SGDIPKRQHW LDWAAEKYPK QLIMDVKALT 300
 25 RVLFYIPLP MFWALLDQCG SRWTLQAIRN NRNLGFFVLQ PDQMQLNPP LVLIFLPLFD 360
 FVIYRLVSKC GINFSLLRKM AVGMILACLA FAVAAVEIK INEMAPAQSG PQEVLQVLN 420
 LADDEVKVTY VGNENSLLI ESIKSPQKTP HYSKLHLKTK SQDFHFLKY HNLSLYTEHS 480
 VQEKWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLHKDVNIS LSTDLSLVNG 540
 EDYGVSAIYT VQRGEYPAHV CRTEKNFSL NLGLLDPGAA YLFVITNTN OGLQAWKIED 600
 IPANKMSIAW LQPGYALVTA GEVMSFVTGL EFSYSQAPSS MKSVLQAAML LTIAVGNIIV 660
 30 LVVAQFSGELV QWAEFILFSC LLLVICLIPS IMGYTYPVK TEDMRGPADK HIPHTQGNMI 720
 KLTBKTQL

35 Seq ID NO: 583 DNA sequence
 Nucleic Acid Accession #: NM_032642.1
 Coding sequence: 184..1263

1 11 21 31 41 51
 40 GACCATTIAGC AGGCACCCAG CCTGTCTTT GGCTGGGAAA CGGTGGCCCC CAATGTAGCC 60
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 ACAGAGGGAA CCTACTCTG GAAACTGTCA GTCCAGGGC ACTGGGGAGG GCTGAGGCGG 180
 ACCATGCCCA GCGTGTCTGT GCTGTTCACG GCTGTCTCTG TGTCCAGCTG GGCTCAGCTT 240
 CTGACAGAGC CCAACTCTGT GTGGTCATTA GCTTTGAACC CGGTGCAGAG ACCCGAGATG 300
 45 TTTATCATCG GTGCCAGCC CGTGTGCACT CAGCTTCCCG GGCTCTCCCC TGGCCAGAGG 360
 AAGCTGTGCC AATTGTACCA GGAGCACATG GCCTACATAG GGGAGGGAGC CAAGACTGGC 420
 ATCAAGGAAT GCCAGCACCA GTTCGGGCG CCGCGGTGGA ATTCAGCAC AGCGGACCAAC 480
 GCATCTGTCT TTTGGGAGAGT CATGCAGATA GGCAGCCGAG AGACCGCCTT CACCCACGCG 540
 GTAGAGCGCG CGGGCGTGGT CAACGCCATC AGCCGGGCGT GCGCGAGAGG CGAGCTCTCC 600
 50 ACCTGCGGCT GCAGCGGAGC GCGCGGCGCC AAGGACCTGC CCCGGGACTG GCTGTGGGGC 660
 GCGTGTGGGG ACAACGTGGA GTACGGCTAC CGCTTGGCCA AGGAGTTTGT GGATGCCCGG 720
 GAGCGAGAGA AGAAGTTTGC CAAAGGATCA GAGGAGCAGG GCGGGTGTCT CATGAACCTG 780
 CAAACCAACG AGGCGGCTCG CAGGGCTGTG TATAAGATGG CAGACGTAGC CTGCAATGTC 840
 CACGCGCTCT CGGGGTCTGT CAGCCTCAAG ACCTGCTGGC TGCAGCTGGC CGAGTTCCGC 900
 55 AAGGTGCGGG ACOCGCTGAA GGAGAATAC GACAGCGCG CGCCATGCG CGTCACCGGC 960
 AAGGCGCGGC TGGAGCTGGT CAACAGCGGC TTCACCCAGC CCACCCCGGA GGACCTGGTC 1020
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 CAGGGCGCGC CTCGCAACAA GACCTCGGAG GGCATGGATG GCTGTGAGCT CATGTGCTG 1140
 GGGCGTGGCT ACAACCAATT CAAGAGCGTG CAGGTGGAGC GCTGCCACTG CAAGTTCCAC 1200
 60 TGGTGTGCT TCGTCAGGTG TAAGAAATGC ACGGAGATCG TGGACCAGTA CATCTGTAAA 1260
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 GAAAGATGAA AATGGAAAGG AAGAGCTTAT TTAAGAGACG CTGGAGATCT CTGAGGAGTG 1440
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 65 GAGGACTCTC AGGATGTAGG GACTTGGAAA TATTACTGT CTGTCCACCA CGGCCCTGGG 1560
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 GTTAGAGGAC TGCTGTGTAT CTGGCCACT AGGCCAAGAG GCCCTATGAA GGTGGCGGGA 1680
 ACTCAGCTTC AACCTGATG TCTTCAGGT CTTGTCCAGA ATGTAGATGG GTTCCTAAG 1740
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 70 GGAACGCTC CTTCCTTAAA ATGAGAAATC CAAAGTATC TCTGGCCAG TGACCAAGA 1860
 GAGATCTGCA CTTCCCGGAC TTCAGGCTG CTTTCCAGC GAGAATTCTT CATCCTCCAC 1920
 GGTTCACATG CTCTCACTG AAGAGGAAAG GGGGCCATT GACCTGACAT GTCAGGAAAG 1980
 CCTTAACTG AATGTTTGG CTTGGCTGC AGAAGCCAG GTGCATGACC AGGCTGCGTG 2040
 GACGTTATAC TGTCTTCCCC CACCCCGGG GAGGGGAAGC TTGAGCTGCT GCTGTCACTC 2100
 75 CTCCACCGAG GGAGGCTCA CAAACCAAG GACGCTGCAA CGGCTCAGGC TGGCGGGCCC 2160
 GCGGTGCTCA TCATCTCTGC CCCAGGTGTA CGTTCCTCT CTGACATTAA ATGCCCTTCA 2220
 TGGAAAAAAA AAAAAGAAAA AAAAAAAAAA AA

80 Seq ID NO: 584 Protein sequence
 Protein Accession #: NP_116031.1

1 11 21 31 41 51
 MPSLLLLFTA ALLSSNAQLL TDANSWWSLA LNPVQRPENF IIGAQPVCQS LPGLSPGQRK 60
 LCQLYQERMA YIGEGAKTGI KECQHQFRQR RWNCSADNA SVFGRVMQIG SRETAFTHAV 120

SAAGVVAIS RACREBELST CGCSRTARPK DLPRDNLWGG CGDNVEYGYR FAKEFVDARE 180
 REKNPAKGE EQGRVLMNLQ NNEAGRRAVY KMADVACKCH GVSQSCSLKT CWLQLAEPRK 240
 VGDRLKEKYD SAAAMRVTRK GRLELVNSRF TQPTPEDLVY VDPSPDYCLR NESTGSLGTQ 300
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Seq ID NO: 585 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1479

1 11 21 31 41 51
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 COGGCTCAOT ACTACCCGTC CCCCGTGCOC CAGTAGCGCC CGAGGGTCTT GACGCGAGCT 180
 TCCAACCCCG TCGTCTGCAC GCAGCCCAAA TCCCATCCG GGACAGTGTG CACCTCAAAG 240
 ACTAAGAAAG CACTGTGCAT CACCTTGACC CTGGGGACCT TCCTCGTGGG AGCTGCGCTG 300
 GCGCTGGCCG TACTCTGGAA GTTTCATGGG AGCAAGTGCT CCAACTCTGG GATAGAGTGC 360
 GACTCTCAG GTACCTGCAT CAACCCCTCT AACTGGTGTG ATGGCGTGTG ACTCTGCCCC 420
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 GTGGATGACA GCGGATCCAC CAGCTTTATG AAACGTGAAC CAAGTGCCGG CAATGTCTGAT 660
 ATCTATAAAA AACTGTACCA CAGTGATGCC TGTTCCTCAA AAGCAGTGGT TTCTTTACGC 720
 TGTATAGCCT GCGGGGTCAA CTTGAATCA AGCCGCCAGA GCAGGATCGT GGGCGGCGAG 780
 AGCGCGCTCC CCGGGGCGCTG GCGCTGGCAG GTCAAGCTGC ACGTCCAGAA CGTCCACGTG 840
 TGGGAGAGCT CCATCATCAC CCGCGAGTGG ATCGTGACAG CGGCCCACTG CGTGGAAAAA 900
 CCTCTTAACA ATCCATGGCA TTGGACGGCA TTTGGGGGGA TTTTGAGACA ATCTTTCATG 960
 TTCTATGGAG CCGGATACCA AGTAGAAAAA GTGATTCTCT ATCCAAATTA TGACTCCAAG 1020
 ACCAAGAAAC ATGACATTGC GCTGATGAAG CTGCAGAAGC CTCTGACTTT CAAAGACCTA 1080
 GTGAACACAG TGTGTCTGCC CAACCCAGGC ATGATGCTGC AGCCAGAAAC GCTCTGCTGG 1140
 ATTTCCGGGT GGGGGGCCAC CGAGAGAGAA GGAAGACCT CAGAAGTGCT GAACCTGCTC 1200
 AAGGTGCTTC TCATTGAGAC ACAGAGATGC AACAGCAGAT ATGTCTATGA CAACCTGATC 1260
 ACACCCAGCA TGATCTGTGC CGGCTTCTCG CAGGGGAACG TCGATTCTTG CCAGGGTGAC 1320
 AGTGGAGGGC CTCTGTCTAC TTCGAAGAAC AATATCTGGT GGCTGATAGG GGATACAAGC 1380
 TGGGGTTCTG GCTGTGCCAA AGCTTACAGA CCAGGAGTGT ACGGGAATGT GATGGTATTC 1440
 ACGGACTGGA TTTATCGACA AATGAGGGCA GACGGCTAA

Seq ID NO: 586 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 SNPVVCTQPK SPGGTCTSK TKKALCITLT LGTFLVGAAL AAGLLWFKMG SKCSNSGIEC 120
 DSSGCTCINFS NWCDGVSHCF GGEDENRCVR LYGFNFILQV YSSQRKSWHP VCQDDWNNENY 180
 GRAACRDMGY KNNFYSSQGI VDDSGSTSPM KLNTSAGNVD IYKRLYHSDA CSSKAVVSLR 240
 CIACGVNLNS SRQSRVGGG SALPGAHPWQ VSLHVQNVHV CGGSIIITPEW IYTAHCVKEK 300
 PLANPWHWTA FAGILRQSPM FYGAGYQVER VISHPNYDSK TKNNIDIALMK LQKPLTFNDL 360
 VKPVCLPNFG MMLQPEQLCW ISGWGATEER GKTSEVLNAA KVLLIETQRC NSRYVYDNL 420
 TPAMICAGFL QGNVDSQGD SGGPLVTSKN NIWMLIGDTS WSGGCAKAYR PGVYGNVMVF 480
 TDHIYRQMA DG

Seq ID NO: 587 DNA sequence
 Nucleic Acid Accession #: NM_005656.1
 Coding sequence: 57..1535

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 CGGAAACCCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCGG 180
 CTCAGTACTA CCGGTCCCCC GTGCCCCAGT ACGCCCGAGG GGTCTGAGC CAGGCTTCCA 240
 ACCCGCTCGT CTGCAAGCAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAAGACTA 300
 AGAAAGCACT GTGCATCAAC TTGACCTTGG GGACCTTCTT CGTGGGAGCT GCGCTGGCCG 360
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 CCTCAGGTAC CTGCATCAAC CCCTCTAACT GGTGTGATGG GGTGTCAAC TGCCCCCGCG 480
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 CATCTCAGAG GAAGTCTTGG CACCTGTGTG GCCAAGACGA CTGGAACGAG AACTACGGGC 600
 GGGCGGCTTG CAGGACATG GGCTATAAGA ATAATTTTTA CTCTAGCCAA GGAATAGTGG 660
 ATGACAGCGG ATCCACCCAG TTTATGAAAC TGAACACAAG TGCCGGCAAT GTCGATATCT 720
 ATAAAAAAT GTACCAAGT GATGCCTGTT CTTCAAAAGC AGTGGTTTCT TTAGCTGTT 780
 TAGCTCGGG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGG GGTGAGAGCG 840
 CGCTCCCGGG GGCCTGGCCC TGGCAGGTCA GCCTGCACGT CCAGAACGTC CACGTGTGG 900
 GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCCGC CCACCTGGTG GAAAAACCTC 960
 TTAACATACC ATGGCAATTG ACGGCATTG CCGGGATTTC GAGCAATCT TCTCATTTCT 1020
 ATGGAGCCGG ATACCAAGTA CAAAAAGTGA TTTCTCATCC AAATTATGAC TCCAGACCA 1080
 AGAACAAATG CATTGGCTG ATGAAGCTGC AGAAGCCTCT GACTTTCAAC GACCTAGTGA 1140
 AACCAGTGTG TCTGCCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTG TCGTGATTT 1200
 COGGGTGGGG GGCACCGAG GAGAAAGGGA AGACCTCAGA AGTGTGAAC GCTGCCAAGG 1260
 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAAC CTGATCACAC 1320
 CAGCCATGAT CTGTGCCGCG TTCTTGCAAG GGAACGTCGA TTTCTGCCAG GGTGACAGTG 1380
 GAGGGCTCTT GGTCACTTGG AACCAATAA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440
 GTTCTGGCTG TGCCAAAGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTACGG 1500
 ACTGGATTTA TCGACAAATG AAGGCAAAAG GCTAATCCAC ATGGTCTTGG TCCTTGAGCT 1560

5 CGTTTACAA GAAACAATG GGGCTGGTTT TGCTTCCCC TGCAATGATT ACTCTTAGAG 1620
 ATGATTGAGA GGTCACTTCA TTTTATTAA ACAGTGAAGT TGTCTGGCTT TGGCACTCTC 1680
 TGCCATAGTG TGCAAGCTGC AGTGGCTCCC CTGCCAGCC TGCTCTCCCT AACCCCTTGT 1740
 COGCAAGGGG TGATGGCCGG CTGGTTGTGG GCATGGCGG TCAATTGTGG AAGGAAGAGG 1800
 GTTGGAGGCT GCCCCATTG AGATCTTCTT GCTGAGTCT TCCAGGGGG CAATTTTGGG 1860
 TGAGCATGGA GCTGTCACTT CTCAGCTGCT GATGACTTG AGATGAAAA GGAGAGACAT 1920
 GGAAGGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTGTGTAGTG 1980
 TCCCCAGCCT ACTTCACAAG GGGATTTTGC TGATGGGTTT TTAGAGCCTT AGCAGCCCTG 2040
 GATGGTGGCC AGAAATAAAG GGACCAAGCC TTCATGGGTG GTGACGTGGT AGTCACTTGT 2100
 10 AAGGGGAACA GAAACATTTT TGTTCCTATG GGGTGAGAAT ATAGACAGTG CCCTTGGTGC 2160
 GAGGGAAGCA ATTGAAAAAG AACTTGCCTT GAGCACTCCT GGTGACGGTC TCCACCTGCA 2220
 CATTTGGTGG GGTCTCTGGG AGGGAGACTC AGCCTTCTCT CTCATCTCTC CTGACCCCTG 2280
 TCCTAGCACC CTGGAGAGTG AATGCCCTTT GGTCCCTGGC AGGGGCGCAA GTTTGGCACC 2340
 15 ATGTCCGGCT CTTCAGGCTT GATAGTCAAT GGAATTTAG GTCCATGGGG GAAATCAAGG 2400
 ATGCTCAGTT TAAGGTACAC TGTTCCTATG TTATGTTTCT ACACATTGAT GGTGTGACC 2460
 CTGAGTTCAA AGCCATCTT

Seq ID NO: 588 Protein sequence
 Protein Accession #: NP_005647.1

20 1 11 21 31 41 51
 MALNSGSPFA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTQA 60
 25 SNPVVCTQPK SPSGTVCSTK TKKALCITLT LGTFLVGAAL AAGLLWKFVG SKCSNSGIEC 120
 DSSGTCINFS NWCQGVSHCF GGEDENRCVR LYGPNFILQM YSSQRKSWHP VQDDWNNENY 180
 GRAACRDMGY KNNFYSSQGI VDDSGSTSPM KLNTSAGNVD IYKLYHSDA CSSKAVVSLR 240
 CLACGVNLNS SRQSRIVGGE SALPGAWFWQ VSLHVQNVHV CGGSIITPEW IVTAACHVEK 300
 PLNNPWNWTA FAGLLRQSFY FYGAGYQVQK VISHPNYDSK TKNDIALMK LQKPLTFNDL 360
 30 VKFVCLNPNP MMLQPEQLCW ISGWGATEEK KKTSEVLNAA KVLIIETQRC NSRYVYDNL 420
 TPAMICAGPL QGNVDSQGD SGGPLVTSNN NIWLLIGDTS WSGCAKAYR PGVYGNVMVF 480
 TDWYRQMKKA NG

Seq ID NO: 589 DNA sequence
 Nucleic Acid Accession #: NM_001935.1
 Coding sequence: 1..2301

35 1 11 21 31 41 51
 40 ATGAAGACAC CGTGAAGAT TCTTCTGGGA CTGCTGGGTG CTGCTGCGCT TGTCAACCATC 60
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 AAAACTTACA CTCTAACTGA TTAATCTAAA AATACTTATA GACTGAAGTT ATACTCCTTA 180
 AGATGGATTT CAGATCAATGA ATATCTCTAC AAACAAGRAA ATAATATCTT GSTATTCAAT 240
 GCTGAATATG GAAACAGCTC AGTTTTCTTG GAGAACAGTA CATTTGATGA GTTTGGACAT 300
 45 TCTATCAATG ATTATTCAT ATCTCCTGAT GGGCAGTTTA TTCTCTTAGA ATACAACATC 360
 GTGAAGCAAT GAGAGCAATC CTACACAGCT TCATATGACA TTTATGATTT AAATAAAAGG 420
 CAGCTGATTA CAGAAGAGAG GATTCCAAAC AACACACAGT GGGTCACATG GTCAACCATG 480
 GGTCAATAAT TGGCATAATG TTGGAACAAT GACATTTATG TTAATAATGA ACCAAATTTA 540
 CCAAGTTACA GAATCACATG GACGGGGAAA GAAGATATAA TATATAATGG AATAACTGAC 600
 TGGGTTTATG AAGAGGAAGT CTTCAGTGCC TACTCTGCTC TGTGGTGGTC TCCAAACGGC 660
 50 ACTTTTTTAG TCATGGCCCA ATTAAACGAC ACAGAAGTCC CACTTATTGA ATACTCCCTC 720
 TACTCTGATG AGTCACTGCA GTACCCAAAG ACTGTACGGG TTCCATATCC AAAGGCAGGA 780
 GCTGTGAATC CAACTGTAAA GTTCTTTGTT GTAAATACAG ACTCTCTCAG CTCAGTCACC 840
 AATGCAACTT CATACAAAT CACTGCTCCT GCTTCTATGT TGATAGGGGA TCACACTTGG 900
 TGTGATGTGA CATGGGCAAC ACAAGAAAGA ATTTCTTTGC AGTGGCTCAG GAGGATTCAG 960
 55 AACTATTCCG TCATGGATAT TTGTGACTAT GATGAATCCA GTGGAAGATG GAACCTGCTTA 1020
 GTGGCAAGGC AACACATTGA AATGAGTACT ACTGGCTGGG TTGGAAGATT TAGGCCTTCA 1080
 GAACCTCATT TTACCTTTGA TGGTAATAGC TTCTACAAGA TCATCAGCAA TGAAGAAGGT 1140
 TACAGACACA TTGTGCTATT CCRAATAGAT AAAAAAGACT GCACATTAT TACAAAGGC 1200
 ACCTGGGAAG TCATCGGGAT AGAAGCTCTA ACCAGTGAAT ATCTATACTA CATTAGTAAT 1260
 60 GAATATAAAG GAATGCCAGG AGGAAGGAAT CTTTATAAAA TCCAACTTAG TGACTATACA 1320
 AAAGTGACAT GCCTCAGTTG TGAGCTGAAT CCGGAAAGGT GTCAGTACTA TTTGTGTCTA 1380
 TTCAGTAAG AGGCGAAGTA TTATCAGCTG AGATGTTCCG GTCCTGGTCT GCCCCTCTAT 1440
 ACTCTACACA GCAGCGTGAA TGATAAAGGG CTGAGAGTCC TGGGAAGCAA TTCAGCTTTC 1500
 GATAAAATGC TGCAGAAATG CCAGATGCCC TCCAAAAAAC TGGACTTCAT TATTTTGAAT 1560
 65 GAAACAAATC TTTGGTATCA GATGATCTTG CCTCCTCATT TTGATAAATC CAAGAAATAT 1620
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 70 TTTGAAGTTG AAGATCAAT TGAAGCAGCC AGACAATTTT CAAAAATGGG ATTTGTGGAC 1860
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 GGATCGGGAA GTGGCGTGTT CAAGTGTGGA ATAGCCGTGG CGCCTGTATC CCGGTGGGAG 1980
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 75 CTCTTATATC ATGGAACAGC AGATGATAAC GTTCACITTC AGCAGTCAGC TCAGATCTCC 2160
 AAAGCCCTGG TCGATGTTGG AGTGGATTTC CAGGCAATGT GGTATACTGA TGAAGACCAT 2220
 GGAATAGCTA GCAGCACAGC ACACCAACAT ATATATACCC ACATGAGCCA TCTCATAAAA 2280
 CAATGTTTCT CTTTACCTTA G

Seq ID NO: 590 Protein sequence
 Protein Accession #: NP_001926.1

80 1 11 21 31 41 51
 MKTPWKILLG LLGAAALVTI ITVPVLLNK GTDDATADSR KTYTLTDYLR NTRYRLKLYSL 60

5 RWISDHEYL KQENNILVFN AEYGNSSVFL ENSTPDEFHG SINDYSISPD GQFILLEYNV 120
 VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVTWSPV GHKLAYVWNN DIYVVKIEPNL 180
 PSYRITWTGK EDIYNGITD WYEEVEVFA YSALMNSPNG TFLAYAQFND TEVPLIEYSF 240
 YSDESLQYPK TVRVYPYKAG AVNPTVKFPV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300
 CDVTWATQER ISLQWLRRIQ NYSVMDICDY DESSGRMNCL VARQHIEMST TGVVGRFRPS 360
 EPHTLDGNS FYKIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYYISN 420
 EYKMPGGRN LYKIQLSDYT KVTCLSCBLN PERCQYYSVS FSKKAKYQL RCSGPGPLPY 480
 TLHSSVNDKG LRVLEDNSAL DRMLQNVQMP SKKLDPIILN ETQFWYQML PPHFDKSKKY 540
 10 PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIVASPDG RSGSYQGDKI MHAINRRLGT 600
 FEVEDQIEAA RQFSKMGFVD NKRIAIWGS YGGYVTSMVL GSGSGVFKCG IAVAPVSRWE 660
 YDVSYYTERY MGLPTPEDNL DHYRNSTVMS RAENFKQVEY LLHGTADDN VHFQSAQIS 720
 KALVDVGVD FQAMWYTDDEH GIASSTAHQH IYTHMSHFIL QCFSLP

15 Seq ID NO: 591 DNA sequence
 Nucleic Acid Accession #: NM_016077.1
 Coding sequence: 128..667

20 1 11 21 31 41 51
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 TOGCTTTGTG ATTCTTGATC CGGAACCTTG TCACCCAGGA ACCCCGGAAG AGGTAGCTCA 60
 COGATAGAA AGTGTTCGC TTGCCAGAA GAAGGGAAGG CGGAGTGAAG GAAAGGAGGT 120
 ACTGTAGATG CCTCCAAAT CCTGGTTAT GGAATATTG GCTCATCCCA GTACACTCGG 180
 CTGGCTGTT GGAGTTGCTT GTGGCATGTG CTGGGCTGG AGCCTTCGAG TATGCTTTGG 240
 25 GATGCTCCCC AAAAGCAAGA CGAGCAAGAC ACACACAGAT ACTGAAAGTG AAGCAAGCAT 300
 CTTGGGAGAC AGCGGGAGT ACAAGATGAT TCTTGTGGT CGAAATGACT TAAAGATGGG 360
 AAAAGGGAAG GTGGCTGCC AGTGCTCTCA TGCTGCTGTT TCAGCTTACA AGCAGATTCA 420
 AAGAAGAAAT CTGAAGATGC TCAACAATG GGAATACTGT GGCACGCCA AGTGGTGGT 480
 CAAAGCTCCT GATGAAGAAA CCCTGATTGC ATTATTGGCC CATGCAAAAA TGCTGGGACT 540
 GACTGTAAGT TTAATTCAAG ATGCTGGAGC TACTCAGATT GCACCAAGCT CTCAACTGT 600
 30 CTTAGGATT GGGCCAGGAC CAGCAGACCT AATTGACAAA GTCACTGGTC ACCTAAACT 660
 TTACTAGGTG GACTTTGATA TGACAACAAC CCCTCCATCA CAAGTGTGTT AAGCCTGTCA 720
 GATTCTAACA ACAAAAGCTG AATTCTTCA CCCAATTAA ATGTTCTTGA GATGAAAATA 780
 AAACCTATTCC CATGTTCTA AAAAAA

35 Seq ID NO: 592 Protein sequence
 Protein Accession #: NP_057161.1

40 1 11 21 31 41 51
 | | | | | |
 MPSKSLVMEY LAHPSTLGLA VGVACGMCLG WSLRVCFGML PKSKTSKTHT DTESEASILG 60
 DSGEYKMLLV VRNDLKMKG KVAACQSHAA VSAYKQIQRR NPEMLKQWEY CGQPKVVVKA 120
 PDEETLIALL AHAKMLGLTV SLIQDAGRTQ IAPGSQTVLG IGPADLID KVTGHLKLY

45 Seq ID NO: 593 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1896

50 1 11 21 31 41 51
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 GCTCCGCGCG CCGCGCCGAG CAGAGCCGAG TCCGTCTCCG GCGCTGGCC CGAACCCGAG 120
 CGCGAGTCCG GGCACCGGCC CGGCGCGGGG CCGGGGAACA CCACCCGGTT TGGGCTGGG 180
 GCGCGGGGCG GCAGCGGCGC CTCCAGCTCC AACAGCAGTG CGGACGCCCT GGTGACCCGC 240
 55 ATTTCATCC TCCCTCGGGA CCTACCCACC CTCAGGCAG CGGTGATCGT GCGGTTCGCC 300
 TTACACACC TCCCTATGCG CTGCTGCTG CTGCGGTCT TCAGTGGGG AAAGAGGTTA 360
 AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGCGCCA 420
 CTAATGAAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TGACATCAA ATACAGAGTG 480
 TCCCTGCCCG CTGCACCTAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCCT 540
 60 GTGCCCCAC CCTTCATCCT CGACATGAC CTTCAGCAA GATGCACTGG AAGGCTGAT 600
 GGTGGAATCA GACCTGGTAA AACCTGTTTC CCAGCTCGGT GGCATCCTGT GGAAAGTTGG 660
 TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGGT CCGAGGTGTT 720
 GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGGGTGTC AGGCACTGTC 780
 TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCAACCAA TGGAGTTGCT TCTGCCACCC 840
 65 TTTGGGCATC CCTTAAAGT GCGCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTCGAG 900
 CTGAATCTCA TGGAAAAGCT GGATTCTCTT GCCTTAAGCA GAACACCCG GGCTCCATCT 960
 GCCAGGTGCT TGCCACTGGT CTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
 CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCCTTACAC ACAAAOCATG 1080
 70 AGTACCTGG GCTTGGATGT TTTCTGTGGT GCGGCGCAGC GGGGCACCTT TTGTGAAGAC 1140
 AGAGCAGTGA CTAAGGTTCT CCAGGGTAGC TCTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
 GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTC TCGCTGAGC 1260
 ACCCATCCTG TCAGGTTGGC TCGTTGAGT GCGCGGGGAC AAGCCAGCCT GAGCGGGAGG 1320
 AGGGTGTTC GCGCTCGCGG GCACTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380
 75 TGCTTTTGG TTTTGAAGAT TCTGTTGAG CGCATCTCT ACCTTGACCT CTTCTACAAA 1440
 ATCTGTCTCC CCGTCTGTGC CGTGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
 GTCTTGGGT CATTTGAGCA GAGCCCACAA AAGGCAGCTG CTGCCACGCG GGAGCCTGTC 1560
 AAAAGAGGGC GAGACTTGGA ATTGACCAAG CACACATGCC CTGGCTGGGG GATCACACAT 1620
 GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCACGTGGA GGATGTCACT 1680
 80 CACCTCGGAG GAGACTTTGA TGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTTCCAG 1740
 GATGGCAGAT GCCAGAAGAT GGTCTGTATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
 TGTGAGAGG TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCTTCTCT 1860
 TCCCCCGAC AGCCCCGTG TCTGTCCAG CCTGTA

Seq ID NO: 594 Protein sequence
 Protein Accession #: FGENESH predicted

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1      11      21      31      41      51
|      |      |      |      |      |
5  MRVAVLPAPL LPLLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNITRFGSG 60
AAGSGSSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAFAP FTTLIIACLL LRVFRSGKRL 120
KRTRKYDIIT TPAERVEMAP LNEEDEDDED STVFDIKYRV SLPAALRRQL PGQTLTLLVP 180
VPPPFILDID LPARCSGRPD GGIRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSCVGGV 240
ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTMELLPP FGHPEKVPPT STPHGFRQLQ 300
10 LNLMEKLDS ALRRNTRAPS ARCLPLVLAE MAAAESDLFN PWWHFSATGS PIKTLTYQTM 360
STLGLDVFPG AGQRGTFCED RAVTKVLQGS SFSKQLRWKP ALESGFPHL RLLRECPPLS 420
THPVRLARSD ARGQASLTGR RVFRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480
ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHAHEPV KRGPSSQLTR HTCPGWGITH 540
ANLQTIPTDQ QGEGPREDVT HPGGDLDGVA NFYLEEBGFQ DGRQCQKMLM SEEGPPSLTG 600
15 CERLTGSHHF SSSKSNWFL SPRQPLFLSR P

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Seq ID NO: 595 DNA sequence
Nucleic Acid Accession #: NM_021614.1
Coding sequence: 1..1740

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20 1      11      21      31      41      51
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CGCCGGAACC TGCACGAGAT GGACTCAGAG CGCAGCGCCC TGCAGCCCCC CGCGTCTGTC 120
GGAGGAGGTG GCGGCGCGTC CTCCCGTCT GCAGCGCGTG CGCGCGCGCG CGCTGTTCOG 180
25 TCCTCAGCCC CGAGATCGT GGTGTCTAAG CCGAGCACA ACACTCCAA CAACCTGGCG 240
CTCTATGGAA CCGCGGCGCG AGGCAGCACT GGAGGAGCG GCGGCGGTGG CCGGAGCGGG 300
CAGGCGAGCA GCAGTGGCAC CAAGTCCAGC AAAAAGAAAA ACCAGAACAT CGGCTACAAG 360
CTGGGCCACC GGGCGGCCCT GTTCGAAAAG CGCAGCGCG TCAGCGACTA CGCGCTCATC 420
TTGCGCTTCT TCGGCATCGT GGTCTATGGT ATCGAGACCG AGCTGTCTGT GGGCGCCTAC 480
30 GACAAGCGGT CGCTGTATTC CTTAGCTCTG AAATGCCTTA TCAGTCTCTC CACGATCATC 540
CTGCTCGGTC TGATCATCGT GTACCAAGCC AGGGAATAT AGTTGTTTCT GGTGGACAAT 600
GGAGCAGATG ATCGGAGAT AGCCATGACT TATGAGCGTA TTTTCTTCAT CTGCTGGAA 660
ATACTGGTGT GTGCTATTCA TCCCATACCT GGGAAATATA CATTACATG GACGCGCCGG 720
35 CTTGCGTCTT CCTATGCCCC ATCCAACAC ACGCTGATG TGGATATTAT TTTATCTATA 780
CCAATGTTCT TAAGACTCTA TCTGATTGCC AGAGTCATGC TTTTACATAG CAACTTTTTC 840
ACTGATGCCT CCTCTAGAAG CATTGGAGCA CTTAATAAGA TAAACTTCAA TACACGTTTT 900
GTTATGAAGA CTTTAATGAC TATATGCCCA GGAAGCTGAC TCTTGTGTTT TAGTATCTCA 960
TTATGGATAA TTGCGCATG GACTGTCCGA GCTGTGTAAA GGTACCATGA TCAACAGGAT 1020
40 GTTACTAGCA ACTTCTCTTG AGCGATGTGG TTGATATCAA TAACTTTTCT CTCCATTGGT 1080
TATGGTGACA TGGTACCTAA CACATACTGT GGAAGAGGAG TCTGCTTACT TACTGGAATT 1140
ATGGGTGCTG GTTGACAGC CCTGTGTGTA GCTGTAGTGG CAAGGAAGCT AGAAGTTACC 1200
AAAGCAGAAA AACACGTGCA CAATTTCATG ATGGATACTC AGCTGACTAA AAGAGTAAAA 1260
AATGCAGCTG CCAATGTACT CAGGGAACA TGGCTAATT ACAAAATAC AAAGCTAGTG 1320
45 AAAAGATAG ATCATGCAA AGTAAGAAAA CATCAACGAA AATTCCTGCA AGCTATTCAT 1380
CAATTAAGAA GTGTAAAAAT GGAGCAGAGG AAAGTGAATG ACCAAGCAAA CACTTTGGTG 1440
GACTTGGCAA AGACCCAGAA CATCATGTAT GATATGATT CTGACTTAAA CGAAGGAGT 1500
GAAGACTTCG AAGAAGAGAT TGTACCCCTG GAAACAAAAC TAGAGACTTT GATTGGTAGC 1560
ATCCAGCCCC TCCCTGGGCT CATAGCCAG ACCATCAGGC AGCAGCAGAG AGATTTCATT 1620
50 GAGGCTCAGA TGGAGAGCTA CGACAGCAC GTCACTTACA ATGCTGAGCG GTCCCCGTCC 1680
TCGTCCAGGA GCGCGCGTC CTCTCCACA GCACCAACAA CTTATCAGA GAGTAGCTAG

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Seq ID NO: 596 Protein sequence
Protein Accession #: NP_067627.1

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55 1      11      21      31      41      51
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SSAPEIVVSK PEHNNNSNLA LYGTGGGGST GGGGGGGGSG HGSSSGTKSS KKKQNIGYK 120
LGHRRALFEK RRRLSDYALI FGMFGIVVMV IETELSWGAY DKASLYSLAL KCLISLSTII 180
60 LLGLIIVYHA REIQLFMVDN GADDWRIAMT YERIFFICLE ILVCAIHPIP GNYTFWTAR 240
LAPSYAPSTT TADVDIILSI FMFLRLYLIA RVMLLHSLKF TDASSRSIGA LNKINFNTFR 300
VMKTLMTICP GTVLLVFSIS LNIIAWTVR ACERYHDQDD VTSNPLGAMW LISITPLSIG 360
YGMVVPNTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVHFM MDTQLTKRVK 420
70 NAAANVLRET WLIYKNTKLK KIDHAKVRK HQRKFLQAIH QLRSVKMEQR KLANDQANTLV 480
DLAKTQNMIM DMISDLNERS EDFEKRICTL ETKLETIGS IHALPLGISQ TIRQQQRDFI 540
EAQMESYDKH VTYNAERSRS SSRRRSSST APPTSSBS

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Seq ID NO: 597 DNA sequence
Nucleic Acid Accession #: NM_016029.1
Coding sequence: 228..1097

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75 1      11      21      31      41      51
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GGCGGTGGCG GCGCGCAATG AACTGGGAGC TGCTGCTGTG GCTGCTGGTG CTGTGCGGCG 120
TGCTCCTGCT CTGTGTGCGG CTGCTGCGCT TCCTGAGGGC TGACGCGGAC CTGACGCTAC 180
TATGGGCGGA GTGGCAGGGA CAGCGCCAGC AATGGGAGCT GACTGATATG GTGTGTGGG 240
TGACTGGAGC CTCGAGTGGG ATTGGTGAGG AGCTGGCTTA CCAGTTGTCT AAACAGGAG 300
70 TTTCTCTGTG GCTGTGACCC AGAAGAGTGC ATGAGCTGGA AAGGCTGAAA AGAAGATGCC 360
TAGAGAAATG CAATTAAAAA GAAAAAGATA TACTTGTTTT GCCCTTGAC CTGACGACA 420
CTGGTTCCCA TGAAGCGGCT ACCAAAGCTG TTCTCCAGGA GTTGTGTAGA ATCGACATTC 480
TGGTCAACAA TGGTGAATG TCCAGCGGTT CTCTGTGCAT GGATACCAGC TTGGATGTCT 540
ACAGAAAGCT AATGAGCTT AACTACTTAG GGACGGTGTC CTTGACAAAA TGTGTTCTGC 600
CTCACATGAT CGAGAGGAGG CAAGGAAAGA TTGTTACTGT GAATAGCATC CTGGGTATCA 660

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TATCTGTACC TCITTTCCATT GGATACTGTG CTAGCAAGCA TGCTCTCCGG GGTITTTTAA 720
 ATGGCCCTTGG AACAGAACTT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTTGCCCCAG 780
 GACCTGTGCA ACATAATATT GTGGAGAATT CCCTAGCTGG AGAAGTCACA AAGACTATAG 840
 GCAATAATGG AGACCACTCC CACAAGATGA CAACCACTGG TTGTGTGCGG CTGATGTTAA 900
 TCAGCATGGC CAATGATTTG AAAGAAGTTT GGATCTCAGA ACAACCTTTC TTGTTAGTAA 960
 CATATTTGTG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCAACAAG ATGGGGAAGA 1020
 AAAGGATTGA GAACTTTAAG AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTTA 1080
 AGACAAAACA TGAAGTAAAA GAGCACCTGT ACTTTTCAAG CCACTGGAGG GAGAAATGGA 1140
 AAACATGAAA ACAGCAATCT TCITATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200
 ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260
 AGATTGCCAT GAATCTTGCA AA

Seq ID NO: 598 Protein sequence
 Protein Accession #: NP_057113.1

1 11 21 31 41 51
 MNWELLWLVL VLCAALLLLV QLLRFLRADG DLTLLWAEWQ GRRPEWELTD MVMVVTGASS 60
 GIGELAYQL SKLGVSLVLS ARRVHELERV KRRCLENGNL KEKDILVLPL DLTDTGSHEA 120
 ATKAVLQBEF RIDILVNNGG MSQRSLOMDT SLDVYRKLIE LNYLGTVSLT KCVLPHMIER 180
 KQKIVTVNS ILGIISVPLS IGYCASKHAL RGFENGLRTE LATYPGIIVS NICPGPVQSN 240
 IVENSLAGEV TKTIGNNGDQ SHKMTTSRCV RLMILISMAND LKEVWIESEP PLLVTVLMQY 300
 MPTWAWWITN KMGKKRIENF KSGVDADSSY FKIFKTKHD

Seq ID NO: 599 DNA sequence
 Nucleic Acid Accession #: NM_000793.2
 Coding sequence: 401..1222

1 11 21 31 41 51
 GCCTGCAGAG AGAGGCCACTT TGCACCACAG ACAGATAGCA AGAAGGGGAAA GACAGAGAGT 60
 GAGAAAAAAG AGGAGTCAGT CGCTCCTGGG AGAGGGAGAG AGTGAGACTG GGAGAAAGAG 120
 AAGCAGACAA AGTGTGTGTA AAACGGAGTA AAGAAAGAAA AAAAAAAAC TACCCTTAAA 180
 GCACATTTAA AAAAAAATAA CTCTGGCAAT TCAAGAAAGA AACAGGCTAC GTTTAAAGAG 240
 CATAGAGACA ATGAAAGGCT AAAGAAAATT TTAATAATCT TGCCACAGTC TCATAGGTGC 300
 TTGGAAATGA AAGTAGAACT GCCTGTCTTT AACGGACTCT GACAGAGAGG GTGAAGGGGA 360
 ACCAGAGCGC ACAAGGGAAC TGACTCAGGA GGCAGAGAAG ATGGGCATCC TCAGCGTAGA 420
 CTGTCTGATC ACACTGCAAA TTCTGCCAGT TTTTCTCTCC AACTGCTCTT TCCTGGCTCT 480
 CTATGACTCG GTCATTCTGC TCAAGCACGT GGTGCTGCTG TTGAGCCGCT CCAAGTCCAC 540
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Seq ID NO: 600 Protein sequence
 Protein Accession #: NP_000784.2

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Seq ID NO: 602 Protein sequence
 Protein Accession #: NP_005224.1

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LVVPAIKRDY GSQEDFTQWV NTKMKGLKCC GFTNYTDFED SPYFKENSAP PPFCCNDNVT 180
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Seq ID NO: 605 DNA sequence
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Coding sequence:

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Seq ID NO: 606 Protein sequence
Protein Accession #: NP_000720.1

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Coding sequence: 219..692

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GGAGGAGGAA AGAGAGTTTG TAAGGTATG CTGGTGGGTT AGCTAAACCA AGAAGGAGAC 1320
CTTTTACAA TGGAAACCTT GGGGGATGGT CAGAGCCAGC TOGAGACCTC ACACACGGCT 1380
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ATCAATATTG AGGATCAGGG CTCCTAGGCT CAGTGGTAGC TCTGGCTTAG ACACCACTGT 1740
GAGTGATCAC CTCCTGGGGA CCCTGCCTAT CCCACTTAC AGGTGAGGCA TGGCAATTCT 1800

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5
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GGAGCTGAT TAAACACAC ATAAACCAAA ACCAAACAAC AGGCCCTTGG GTGAAAGGTG 1860
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GCATTTCCCG GAAATACGA AAATCCCATG AGATAAATAA AAATATAGGT GATGGGCAGA 1980
TCTTTTCTTT AAAATAAAAA AGCAAAAACCT CTGTGGTGTAC CTAGTCAGAT GGTAGACGAG 2040
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CAGACATATC CAAAGGGAAT ACTCACATTT TGTAAAGAAG TTGAACATAG ACTGGAGTAA 2580
ACCATGTATT CCCTTATCTT TTACTTTTTT TCTGTGACAT TTATGTCTCA TGTAAATTTGC 2640
ATTACTCTGG TGGATTGTTT TAGTACTGTA TTGGGCTTCT TCGTTAATAG ATTATTTTCA 2700
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20 Seq ID NO: 608 Protein sequence
Protein Accession #: NP_001414.1

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LKTQVAFMIL SIIFCVIAL VVVFQLFTME KGNRPFLSGA TTLVCHLCL VGVSIYTSY 120
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30 Seq ID NO: 609 DNA sequence
Nucleic Acid Accession #: NM_004961.2
Coding sequence: 55..1575

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CCTCAGACTG AATCAAGAA TGAAGCCTCT TCCCGTGATG TTGTCTATGG CCCCAGGCC 180
CAGCCTCTGG AAAATCAGCT CCTCTCTGAG GAAACAAAGT CAACTGAGAC TGAGACTGGG 240
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GACCACAAAC TGCGCCCTGG CATTTGGAGAG AAGCCCACCTG TGGTCACTGT TGAGATCGCC 360
GTCAACAGCG TTGGTCCCTCT CTCTATCCTA GACATGGAAT ACACCATTTGA CATCATCTTC 420
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TTCCAGTTTG ATTTTACAGG AGTGAGCAAC AAAACTGAAA TAATCACAA CCAAGTTGGT 840
GACTTCAATG TCATGACGAT TTTCTTCAAT GTGAGCAGGC GGTTTGGCTA TGTGCTCTTT 900
CAAAACTATG TCCTCTCTTC CGTGACCACG ATGCTCTCCT GGGTTTCCCT TTGGATCAAG 960
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ACTTTCCAG TGACTTCCCC TAGCCCTGAC CCAGGCACTA GGCCCTGGTG ACTTCTGGG 2460
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5 Seq ID NO: 610 Protein sequence
Protein Accession #: NP_004952.1

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	TGSRVGLKPE	ASRILNTILS	NYDHKLRLPGI	GEKPTVVTVVE	IAVNSLGLPLS	ILDMEYTIDI	120
	IFSQTWYDER	LCYNDTFESL	VLNGNVVSQL	WIPDTFFRNS	KRTHEHEITM	PNQMVRIYKD	180
	GKVLTYTIRM	IDAGCSLHML	RFPMDSHSCP	LSPSSPSYPE	NEMIKWENP	KLEINBKNSW	240
	KLFQDFDTGV	SNKTEIITTP	VGDFMVMITF	FNVSRRFQIV	AFQNYVPSSV	TTMLSNVSWF	300
15	IKTESAPART	SLGITSVLTM	TTLGTFSRKN	FPRVSYITAL	DFYIAICFVF	CFCALLEFAV	360
	LNFLIYNQTK	AHASPKLRHP	RINSRAHART	RARSRACARQ	HQBAFVQIV	TTGSGDGEER	420
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	DNYSRVVFPV	TPFFPNVLYW	LVCNL				

20 Seq ID NO: 611 DNA sequence
Nucleic Acid Accession #: NM_021984.1
Coding sequence: 572..1753

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	CAGAGAAGTG	CTCAAAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAAAT	GACCACAGCG	180
	GTGTAAAGAA	AGCCAAATCA	AGGACCGGAA	TGTGAGCAGG	ACCTCAGAAG	CCCCCTTGT	240
	CACCTGCTCC	CAGCAAAAGC	AGCACTATCC	GGACTTCTAA	CACCATCGGG	TCGAGGGACC	300
30	TCAGACTGAA	TCAAAGAATG	AAGCCTCTTC	COGTGATGTT	GTCTATGGCC	CCCAGCCCCA	360
	GCCTCTGGAA	AATCAGCTCC	TCTCTGAGGA	AACAAAGTCA	ACTGAGACTG	AGACTGGGAG	420
	CAGAGTTGGC	AAACTGCCAG	AAGCCTCTCG	CATCTGAAC	ACTATCCTGA	GTAATTATGA	480
	CCACAACTG	CGCCCTGGCA	TTGGAGAGAA	GCCCACTGTG	GTCACTGTTG	AGATCTCCGT	540
	CAACAGCCTT	GGTCTCTCT	CTATCTTAGA	CATGGAATAC	ACCATTGACA	TCATCTTCTC	600
35	CCAGACCTGG	TACGACGAAC	GCCTCTGTTA	CAACGACACC	TTTGAGTCTC	TTGTTCTGAA	660
	TGGCAATGTG	GTGAGCCAGC	TATGGATCCC	GGACACCTTT	TTTAGGAATT	CTAAGAGGAC	720
	CCACGAGCAT	GAGATCACCA	TGCCCAACCA	GATGTCGCG	ATCTACAAGG	ATGGCAAGGT	780
	GTGTATACAC	ATTAGGATGA	CCATTGATGC	CGGATGCTCA	CTCCACATGC	TCAGATTTC	840
	AATGGATTCT	CACCTCTGCC	CTCTATCTTT	CTCTAGCTTT	TCCTATCCTG	AGAAATGAGAT	900
40	GATCTACAG	TGGGAAAATT	TCAAGCTTGA	AATCAATGAG	AAGAATCCT	GGAAGCTCTT	960
	CCAGTTGATG	TTTACAGGAG	TGAGCAACAA	AACTGAATA	ATCACAAACC	CAGTTGGTGA	1020
	CTTCATGGTC	ATGACGATT	TCCTCAATGT	GAGCAGGCG	TTTGGCTATG	TTGCCTTTCA	1080
	AAACTATGTC	CCCTCTCTCG	TGACCAAGAT	GCTCTCTGG	GTTCCTTTT	GGATCAAGAC	1140
	AGAGTCTGCT	CCAGCCCGGA	CCTCTCTAGG	GATCACTCT	GTTCGACCA	TGACCAAGTT	1200
45	GGGCACTTT	TCTGTAAAG	ATTTCGCGG	TGTCTCTAT	ATCACAGCCT	TGGATTCTTA	1260
	TATCGCCATC	TGCTTGCTCT	TCTGCTCTG	CGCTCTGTT	GAGTTTGTG	TGCTCAACTT	1320
	CTGATCTAC	AACACAGCAA	AAGCCCATGC	TTCTCCTAAA	CTCCGCCATC	CTCGTATCAA	1380
	TAGCCGTGCC	CATGCCCGTA	CCCGTGACCG	TTCCGAGCC	TGTGCCCGCC	AACATCAGGA	1440
	AGCTTTTGTG	TGCCAGATTG	TCACCACTGA	GGGAAGTGAT	GGAGAGGAGC	GCCCGTCTTG	1500
50	CTCAGCCCG	CAGCCCGCTA	GCCAGGTAG	CCCTGAGGGT	CCCGCAGCG	CTGCTCCAAA	1560
	GCTGGCCTGC	TGTGAGTGT	GCAAGOGTTT	TAAGAAGTAC	TTCTGATGG	TCGCCGATTG	1620
	TGAGGGCAGT	ACCTGGCAGC	AGGCCCGCCT	CTGCATCCAT	GTCTACCGCC	TGGATAACTA	1680
	CTGAGAGATT	GTTTTCCTAG	TGACTTTCTT	CTTCTTCAAT	GTGCTCTACT	GGCTTGTGTT	1740
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55	TCCAAGCCCC	TTGCCAAGGG	AGTTGGGGGA	AAGCAGCAGC	AGCAGCAGGA	GCGACTAGAG	1860
	TTTTTCTGTC	CCCATTTCCC	AAACAGAAGC	TTGCAGAGGG	TTTGTCTTTG	CTGCCCTCT	1920
	CCCTACCTG	GCCCATCTAC	TGAGTTTCT	CAGCAGACCA	TTTCAAATTA	TTAATAAATG	1980
	GGCCACCTCC	CTCTCTTCA	AGGAGCATCC	GTGATGCTCA	GTGTTCAAAA	CCACAGOCAC	2040
	TTAGTGATCA	GCTCCCTAAA	ACCATGCCTA	AGTACAGGCG	GATTAGCTAT	CTTCCAACAA	2100
60	TGCTGACCAC	CAGACAATTA	CTGCATTTT	CCAGAAGCCC	ACTATTGCTT	TTGCACTGCT	2160
	TTCCGCCCA	TTTGGCCTC	AGCCTCAAAG	TGCACGACT	AGTTGCTTGC	CTATACCTGG	2220
	CACCTCATTA	AGATGCTGGG	CAGCAGTATA	ACAGAGGAA	GAGATCCCTC	TCCTTTGGTC	2280
	AGATTATTAT	GTTCTCAGTT	CTCTCTCCCT	GCTACCCCTT	TCTCTGCAGA	TAGATAGACA	2340
	CTGGCATTAT	CCCTTTAGGA	AGAGGGGGGG	GCAGCAAGAG	AGCCTATTTG	GGACAGCATT	2400
65	CCTCTCTCTC	TGCTGCTGTG	ACATCTCCCT	CTCCTTGCTG	GCTCCATCTT	TGCTCTGCAC	2460
	TACCAATTCA	ATGCCCTTCA	TCCRAATGGT	ATCTATTTTT	GTGTGTGATT	ATAGTAACCTA	2520
	CTCCTGCTT	TATATGCCAC	CCTCTTCTT	CTCTTTGACC	CCTGTGACTC	TTCTGTAAAC	2580
	TTTCCAGTG	ACTTCCCTTA	GCCCTGACCC	AGGCACTAGG	CCTTGGTGAC	TTCCCTGGGC	2640
	CAAGAACTA	AGGAACTCG	GCTTTGCAAC	AGGCATTACT	OGCCATTGAT	TGGTGCCAC	2700
70	CCAGGGCACA	CTGTGGAGT	TCTATCACTT	GCTTGACCCC	TGGACCCATA	AACAGTCCA	2760
	CTGTTATACC	CGGGGCACTC	TAACCATCAC	AATCAATCAA	TCAAATTCCT	TTAAATTTGT	2820
	ATGGCACTGG	AACCTTGGCA	AAGCACTTTT	GACAAGTTGT	GTCTGATTGG	AGCTTCATGA	2880
	TAGCCTTTGT	ACATCTTTAG	GGCAGGATTC	TTATCCCAT	TTTGAGATG	AAAACTCTGA	2940
	GTCACAGATT	TCTGTGGGAC	TGTGGATCTC	ACTGGAAGCT	ATCCAAGAGC	CCACTGTCTC	3000
75	CTTCTAGACC	ACATGATAGG	GCTAGACAGC	TCACTTACCC	ATGATTCTCT	TCTGTCACTC	3060
	CTGCTGGCAG	ACCACTGGCA	AGGCCAGAG	TGGGACCTC	TCTTTAGCTC	AATTTCTGGG	3120
	CCTGAGGTGC	TCAGACTGCC	CCCAAGATCA	AATCTCTCCT	GCTGTAGTGA	ACCCAGTGGG	3180
	ATGAATTGG	ACATGCCCCA	ATGCTTCTAT	ATGCTAAGTG	AAATCTGTGT	CTGTAATTTG	3240
80	TTGGGGGGTG	GATAGGGTGG	GGTCTCCATC	TACTTTTTGT	CACCATCATC	TGAAATGGGG	3300
	AAATATGTAA	ATAAATATAT	CAGCAAAGC				

Seq ID NO: 612 Protein sequence
Protein Accession #: NP_068819.1

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5	MVRIYKDGKV	LYTIRMTIDA	GCSLHMLRFP	MDSHSCPLSF	SSFSYPENEM	IYKWNFKLE	120
	INEKNSWKLF	QLDPTGVSNK	TEIITTPVGD	FMVMTIFPNV	SRRFYGVAFQ	NYVPSVITTM	180
	LSWVSFWIKT	ESAPARTSLG	ITSVLMTTL	GTFSRKNFPR	VSYYTALDFY	IAICFVFCFC	240
	ALLEFAVLNF	LIYNQTKAHA	SPKLRHPRIN	SRAHARTRAR	SRACARQHQE	AFVCQIVTTE	300
	GSDGEERPSC	SAQQPPSPGS	PEGPRSLCSK	LACCEWCKRF	KKYFCMVPCD	EGSTWQQARL	360
10	CIHVYRLDNY	SRVVPVPTFP	FFNVLYWLVC	LNL			

Seq ID NO: 613 DNA sequence
Nucleic Acid Accession #: NM_021987.1
Coding sequence: 572..1657

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	CAGAGAAGTG	CTCAAAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAAAT	GACCAACGCG	180
20	GTGTAAAGAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAA	CCCCCTTGT	240
	CACGTGCTCC	CAGCAAAAGC	AGCACTATCC	GGACTTCTAA	CACCATCCGG	TCGAGGGACC	300
	TCAGACTGAA	TCAAAGAATG	AAGCCTCTTC	CGGTGATGTT	GTCTATGGCC	CCCAGCCCCA	360
	GCCTCTGGAA	AATCAGCTCC	TCTCTGAGGA	AACAAAGTCA	ACTGAGACTG	AGACTGGGAG	420
	CAGAGTTGGC	AAACTGCGAG	AAGCCTCTCG	CATCTGAAAC	ACTATCCTGA	GTAATTATGA	480
25	CCACAACTG	CGCCTGGCA	TGGAGAGAA	GCCACTGTG	GTCACTGTG	AGATCTCCGT	540
	CAACAGCCTT	GGTCTCTCT	CTATCCTAGA	CATGGAATAC	ACCATTGACA	TCATCTTCTC	600
	CCAGACCTGG	AATTCTAAGA	GGACCCACGA	GCATGAGATC	ACCATGCCCA	ACCAGATGGT	660
	CCGCACTTAC	AAGGATGGCA	AGGTGTTGTA	CACAATTAGG	ATGACCATTG	ATGCCGGATG	720
	CTCACTCCAG	ATGCTCAGAT	TTCCAATGGA	TTCTCACTCT	TGCCCTCTAT	CTTCTCTAG	780
30	CTTTTCTTAT	CCTGAGAATG	AGATGATCTA	CAAGTGGGAA	AATTTCAAGC	TTGAAATCAA	840
	TGAGAAGAAC	TCTTGGGAAG	TCTTCCAGTT	TGATTTTACA	GGAGTGAGCA	ACAAAACCTGA	900
	AATAATCACA	ACCCAGTGT	GTGACTTCAT	GGTCATGACG	ATTTCTCTCA	ATGTGAGCAG	960
	GCGGTTTGGC	TATGTTGCC	TTCAAACTA	TGTCCCTTCT	TCCGTGACCA	CGATGCTCTC	1020
	CTGGGTTTCC	TTTGGATCA	AGACAGAGTC	TGCTCCAGCC	CGGACCTCTC	TAGGGATCAC	1080
35	CTCTGTCTTG	ACCATGACCA	CGTTGGGCAC	CTTTTCTCGT	AAGAATTTCC	CGCGTGTCTC	1140
	CTATATCACA	GCCTTGGATT	TCTATATGCG	CATCTGCTTC	GTCTTCTGCT	TCTGCGCTCT	1200
	GTGAGAGTTT	GCTGTGCTCA	ACTTCTGTAT	CTACAACCAG	ACAAAAGCCC	ATGCTTCTCC	1260
	TAAACTCCGC	CATCTCGTA	TCAATAGCCG	TGCCCATGCC	CGTACCCGTG	CAGTTCCCG	1320
	AGCCTGTGCC	CGCCAAATC	AGGAAGCTTT	TGTGTGCCAG	ATTGTCAACA	CTGAGGGAGG	1380
40	TGATGGAGAG	GAGCGCCCGT	CTTGCTCAGC	CCAGCAGCCC	CCTAGCCGAG	GTAGCCCTGA	1440
	GGGTCCCGCG	AGCCTCTGCT	CCAAGCTGGC	CTGCTGTGAG	TGTTGCAAGC	GTTTTAAAGAA	1500
	GTACTTCTGC	ATGTGTCGCC	ATTGTGAGGG	CAGTACCTGG	CAGCAGGGCC	GCTCTGCAAT	1560
	CCATGTCTAC	CGCCTGGATA	ACTACTCGAG	AGTTGTTTTT	CCAGTGACTT	TCTTCTTCTT	1620
	CAATGTGCTC	TACTGGCTTG	TTTGCCCTFA	CTTGTAGGTA	CCAGCTGGTA	CCCTGTGGGG	1680
45	CAACCTCTCC	AGTTCCCCAG	GAGGTCCAAG	CCCCTTGCCA	AGGGAGTTGG	GGGAAAGCAG	1740
	CAGCAGCAGC	AGGAGCGACT	AGAGTTTTTC	CTGCCCCATT	CCCCAAACAG	AAGCTTGCA	1800
	AGGGTTTGT	TTTGTGCC	CTCTCCCTTA	CCTGGCCCAT	TCACTGAGTT	TTCTCAGCAG	1860
	ACCATTTCAA	ATTATTAATA	AATGGGCCAC	CTCCCTCTTC	TTCAAGGAGC	ATCCGTGATG	1920
	CTCAGTGTTC	AAAACACAG	CCACTTAGTG	ATCAGCTCCC	TAAAACCATG	CCTAAGTACA	1980
50	GGCGGATTAG	CTATCTTCCA	ACAATGCTGA	CCACCAGACA	ATTACTGCAT	TTTTCCAGAA	2040
	GCCCACTAAT	GCCTTTGCGC	TGCTTTGCGC	CCAGTTCCTG	CCTCAGCCCT	AAAGTGACAC	2100
	GACTAGTCTG	TTGCTATATC	CTGGCACCTC	ATTAAGATGC	TGGGCAGCAG	TATAACAGGA	2160
	GGAAGAGATC	CCTCTCCTTT	GGTCAGATTA	TTATGTTCTC	AGTTCTCTCT	CCCTGCTACC	2220
	CCTTTCTCTG	CAGATAGATA	GACACTGGCA	TTATCCCTTT	AGGAAGAGGG	GGGGGAGGCA	2280
55	AGAGAGGCTA	TTTGGGACAG	CATTCTCTCT	TCTCTGCTGC	TGTGACATCT	CCCTCTCCTT	2340
	GCTGGCTCCA	TCTTCTGCT	GCACTACCAA	TTCAATGCC	TTTCAATCCA	GGGTATCTAT	2400
	TTTGTGTGT	GATTATAGTA	ACTACTCCCT	GCCTTATATG	CCACCTCTCT	CCCTCTCTTT	2460
	GACCCCTGTG	ACTCTTTCTG	TAACCTTTCC	AGTGACTTCC	CCTAGCCCTG	ACCAGGCAC	2520
	AGGCCTTGGT	GACTTCTCTG	GGCCAGAGAA	CTAAGGAAAC	TGGGCTTTGC	AACAGGCATT	2580
60	ACTCGCCATT	GATTGGTGCC	CACCCAGGGC	ACACTGTCCG	AGTTCTATCA	CTTGCTTGAC	2640
	CCCTGGACCC	ATAAACCACT	CCACTGTAT	ACCGGGGCA	CTCTAACCAT	CACAATCAAT	2700
	CAATCAAATT	CCCTTAAATT	TGTATGGCAC	TGGAACCTTG	GCAAGCACT	TTTGACAAGT	2760
	TGTGTCTGAT	TGGAGCTTCA	TGATAGCCTT	GTGACATCTT	TAGGGCAGGA	TTCTTATCCC	2820
	CATTTTGAG	ATGAAAACCC	TGAGTCACAG	ATTCTGTGG	GACTGTGGAT	CTCACTGGAA	2880
65	GCTATCCAAG	AGCCCACTGT	CACCTTCTAG	ACCAATGAT	AGGGCTAGAC	AGCTCAGTTC	2940
	ACCATGATTC	TCTTCTGTCA	CCTCTGCTGG	CACACCACTG	GCAAGGCCCA	GAATGGCGAC	3000
	CTCTCTTTAG	CTCAATTTCT	GGGCTGAGG	TGCTCAGACT	GCCCCAAGA	TCAATCTCT	3060
	CCTGGCTGTA	GTAACCCAGT	GGAATGAATT	TGGACATGCC	CCAATGCTTC	TATATGCTAA	3120
	GTGAAATCTG	TGCTGTAAAT	TTGTGGGGGG	GTGGATAGGG	TGGGGTCTCC	ATCTACTTTT	3180
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Seq ID NO: 614 Protein sequence
Protein Accession #: NP_068822.1

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80	VMTIFPNVSR	RFYGVAFQNY	VPSSVTMLLS	WVSFWIKTES	APARTSLGIT	SVLMTTLTGT	180
	FSRKNFPRVS	YITALDFYIA	ICFVFCFCAL	LEFAVLNPLI	YNQTKAHASP	KLRHPRINSR	240
	AHARTRARSR	ACARQHQAEP	VQIVTTTSGS	DGEERPSCSA	QPPSPGSPSE	GPRSLCSKLA	300
	CCEWCKRFFK	YFCMVPCDCE	STWQQRLCI	HVYRLDNYSR	VVFPVTPFPF	NVLVYLVLN	360

Seq ID NO: 615 DNA sequence
Nucleic Acid Accession #: NM_021990.1
Coding sequence: 1309..2490

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Seq ID NO: 616 Protein sequence
Protein Accession #: NP_068830.1

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MVIYKDGKV LYTIKRTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120
INEKSNWKLQ QFDFTGVSNK TBIITPVGD FMVMTIFFNV SRRPGYVAFQ NYVPSSVTM 180
LSWVFWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDPY IAICFVPCFC 240

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ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQB AFVQIVTTE 300
 GSDGGERPSC SAQQPPSPGS PBGPRLSLCSK LACCWCKRF KKYFCMVPCD EGSTWQGGRL 360
 CIHVYRLDNY SRVVPVTFP FPNVLYWLVC LNL

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Seq ID NO: 617 DNA sequence
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 Coding sequence: 26..952

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 15 ATTCCGAGAG TTGCGGAAC GCTACGAGGA CCTGCTAACC AGGCTGCGGG CCACCCAGAG 240
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Seq ID NO: 618 Protein sequence
 Protein Accession #: NP_004855.1

35

1 11 21 31 41 51
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 EDLLRLRLAN QSWEDSNTDL VPAPAVRILT PEVRLGSGGH LHLRISRAAL PEGLEASRL 120
 40 HRLFLRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPPSQSDQLL AESSARPLQL 180
 ELHLRPQAA RRRRARARNG DDCLPLGPRC RLRLTVRASL EDLWADWVL SPREVQVTMC 240
 IGACPSQFRA ANMHAQIKTS LHRLKPDTEP APCCVPASYN FMVLIQKTDV GVSILQTYDDL 300
 LAKDCHCI

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Seq ID NO: 619 DNA sequence
 Nucleic Acid Accession #: NM_003979.2
 Coding sequence: 254..1357

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 55 CTGCGCTGCT GCGCTCTTGC GCGCGGGAAG CAGCACCAGG TTCAAGGCCA ACGCCTTGGC 240
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 65 CTTTGTCTCT CTGCTCACT ACGTCTCTT CTGTATGGCG CTGACCTTCC TCATGTCTCT 840
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 75 TCAAGGGGAT GTGGGCGAAA TCTTGAGTCT TCTGAGAAAA CTGTACAAGA CACTACGGGA 1440
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 TTGCTGGCAC CCCGCTCCC CAACCTTCT TGCTGGGTA GAGAGGCTA AAGATCAACC 2040

5
TAAATTACT CATCTCTCTA GTGCTGCCTC ACATTGGGCC TCAGCAGCTC CCCAGCACCA 2100
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Seq ID NO: 620 Protein sequence
Protein Accession #: NP_003970.1

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1 11 21 31 41 51
MATTVPDGR NGLESKYYRL CDKABAWGIV LETVATAGVV TSVAFMLTLP ILVCKVQDSN 60
RRKMLPTQFL FLLGVLFIFG LTFAPFIIGLD GSTGPTRFLL FGILFSICFS CLLAHAVSLT 120
KLVRGRKPLS LLVILGLAVG FSLVQDVIAI EYIVLTMNRT NVNVFSELSA PRNEDFVLL 180
LTYVLFMLAL TFLMSSFTFC GSFTGWKRHG AHYLTMLLS IAIWVAVITL LMLPDFDRRW 240
DDTLSSALA ANGVVFLAY VSPFVLLTK QRNPMDYPVE DAFCKPQLVK KSYGVENRAY 300
SQEBITQGF ETDGLYAPY STHFQLQNP PQKEFSIPRA HAMPSPYKDY EVKKEGS

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Seq ID NO: 621 DNA sequence
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Coding sequence: 48..851

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GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT 180
30 ATGACTCAGA AACAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAT 240
TCTTTGSCCT ACCATATACT GGAATGTAA ACTCCGCGT CATAGAAATA ATGCAGAAGC 300
CCAGATGTGG AGTGCCAGAT GTTGCAAGAT ACTCACTATT TCCAATAGC CCAAAATGGA 360
CTTCCAAAGT GGTCACTTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG 420
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35 GGAAAGTTGT ATGGGGAAC TGTGACATCA TGATTGGCTT TGGCGAGGA GCTCATGGGG 540
ACTCCTACCC ATTTGATGGG CCAGGAAACA CGCTGGCTCA TGCCCTTGGG CCGTGGGACAG 600
GTCTCGGAGG AGATGCTCAC TTCGATGAGG ATGAAOCTG GACGGATGGT AGCAGTCTAG 660
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CCTCTGATCC TAATGCAGTG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA 780
40 AACTTCCCA GGATGATATT AAAGGCATT AGAACTATA TGGAAAGAGA AGTAATTCAA 840
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TGTGTCAGT CAGAAATTGA TAAGCACTGT TCCTCCACTC CATTAGCAA TTATGTCAAC 960
CTTTTITATT GCAGTTGGTT TTTGAATGTC TTTCACTCCT TTTATTGGTT AAACCTCTTT 1020
45 ATGGTGTGAC TGTGCTTAT TCCATCTATG AGCTTTGTCA GTGCGGTAG ATGTCAATAA 1080
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Seq ID NO: 622 Protein sequence
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55 PHITVDRLS KALNMWKEI PLHFRKVVWG TADIMIGPAR GAHGDYPPD GPGNTLAHAF 180
APGTGLGGDA HFDEDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYNGED 240
PQNFILSQDD IKGIQKLYGK RSNSRKK

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ACGTGGCTGC TGSCAGAGCA AGCATGAATT CGATGACTTC AGCAGTTCG GTGGCCAATT 240
CTGTGTTGGT GGTGGCACCC CACAATGGT ATCCTGTGAC CCCAGGAATT ATGTCTCACG 300
70 TGCCCCGTGA TCCAACAGC CAGCGCAAG TCCACCTAGT TCCTGGGAAC CCACTAGTT 360
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GGGCCATCCA GATCATATT GGCTGGCTC ACATGGGCTC GCGCTCCATC ATGGCGACGG 480
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75 GCTGCTGTC TGSCAGTTTG GGCTTGAACA TCGTCAGTGC AATCTGCTCT GCAGTTGGAG 660
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TATGTGGGCA TCCAGCTCT GGGGCTTGG CACACACACA TTGTTGTCT CTGCTGCATG 1260

TGAGCTTGTG GGTAGAGGA ACAAATATCT AGACATTCAA TCTTACTCT TTCAATTGTG 1320
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Seq ID NO: 624 Protein sequence
Protein Accession #: NP_113645.1

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1 11 21 31 41 51
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10 PVQKALKEGK TLGAIQIIIG LAHIGLGSIM ATVLVGEYLS ISFYGGFFPW GGLWFIISGS 120
LSVAAENQFY SYCLLSGSLG LNIVSAICSA VGVILFITDL SIPHPYAYPD YYPYANGVNP 180
GMAISGVLLV FCLLEPGIAC ASSHFGCQLV CCQSSNVSVI YPNIIAANPV ITPEPVTSP 240
SYSSEIQANK

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Coding sequence: 1..870

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25 CCTACCTCGG CTTCCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCAOGGCGTG 240
AACGGCTCCG CCGGAGGCTA CCCAGCCAAA GCTTATGCCG ACTATAGCTA CGCTAGCTCC 300
TACCACCACT ACGGGGGGCG CTACAACCGC GTCCCAAGCG CCACCAACCA GCCAGAGAAA 360
GAAGTGAACG AGCCGAGGTG GAGAATGGTG AATGGCAAC CAAGAAAGT TCGTAAACCC 420
AGGACTATTT ATTCCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG 480
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30 GTGAAATCTT GGTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AAACGGGGAG 600
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CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACCC TCATGCCAC 720
CCTCGGACCT CCAACCACTC CCCAGCGTCC AGCTACCTCG AGAAGCTCTG ATCTGGTAC 780
35 ACAAGTGCAG CAGCTCAAT CAATCCAC CTGCGCGCGC CGGCTCCTT ACAGCACCG 840
CTGCGCTG CTGCGGAC ACTCTATTAG

Seq ID NO: 626 Protein sequence
Protein Accession #: NP_005212.1

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45 EVTEPEVRMV NGKPKKVRKP RTIYSSPQLA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ 180
VKIWFQNKRS KIKKIMKNGE MPPEHSPSSS DPMACNSPQS PAVWEPQSSS RSLSHHFAH 240
PPTSNQSPAS SYLENSASWY TSAASSINSH LPPFGSLQHP LALASGTLV

Seq ID NO: 627 DNA sequence
Nucleic Acid Accession #: NM_014420
Coding sequence: 118..792

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CTGTCTGACA CGGACTGCAA TACCAGAAAG TTCTGCCTCC AGCCCCGCGA TGAGAAGCCG 300
TTCTGTGCTA CATGTGCTGG GTTGGGAGG AGGTGCCAGC GAGATGCCAT GTGCTGCCCT 360
60 GGGACACTCT GTGTGAACGA TGTGTGTACT ACGATGGAAG ATGCAACCCC AATATTAGAA 420
AGGCAGCTTG ATGAGCAAGA TGGCACACAT GCAGAAGGAA CAACTGGGCA CCCAGTCCAG 480
GAAAACCAAC CCAAAAGGAA GCCAAGTATT AAGAAATCAC AAGGCAGGAA GGGACAAGAG 540
GGAGAAAGTT GTCTGAGAAC TTTTACTGTG GGCCCTGGAC TTGTCTGTGC TGTCTATTT 600
TGGACGAAAA TTTGTAAAGC AGTCCTTTTG GAGGACAGG TCTGCTCCAG AAGAGGGCAT 660
65 AAGACACTG CTCAAGCTCC AGAAATCTTC CAGCGTTGCG ACTGTGGCCC TGGACTACTG 720
TGTGGAAGCC AATTGACCAG CAATCGGCAG CATGCTCGAT TAAGAGTATG CCAAAAAATA 780
GAAAAGCTAT AAATATTTC AATAAAGAA GAATCCACAT TGCAAAAAA AAAAAAATA 840
A

70
Seq ID NO: 628 Protein sequence
Protein Accession #: NP_055235

75 1 11 21 31 41 51
MVAALLGLS WLCSPLGALV LDFNNIRSSA DLHGARKGSQ CLSDTDCNTR KFCLOPRDEK 60
PFCATCRGLR RRCQRDAMCC PGTLCVNDVC TTMEDATPIL ERQLDEQDGT HAEGTGHFV 120
QENQPKRKPS IKKSQGRKQG EGESCLRTFD CGPGLCCARH FMTKICKPVL LEGQVCSRRG 180
HKDTAQAPFI FQRCDCGPGI LCRSGLTSNR QHARLRVCQK IEKL

80
Seq ID NO: 629 DNA sequence
Nucleic Acid Accession #: NM_002448.1
Coding sequence: 241..1134

1 11 21 31 41 51

Seq ID NO: 630 Protein sequence
Protein Accession #: NP_002439.1

Seq ID NO: 631 DNA sequence
Nucleic Acid Accession #: NM_002557.1
Coding sequence: 13..2049

1192

CTCTTTTCCA TTAATAAAC TGTAACACA AGAACCCA

Seq ID NO: 632 Protein sequence
Protein Accession #: NP_002548.1

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1	11	21	31	41	51	
MMKLLLVVGL	VLVLKHHHDA	AHKLVCYPTN	WAHSRPGPAS	ILPHDLDPFL	CTHLIPAFAS	60
MNNNQIVAKD	LQDEKILYPE	FNKLKERNRE	LKTLLSIGGW	NFGTSRFTTM	LSTFANREKF	120
IASVISLLRT	HDPDGLDLFF	LYPGLRGSPM	HDRWTFLELI	EELLFAFRKE	ALLTMRPRL	180
LSAAVSGVPH	IVQTSVDVRF	LGRLLDPIV	LSYDLHGSWE	RFTGHNSPLF	SLPEDPKSSA	240
YAMNYWRKLG	APSEKLIMGI	PTYGRTFRLL	KASKNGLQAR	AIGPASPGKY	TKQEGFLAYF	300
EICSFVWGAK	KHWIDYQYVP	YANKGKEWVG	YDNAISFSYK	AWFIRREHFG	GAMVNTLDM	360
DVRGTFCGTG	PFPLVYVLND	ILVRAEFSST	SLPQFWLSSA	VNSSSTDPER	LAVTTAWTTD	420
SKILPFGGEA	GVTEIHGKCE	NMTITPRGTT	VTPTKETVSL	GKHTVALGEK	TEITGAMTMT	480
SVGHQSMTPG	EKALTPVGHQ	SVTTGQKTLT	SVGYQSVTPG	EKTLTPVGHQ	SVTPVSHQSV	540
SPGGTMTMPV	HFQTETLRQN	TVAPRRKAVA	REKVTVPSEN	ISVTFEGQTM	PLRGENLTSE	600
VGTHPRMGNL	GLQMEANENM	MLSSSPVIQL	BEQTPLAFDN	RFVPIYGNHS	SVNSVTPTQS	660
PLSLKKEIPE	NSAVDEEA					

Seq ID NO: 633 DNA sequence
Nucleic Acid Accession #: NM_003885.1
Coding sequence: 98..1021

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30
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1	11	21	31	41	51	
AAACTCAGAA	TTTTGCGGG	CTCGGTGAGC	GGTTTTATCC	CTCCGGCCGG	CAGGCTGGGC	60
GCAGGGGGCG	AGCCCCCGCC	CGGCGCGCAG	CAGCACCATG	GGCACGGTGC	TGTCCTCTGT	120
TCCAGCTACT	CGGAAGGCCA	CGCTGTTTGA	GGATGCGCGC	GCCACCGTGG	GCCACTATAC	180
GGCGGTACAG	AACAGCAAGA	ACGCCAAGGA	CAAGAACCTG	AAGCGCCACT	CCATCATCTC	240
CGTGCTGCTT	TGGAAGAGAA	TCGTGGCCGT	GTGCGCCAAG	AAGAAGAACT	CCAAGAAGGT	300
GCAGCCTAAC	AGCAGCTACC	AGAACAACAT	CACGCACCTC	AACAATGAGA	ACCTGAAGAA	360
GTGCTGTGCG	TGCGCCAACC	TGTCCACATT	CGCCAGCCCG	CCACCGGCCG	AGCCGCTGTC	420
ACCCCGCGCC	AGCCAGCTCT	CGGTTTCCCA	GACCGGGGGC	TCCTCTCTAG	TCAAGAAAGC	480
CCCTCACCTT	CGCGTCACCT	CCGCAGGGAC	GCCCAAAACG	GTCTCTGTCC	AGGCGTCCAC	540
CAGTGAGCTG	CTTCGCTGCC	TGGGTGAGTT	TCTCTGCGCG	CGGTGCTACC	GCCTGAAGCA	600
CCTGTCCCCC	ACGGACCCCG	TGCTCTGGCT	GCGCAGCGTG	GACCGCTGCG	TGCTTCTGCA	660
GGGCTGGCAG	GACCAGGGCT	TCATCACGCC	GGCCAACGTG	GTCTTCTCTT	ACATGCTCTG	720
CAGGGATGTT	ATCTCTCTCG	AGGTGGGCTC	GGATCACGAG	CTCCAGGCCG	TCCTGTCTGAC	780
ATGCGCTGAC	CTCTCTACT	CCTACATGGG	CAACGAGATC	TCCTACCCCG	TCAAGCCCTT	840
CCTGGTGAGG	AGCTGCAAGG	AGGCCTTTTG	GGACCGTTGC	CTCTCTGTCA	TCAACCTCAT	900
GAGCTCAAAG	ATGCTGCAGA	TAAATGCGGA	CCCACTACT	TTCACACAGG	TCTTCTCCGA	960
CCTGAAGAAC	GAGAGCGGCC	AGGAGGACAA	GAAGCGGCTC	CTCCTAGGCC	TGGATCGGTG	1020
AGCACTGTAG	CCTGCGTCAT	GGCTCAAGGA	TTCAATGCAT	TTTAAAGAAT	TATATTATTA	1080
ATCAGTTTGG	TGTACAG					

Seq ID NO: 634 Protein sequence
Protein Accession #: NP_003876.1

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55

1	11	21	31	41	51	
MGTVLSLSPS	YRKATLFEDG	AATVGHYTA	QNSKQAKDRN	LKRHSIISVL	PWKRIVAVSA	60
KKQNSKKVQP	NSSYQNNITH	LNENLKKSL	SCANLSTPAQ	PPPAQPPAPP	ASQLSGSQTG	120
GSSSVKKAPH	PAVTSAGTPK	RVIVQASTSE	LLRCLGEFLC	RRCYRLKHL	PTDPVLWLRS	180
VDRSLLLQGW	QDQGFITPAN	VVFLYMLCRD	VISSEVGS DH	ELQAVLLTCL	YLSYSYMGNE	240
ISYPLKPFIV	ESCKEAFWDR	CLSVINLMSS	KMLQINADPH	YFTQVPSDLK	NESGQEDKKR	300
LLGLGLDR						

TABLE 79A:

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelD:	Unigene number			
	Unigene Title:	Unigene gene title			
	Seq ID No.:	Sequence identification number linking information in Table 79A to sequences in Table 80			
10	Pkey	ExAccn	UnigenelD	Unigene Title	Seq ID No.
	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	Seq ID No. C1 & C217
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	Seq ID No. C2 & C218
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C3 & C219
15	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C4 & C220
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID No. C5 & C221
	443646	AI085198	Hs.164226	Thrombospondin 1	Seq ID No. C6 & C222
	409556	AW103364	Hs.727	Inhibin, beta A (activin A, activin AB a	Seq ID No. C7 & C223
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (psa	Seq ID No. C8 & C224
20	444381	BE387335	Hs.283713	hypothetical protein BC014245	Seq ID No. C9 & C225
	421582	AI910275	Hs.350470	trefoil factor 1 (breast cancer, estrogen	Seq ID No. C10 & C226
	411789	AF245505	Hs.72157	Adfican	Seq ID No. C11 & C227
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	Seq ID No. C12
	428698	AA852773	Hs.334838	KIAA1866 protein	Seq ID No. C13 & C228
25	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	Seq ID No. C14 & C229
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	Seq ID No. C15 & C230
	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	Seq ID No. C16 & C231
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	Seq ID No. C17 & C232
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	Seq ID No. C18 & C233
30	418888	AU076801	Hs.49436	cadherin 17, LI cadherin (liver-intestin	Seq ID No. C19 & C234
	432179	X75208	Hs.2913	EphB3	Seq ID No. C20 & C235
	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	Seq ID No. C21 & C236
	409889	AW630041	Hs.56937	suppression of tumorigenicity 14 (colon	Seq ID No. C22 & C237
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C23 & C238
35	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C24 & C239
	411975	AI916058	Hs.144583	3'UTR of: dead ringer (Drosophila)-like	Seq ID No. C25 & C240
	434206	AW136973	Hs.362915	ESTs, Weakly similar to S69890 mitogen i	Seq ID No. C26 & C241
	423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	Seq ID No. C27 & C242
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	Seq ID No. C28 & C243
40	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	Seq ID No. C29 & C244
	415214	AI445236	Hs.125124	EphB2	Seq ID No. C30 & C245
	443247	BE614387	Hs.333893	c-Myc target JPO1	Seq ID No. C31 & C246
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	Seq ID No. C32 & C247
	410418	D31382	Hs.63325	transmembrane protease, serine 4	Seq ID No. C33 & C248
45	446342	BE298665	Hs.14846	solute carrier family 7 (cationic amino	Seq ID No. C34 & C249
	411274	NM_002776	Hs.69423	kallikrein 10	Seq ID No. C35 & C250
	104978	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	Seq ID No. C36 & C251
	422260	AA315993	Hs.105484	regenerating gene type IV	Seq ID No. C37 & C252
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C38 & C253
50	420344	BE463721	Hs.97101	putative G protein-coupled receptor	Seq ID No. C39 & C254
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	Seq ID No. C40 & C255
	437935	AW939591	Hs.6940	mucin 13, epithelial transmembrane	Seq ID No. C41 & C256
	422330	D30783	Hs.115263	epiregulin	Seq ID No. C42 & C257
	408908	BE296227	Hs.250822	serine/threonine kinase 15	Seq ID No. C43 & C258
55	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	Seq ID No. C44 & C259
	437852	BE001836	Hs.256897	putative GPCR	Seq ID No. C45 & C260
	408243	Y00787	Hs.624	interleukin 8	Seq ID No. C46 & C261
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	Seq ID No. C47 & C262
	439738	BE246502	Hs.9598	sera domain, immunoglobulin domain (Ig),	Seq ID No. C48 & C263
60	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	Seq ID No. C49 & C264
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	Seq ID No. C50 & C265
	417771	AA804698	Hs.82547	retinoic acid receptor responder (Iazaro	Seq ID No. C51 & C266
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No. C52 & C267
	442006	AW975183	Hs.372210	ESTs, Weakly similar to S72482 hypotheti	Seq ID No. C53 & C268
65	413048	M93221	Hs.75182	mannose receptor, C type 1	Seq ID No. C54 & C269
	443324	R44013	Hs.164225	ESTs	Seq ID No. C55 & C270
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C56 & C271
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C57 & C272
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	Seq ID No. C58 & C273
70	442652	AI005163	Hs.201378	Homo sapiens cDNA FLJ40427 fis	Seq ID No. C59 & C274
	450726	AW204600	Hs.355462	HUMPSPBA Human pulmonary surfactant-asso	Seq ID No. C60 & C275
	416955	N26223	Hs.160436	MDAC1	Seq ID No. C61 & C276
	442275	AW449467	Hs.54795	Homo sapiens secretoglobulin, family 3A, m	Seq ID No. C62 & C277
	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C63 & C278
75	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C64 & C279
	453142	AA033648	Hs.7473	Homo sapiens gap junction protein, alpha	Seq ID No. C65 & C280
	421659	NM_014459	Hs.106511	protocadherin 17	Seq ID No. C66 & C281
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	Seq ID No. C67 & C282
	421563	NM_006433	Hs.105806	granulysin	Seq ID No. C68 & C283
80	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	Seq ID No. C69 & C284
	414991	C17898		Homo sapiens up-regulated by BCG-CWS (LO	Seq ID No. C70 & C285
	419833	AA251131	Hs.220697	Homo sapiens tryptophanyl-IRNA synthetas	Seq ID No. C71 & C286
	424943	AU077260	Hs.153924	death-associated protein kinase 1	Seq ID No. C72 & C287

	430890	X54232	Hs.2699	glypican 1	Seq ID No. C73 & C288
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	Seq ID No. C74 & C289
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	Seq ID No. C75 & C290
	410407	X66839	Hs.63287	carbonic anhydrase IX	Seq ID No. C76 & C291
5	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	Seq ID No. C77 & C292
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	Seq ID No. C78 & C293
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	Seq ID No. C79 & C294
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C80 & C295
10	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C81 & C296
	431846	BE019924	Hs.271580	uroplakin 18	Seq ID No. C82 & C297
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	Seq ID No. C83 & C298
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	Seq ID No. C84 & C299
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	Seq ID No. C85 & C300
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	Seq ID No. C86 & C301
15	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	Seq ID No. C87 & C302
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	Seq ID No. C88 & C303
	457819	AA057484	Hs.35406	FLJ20522 Hypothetical protein FLJ20522	Seq ID No. C89 & C304
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	Seq ID No. C90 & C305
	418462	BE001596	Hs.85266	integrin, beta 4	Seq ID No. C91 & C306
20	439606	W79123	Hs.58561	G protein-coupled receptor 87	Seq ID No. C92 & C307
	407720	AB037776	Hs.38002	immunoglobulin superfamily, member 9	Seq ID No. C93 & C308
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	Seq ID No. C94 & C309
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	Seq ID No. C95 & C310
25	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C96 & C311
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C97 & C312
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C98 & C313
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C99 & C314
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C100 & C315
30	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C101 & C316
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C102 & C317
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C103 & C318
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C104 & C319
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C105 & C320
35	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalini	Seq ID No. C106 & C321
	440659	AF134160	Hs.7327	claudin 1	Seq ID No. C107 & C322
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C108 & C323
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C109 & C324
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C110 & C325
40	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	Seq ID No. C111 & C326
	414774	X02419	Hs.77274	plasminogen activator, urokinase	Seq ID No. C112 & C327
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	Seq ID No. C113 & C328
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	Seq ID No. C114 & C329
	449101	AA205847	Hs.23016	G protein-coupled receptor	Seq ID No. C115 & C330
45	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	Seq ID No. C116 & C331
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	Seq ID No. C117 & C332
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	Seq ID No. C118 & C333
	408482	NM_000676	Hs.45743	adenosine A2b receptor	Seq ID No. C119 & C334
	426761	AI015709	Hs.172089	PORIMIN Pro-oncogene receptor inducing me	Seq ID No. C120 & C335
50	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	Seq ID No. C121 & C336
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	Seq ID No. C122 & C337
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	Seq ID No. C123 & C338
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	Seq ID No. C124 & C339
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	Seq ID No. C125 & C340
55	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	Seq ID No. C126 & C341
	428513	BE220806	Hs.184697	plaxin C1	Seq ID No. C127 & C342
	430280	AA361258	Hs.237868	interleukin 7 receptor	Seq ID No. C128 & C343
	428486	AW583497	Hs.184604	pancreatic polypeptide	Seq ID No. C129 & C344
	457489	AI693815	Hs.127179	cryptic gene	Seq ID No. C130 & C345
60	432874	W94322	Hs.279651	melanoma inhibitory activity	Seq ID No. C131 & C346
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C132 & C347
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C133 & C348
	404682			ortholog of mouse polydomain protein	Seq ID No. C134 & C349
	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	Seq ID No. C135 & C350
65	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C136 & C351
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C137 & C352
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C138 & C353
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	Seq ID No. C139 & C354
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	Seq ID No. C140 & C355
70	432596	AJ224741	Hs.278461	matrilin 3	Seq ID No. C141 & C356
	444006	BE395085	Hs.334762	type I transmembrane protein Fn14	Seq ID No. C142 & C357
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	Seq ID No. C143 & C358
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C144 & C359
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C145 & C360
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protel	Seq ID No. C146 & C361
75	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	Seq ID No. C147 & C362
	422109	S73265	Hs.1473	gastrin-releasing peptide	Seq ID No. C148 & C363
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	Seq ID No. C149 & C364
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	Seq ID No. C150 & C365
80	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	Seq ID No. C151 & C366
	426227	U57058	Hs.154299	Human proteinase activated receptor-2 mR	Seq ID No. C152 & C367
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	Seq ID No. C153 & C368
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	Seq ID No. C154 & C369
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	Seq ID No. C155 & C370

5	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	Seq ID No. C156 & C371
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	Seq ID No. C157 & C372
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	Seq ID No. C158 & C373
	413095	AA494359	Hs.30715	potassium voltage-gated channel, Isk-rel	Seq ID No. C159 & C374
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	Seq ID No. C160 & C375
	436729	BE621807	Hs.351316	transmembrane 4 superfamily member 1	Seq ID No. C161 & C376
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	Seq ID No. C162 & C377
	451820	AW058357	Hs.199248	ESTs	Seq ID No. C163 & C378
10	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	Seq ID No. C164 & C379
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	Seq ID No. C165 & C380
	421340	F07783	Hs.1369	decay accelerating factor for complement	Seq ID No. C166 & C381
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C167 & C382
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C168 & C383
15	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	Seq ID No. C169 & C384
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	Seq ID No. C170 & C385
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	Seq ID No. C171 & C386
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	Seq ID No. C172 & C387
	439659	AW970780	Hs.59483	leucine-rich repeat-containing G protein	Seq ID No. C173 & C388
20	411825	AK000334	Hs.352415	solute carrier family 39 (zinc transport	Seq ID No. C174 & C389
	412314	AA825247	Hs.356084	G protein-coupled receptor 27 (GPR27) (S	Seq ID No. C175 & C390
	429150	AF120103	Hs.197366	smoothened (Drosophila) homolog	Seq ID No. C176 & C391
	419073	AW372170	Hs.183918	transmembrane receptor Unc5H2 mRNA	Seq ID No. C177 & C392
	411828	AW161449	Hs.72290	wingless-type MMTV integration site fami	Seq ID No. C178 & C393
25	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C179 & C394
	421779	AI879159	Hs.108219	wingless-type MMTV integration site fami	Seq ID No. C180 & C395
	439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	Seq ID No. C181 & C396
	433336	AF017988	Hs.31386	secreted frizzled-related protein 2 (str	Seq ID No. C182 & C397
	436972	AA284679	Hs.25640	claudin 3	Seq ID No. C183 & C398
30	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	Seq ID No. C184 & C399
	416370	N90470	Hs.203697	CD38 antigen (p45)	Seq ID No. C185 & C400
	437052	AA861697	Hs.120591	ESTs	Seq ID No. C186 & C401
	421481	AW391972	Hs.104696	KIAA1324 protein	Seq ID No. C187 & C402
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	Seq ID No. C188 & C403
35	426174	AA547959	Hs.115838	Homo sapiens similar to Echinoidin (LOC1	Seq ID No. C189 & C404
	410037	AB020725	Hs.58009	KIAA0918 protein	Seq ID No. C190 & C405
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	Seq ID No. C191 & C406
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	Seq ID No. C192 & C407
	418576	AW968159	Hs.302740	Epithelial calcium channel 2, CaT-like A	Seq ID No. C193 & C408
40	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C194 & C409
	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C195 & C410
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C196 & C411
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C197 & C412
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C198 & C413
45	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C199 & C414
	430144	AF732722	Hs.98927	ERGL protein; ERGIC-53-like protein	Seq ID No. C200 & C415
	408833	AW612232	Hs.254835	ESTs	Seq ID No. C201 & C416
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	Seq ID No. C202 & C417
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C203 & C418
50	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C204 & C419
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	Seq ID No. C205 & C420
	425976	C75094	Hs.334514	NG22 protein	Seq ID No. C206 & C421
	432800	BE391046	Hs.278962	AlM-1 protein	Seq ID No. C207 & C422
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	Seq ID No. C208 & C423
55	424339	BE257148	Hs.145416	endoglycan	Seq ID No. C209 & C424
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	Seq ID No. C210 & C425
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	Seq ID No. C211 & C426
	434293	NM_004445	Hs.3796	EphB6	Seq ID No. C212 & C427
	427715	BE245274	Hs.180428	KIAA1181 protein	Seq ID No. C213 & C428
60	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	Seq ID No. C214 & C429
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	Seq ID No. C215 & C430
	422424	AF186431	Hs.296638	prostate differentiation factor	Seq ID No. C216 & C431
	432378	AF93046	Hs.146133	ESTs	Seq ID No. C432 & C433
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C434 & C435

TABLE 79B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414991	1785136_1	D78831 C17898 D78863

TABLE 79C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
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5

404682	9797231	Minus	40977-41150
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281

Table 80:

Seq ID NO: C1 DNA Sequence
Nucleic Acid Accession #: NM_005814
Coding sequence: 345..1304

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10	CTACCCCTTT	GTGAGCAGTC	TAGGACTTTG	TACACCTGTT	AAGTAGGGAG	AAGGCAGGGG	60
	AGGTGGCTGG	TTTAAGGGGA	ACTGAGGGGA	AGTAGGGGAG	ACTCCTCTTG	GGACCTTTGG	120
	AGTAGGTGAC	ACATGAGCCC	AGCCCCAGCT	CACCTGCCAA	TCCAGCTGAG	GAGCTCACCT	180
	GCCAAATCCAG	CTGAGGCTGG	GCAGAGGTGG	GTGAGAAGAG	GGAAAATTGC	AGGGACCTCC	240
	AGTTGGGCCA	GGCCAGAAGC	TGCTGTAGCT	TTAACCAGAC	AGCTCAGACC	TGCTGGAGG	300
15	CTGCCAGTGA	CAGGTTAGGT	TTAGGGCAGA	GAAGAAGCAA	GACCATGGTG	GGGAGATGT	360
	GGCCTGTGTT	GTGGACACTC	TGTGCAGTCA	GGGTGACCGT	CGATGCCATC	TCTGTGGAAA	420
	CTCCGCAGGA	CGTTCTTCGG	GCTTCGCAGG	GAAAGAGTGT	CACCTGCCCC	TGCACCTACC	480
	ACACTTCCAC	CTCCAGTCGA	GAGGGACTTA	TTCAATGGGA	TAAGCTCCTC	CTCACTCATA	540
	CGGAAAGGGT	GGTCATCTGG	CGGTTTTCAA	ACAAAACTA	CATCCATGGT	GAGCTTTATA	600
20	AGAATCGGCT	CAGCATATCC	AACAATGCTG	AGCAGTCCGA	TGCCTCCATC	ACCAATTGATC	660
	AGCTGACCAT	GGCTGACAAC	GGCACCTACG	AGTGTTCTGT	CTCGCTGATG	TCAGACCTGG	720
	AGGGCAACAC	CAAGTCACGT	GTCCGCCTGT	TGGTCCCTCG	GCCACCTGCC	AAACCAAGAT	780
	GCGGCATCGA	GGGAGAGACC	ATAATTGGGA	ACAACATCCA	GCTGACCTGC	CAATCAAAGG	840
	AGGGCTCACC	AACCCCTCAG	TACAGCTGGA	AGAGGTACAA	CATCCTGAAT	CAGGAGCAGC	900
25	CCCTGGCCGA	GCCAGCTCCA	GCTCAGCCTG	TCTCCCTGAA	GAATATCTCC	ACAGACACAT	960
	CGGGTTACTA	CATCTGTACC	TCCAGCAATG	AGGAGGGGAC	GCAGTTCTGC	AACATCACGG	1020
	TGGCCGTGAG	ATCTCCCTCC	ATGAACGTGG	CCCTGTATGT	GGGCATCGCG	GTGGCCGTGG	1080
	TTGCACGCCCT	CATTATCATT	GGCATCATCA	TCTACTGCTG	CTGCTGCCGA	GGGAAGGACG	1140
	ACAACACTGA	AGACAAGGAG	GATGCAAGGC	CGAACCGGGA	AGCCTATGAG	GAGCCACCAG	1200
30	AGCAGCTAAG	AGAACTTTCC	AGAGAGAGGG	AGGAGGAGGA	TGACTACAGG	CAAGAAGAGC	1260
	AGAGGAGCAC	TGGGCGTGAA	TCCCGGAGCC	ACCTCGACCA	GTGACAGGCC	AGCAGCAGAG	1320
	GGCGGGGAGG	GAAGGGTTAG	GGGTTCAATC	TCCCGCTTCC	TGGCCTCCCT	TCTCCTTTCT	1380
	AAGCCCTGTT	CTCCTGTCCC	TCCATCCGAG	ACATGTATGG	GGACATTTCT	TCCCCAGTGT	1440
	CAGCTGTGGG	GAACATGGCT	GGCCTGGTAA	GGGGGTCCCT	GTGCTGATCC	TGCTGACCTC	1500
35	ACTGTCTGTT	GAAGTAACCC	CTCCTGGCTG	TGACACCTGG	TGCGGGCCTG	GCCCTCACTC	1560
	AAGACCAAGC	TGCAGCTCCC	ACTTCCCTCG	TAGTTGGCAG	GAGCTCCTGG	AAGCACAGCG	1620
	CTGAGCATGG	GGGCTCCCA	CTCAGAACTC	TCCAGGGAGG	CGATGCCAGC	CTTGGGGGGT	1680
	GGGGGCTGTC	CTGCTCACTC	GTGTGCCAG	CACCTGGAGG	GGCACCAGGT	GGAGGGTTTG	1740
40	CACCTCCACAC	ATCTTTCTTG	AATGAATGAA	AGAATAAGTG	AGTATGCTTG	GGCCCTGCAT	1800
	TGGCCTGGCC	TCCAGCTCCC	ACTCCCTTTC	CAACCTCACT	TCCCGTAGCT	GCCAGTATGT	1860
	TCCAAACCCCT	CCTGGGAAGG	CCACCTCCCA	CTCCTGCTGC	ACAGGCCCTG	GGGAGCTTTT	1920
	GCCCAACACAC	TTTCCATCTC	TGCCTGTCAA	TATGTAAGCT	GTCCCTCCAG	GCCCATCTCA	1980
	AATCAACAAGG	ATTCTCTCTA	CCCTATCTTA	ATTGTCCACA	TACGTGGAAG	CAATCCTGTT	2040
45	ACTCTGTCCC	ACGTCCAATC	ATGGGCCACA	AGGCACAGTC	TTCTGAGGGA	GTGCTCTCAC	2100
	TGTATTAGAG	CGCCAGCTCC	TTGGGGCAGG	GCCCTGGGCT	CATGGCTTTT	GCTTTCCCTG	2160
	AAGCCCTAGT	AGCTGGGCCC	CATCTAGTGG	GGCACTTAAG	CTTAATTGGG	GAAGCTGCTT	2220
	TGATTGGTTG	TGCCTTCCCT	TCTCTGTGCT	CCTTGAGATG	ATCGTAGACA	CAGGGATGAT	2280
	TCCACCCCAA	ACCACGATAT	TCATTCAGTG	AGTTAAACAC	GAATTGATTT	AAAGTGAACA	2340
50	CACACAAGGG	AGCTTGCTTG	CAGATGGTCT	GAGTTCTTGT	GTCCCTGGTAA	TTCCCTCCCA	2400
	GGCCAGAAAT	ATTGGCATGT	CTCCTCAACC	CACATGGGGT	TCCTGGTTGT	TCCTGCATCC	2460
	CGATACCTCA	GCCCTGGCCC	TGCCAGCCCC	ATTGGGGCTC	TGGTTTCTTG	GTGGGGCTGT	2520
	CCTGCTGCCC	TCCACAGACC	TCCTTCTGTT	TGTCCAGCAT	TTCTTCTACT	CTTGAGAGCT	2580
	CAGGCAGCGT	TAGGGCTGCT	TAGGTCTCAT	GGACCACTGG	CTGGTCTCAC	CCAACCTGAC	2640
55	TTTACTATTG	CTATCTTTTC	TGGATGATCA	GAATAATAAT	TCCATAAATC	TATTGTCTAC	2700
	TGCGATTTT	TTAAAAAATG	TATATTTTAA	TATATATTGT	TAAATCCITT	GCTTCATTCC	2760
	AAATGCITTC	AGTAATAATA	AAATTGTGGG	TGG			2793

Seq ID NO: C2 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3150

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	CGCCGACCCC	CGCTSSSTGCC	GCTGCTGTGG	CTGCTSSSTGC	CGCCGCCACC	CAGGGTCGGG	120
	GGCTTCAACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
	GGATTCTCAG	TGGAGTTTAA	CGGGCCGGGA	ACAGAGCGGG	TCAGTGTGCT	GGTGGGAGCA	240
	CCCAAGGCTA	ATACAGCCCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCCCT	300
70	TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTGG	ACAGCAAAGG	CTCTGGGCTC	360
	CTGGAGTCCT	CACCTGCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCCCTGTCAG	420
	TGGTTGCGGG	CAACAGTTCC	AGCCCATGGC	TCCCTCATCT	TGGCATGGGC	TCCACTGTAC	480
	AGCTGGGSCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
	GATAACTTCA	CCCGAATTCT	GGAGTATGCA	CCCTGCGGCT	CAGATTTCAG	CTGGGCAGCA	600
	GGACACGGTT	ACTGCCAAGG	AGGCTTCAGT	GCGGAGTTCA	CCAAGACTGG	CGGTGTGGTT	660
75	TTAGGTGGAC	CAGGAAGCTA	TTTCTGGCAA	GGCCAGATCC	TGTCTGCCAC	TCAGGAGCAG	720
	ATTGCAGAAT	CTTATTACCC	CGAGTACCTG	ATCAACCTGG	TTCAGGGGCA	GCTGCAGACT	780
	CGCCAGGCCA	GTTCCATCTA	TGATGACAGC	TACCTAGGAT	ACTCTGTGGC	TGTTGGTGAA	840
	TTCACTGGTG	ATGACACAGA	AGACTTGTGT	GCTGGTGTGC	CCAAAGGGAA	CCTCACTTAC	900
80	GGCTATGTCA	CCATCCTTAA	TGGCTCAGAC	ATTCCATCCC	TCTACAACTT	CTCAGGGGAA	960
	CAGATGGCCT	CCTACTTTGG	CTATGCAGTG	GCCGCCACAG	ACGTCAATGG	GGACGGGCTG	1020
	GATGACTTGC	TGGTGGGGGG	ACCCCTGCTC	ATGGATGGGA	CCCTGACGGG	GCGGCTCAG	1080
	GAGGTGACCT	GCTGCTACGT	CTACCTGCAG	CACCCAGCGG	GCAATAGAGCC	CAGGCCACCC	1140
	CTTACCCTCA	CTGGCCATGA	TGAGTTTGGC	CGATTGGGCA	GCTCCTTGAC	CCCCCTGGGG	1200
	GACCTGGACC	AGGATGGCTA	CAATGATGTG	GCCATCGGGG	CTCCCTTTGG	TGGGGAGACC	1260
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GTGGACAAGG CTGTGGTATA CAGGGGCCCG CCCATCGTGT CCGCTAGTGC CTCCTCACC 1500
ATCTTCCCGG CCATGTTCAA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTGTG 1560
GCCTGCATCA ACCTTAGCTT CTGCCTCAAT GCTTCTGGAA AACACGTTGC TGACTCCATT 1620
GGTTTCACAG TGGAACTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA 1680
CTGTTCTCTGG CCTCCAGGCA GGCAACCCCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAAAT TCGAGACAAA 1800
CTCTCGCCGA TTCACATGCG TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC 1860
CACGGCCTCA GGCCAGCCCT ACATTATCAG AGCAAGAGCC GATAGAGGA CAAGGCTCAG 1920
ATCTTGTCTGG ACTGTGGAGA AGACAACATC TGTGTGCTGT ACCTGCAGCT GGAAGTGTTT 1980
GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCC TGAACTCAC TTTCCATGCC 2040
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GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC 2160
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GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC 2280
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TCCTTTCCGG TCTCGTGGG GGCTCAGGCC CAGGTCAACC TGAACGGTGT CTCCAAGCCT 2400
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TACAAAGCCC TGAAGATGCC CTACCGAATC TCGCTCGGC AGCTGCCCCA AAAAGAGCGT 2940
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ATCATCATCC TAGCCATCCT GTTGGGCTTC CTGCTCCTAG GTCTACTCAT CTACATCCTC 3060
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CTCAAGCCTC CAGCCACCTC TGATGCCTGA 3150

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Seq ID NO: C3 DNA Sequence

Nucleic Acid Accession #: NM_002421.2

Coding sequence: 1..1410

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CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120
TACTACAACC TGAAGAAATGA TGGGAGGCAA GTTGAAAGC GGAGAAATAG TGGCCAGTG 180
GTTGAAAAAT TGAAGCAAT GCAGGAATTC TTTGGGCTGA AAGTGAAGTG GAAACAGAT 240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGCTCAGTTT 300
GTCTCAGTGT AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAA 360
TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC 420
TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGCATCATG 480
ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
CTTGCTCATG CTTTTCACCC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTGTGGGC TCATGAAGTC 660
GGCCTATCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGAATGA CCCTAGCTAC 720
ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCAAAA CCCCAAAAGC ATGTGACAGT 840
AAGCTAAACT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
TTCTACATGC GCACAAATCC CTCTACCCG GAAGTTGAGC TCAATTTCTT TCTGTTTTT 960
TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
CGGTTTTTTC AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
CCCAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAAGTG TGAAGCATAT CGATGCTGCT 1140
CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
GATGAATATA AAGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCT 1260
GGAATTGGCC ACAAAGTTGA TGCAAGTTTC ATGAAAGATG GATTTTCTTA TTTCTTTCT 1320
GGAACAAGAC AATACAAATT TGATCTCTAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
AATAGCTGGT TCAACTGCAG GAAAAATTAG 1410

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Seq ID NO: C4 DNA Sequence

Nucleic Acid Accession #: E08 sequence

Coding sequence: 1..1410

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CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCT 1260
GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTTA TTTCTTTTCT 1320
GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
AATAGCTGGT TCAACTGCAG GAAAAATTAG                                     1410

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Seq ID NO: C5 DNA Sequence

Nucleic Acid Accession #: NM_014331.2

Coding sequence: 1..1506

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TTTAAAGACG CGTTTTCAGG AAGAGATTCA AGTATTACGC GGTTCGCACT GGCTTTTAT 720
TATGGAATGT ATGCATATGC TGGCTGGTTT TAOCCTCACT TTGTTACTGA AGAAGTAGAA 780
AACCTCGAAA AAACCAATCC CCTTGCAATA TGTATATCCA TGGCCATTGT CACCATGGCC 840
TATGTGCTGA CAAATGTGGC CTACTTTACG ACCATTAAAT CTGAGGAGCT GCTGCTTTCA 900
AATGCAGTGG CAGTGACCTT TTCTGAGCGG CTACTGGGAA ATTTCTCAT 960
ATCTTTGTTG CCCTCTCTCG CTTTGGCTCC ATGAACGGTG GTGTGTTTGC TGTCTCCAGG 1020
TTATTTCTAT TTGGCTCTCG AGAGGGTCA CTTCCAGAAA TCCTCTCCAT GATTCTATGC 1080
CGCAAGCACA CTCCTCTACC AGCTGTTATT GTTTGCAACC CTTTGACAAAT GATAATGCTC 1140
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GGGCTGGCAG TTGCTGGGCT GATTTATCTT CGATACAAAT GCCCAGATAT GCATCTCTCT 1260
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AAAAATCCTT GAGAAATTTT TATGTCAGAT GTTTTTCAT TCAATTATCAG GAAGTTTATG 2220
TTATCTGTGA TTTTTTTTTT TCACATCAGT TTGATCAGGA AAGTGATATA CACATCTTAG 2280
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TACCCCTGAT GAGTCTATCT AAACATATGC ATTTTAAAGC TTCAAAATAC ATTATCAACA 2400
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AAGAAATGTC GCTGTAAATA AGATTTACAA CTGATGTTTC TAGAAAAATT CCACCTCTAT 2700
ATCTAGGCTT TGTCAATAT TTCCACACCT TAATTATCAT TCAACTTGCA AAAGAGACAA 2760
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GTTTTGCCAG TATTAGAAAA TACTGTGAGC CGGSCATGGT GGCCTACATC TGTAATCCCA 2880
GCATTTGGG AGGCTGAGGG GGTGGATCAC CTGAGGTCCG GAGTTCTAGA CCAGCCTGAC 2940
CAACATGGAG AAACCCATC TCTACTAAAA ATACAAAATT AGCTGGGCAT GGTGGCACAT 3000
GCTGTGTAAT TCAGCTATTG AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGGAGGCG 3060
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CCATCTCCAA AAAAAAAA AAAA                                     3144

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Seq ID NO: C6 DNA Sequence

Nucleic Acid Accession #: NM_003246.1

Coding sequence: 112..3624

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CGCCGCGCTC CGGTACACAC AGGATCCCTG CTGGGCAACA ACAGCTCCAC CATGGGGCTG 120
GCCTGGGGAC TAGGCTCTCT GTTCTGATG CATGTGTGTG GCACCAACCG CATTCAGAG 180
TCTGGCGGAG AACAACAGCT GTTTGACATC TTTGAACCTA CCGGGGCGGC CCGCAAGGGG 240
TCTGGGCGCC GACTGTGTAA GGGCCCGGAC CCTTCCAGCC CAGCTTTCCG CATCGAGGAT 300
GCCAACCTGA TCCCCCTGT GCTGATGAC AAGTTCCAAG ACCTGGTGA TGCTGTGCGG 360
GCAGAAAGGG GTTTCCTCTCT TCTGGCATCC CTGAGGCAGA TGAAGAAGAC CGGGGGCACG 420

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5	CTGCTGGCCC	TGGAGCGGAA	AGACCACCTCT	GGCCAGGTCT	TCAGCGTGGT	GTCCAATGGC	480
	AAGGCGGGCA	CCCTGGACCT	CAGCCTGACC	GTCCAAGGAA	AGCAGCACGT	GGTGTCTGTG	540
	GAAGAAGCTC	TCTTGGCAAC	CGGCCAGTGG	AAGAGCATCA	CCCTGTTTGT	GCAGGAAGAC	600
	AGGGCCAGC	TGTACATDGA	CTGTGAAAAG	ATGGAGAATG	CTGAGTTGGA	CGTCCCATC	660
	CAAAAGCGTCT	TACACAGAGA	CCTGGCCAGC	ATGCCAGAC	TCCGCATCGC	AAAGGGGGGC	720
	GTCAATGACA	ATTTCACGGG	GGTGTCTGAC	AATGTGAGGT	TTGTCTTTGG	AACCACACCA	780
	GAAGACATCC	TCAGGAACAA	AGGCTGTCTC	AGCTCTACCA	GTGTCTCTCT	CACCCCTGAC	840
	AACAACGTGG	TGAATGGTTC	CAGCCCTGCC	ATCCGCACTA	ACTACATTGG	CCACAAGACA	900
10	AAGGACTTGC	AAGCCATCTG	CGGCATCTCC	TGTGATGAGC	TGTCCAGCAT	GGTCTCGGAA	960
	CTCAGGGGCC	TGCGCACCAT	TGTGACCACG	CTGCAGGACA	GCATCCGCAA	AGTGAAGTAA	1020
	GAGAACAAG	AGTTGGCCAA	TGAGCTGAGG	CGGCCTCCCC	TATGCTATCA	CAACGGAGTT	1080
	CAGTACAGAA	ATAACGAGGA	ATGGACTGTT	GATAGCTGCA	CTGAGTGTCA	CTGTGAGAAC	1140
	TCAGTTACCA	TCTGCAAAAA	GGTGTCTCTG	CCCATCATGC	CCTGCTCCAA	TGCCACAGTT	1200
15	CCTGATGGAG	AATGCTGTCC	TCGCTGTTGG	CCCAGCGACT	CTGCGGACGA	TGGCTGGTCT	1260
	CCATGGTCCG	AGTGGACCTC	CTGTTCTACG	AGCTGTGGCA	ATGGAATTCA	GCAGCGCGGC	1320
	CGCTCCTGCG	ATAGCCTCAA	CAACCGATGT	GAGGGCTCCT	CGGTCCAGAC	ACGGAACCTGC	1380
	CACATTTCAG	AGTGTGACAA	AAGATTAAAA	CAGGATGGTG	GCTGGAGCCA	CTGGTCCCCG	1440
	TGGTCATCTT	GTCTGTGAC	ATGTGGTGAT	GGTGTGATCA	CAAGGATCCG	GCTCTGCAAC	1500
20	TCTCCAGGCC	CCCAGATGAA	TGGGAAACCC	TGTGAAGGCG	AAGCGCGGGA	GACCAAGGCC	1560
	TGCAGAAAG	ACGCCCTGCC	CATCAATGGA	GGCTGGGGTC	CTTGGTCACC	ATGGGACATC	1620
	TGTTCTGTCA	CTGTGGGAGG	AGGGGTACAG	AAAGCTAGTC	GTCTCTGCAA	CAACCCCGCA	1680
	CCCCAGTTTG	GAGGCAAGGA	CTGCGTTGGT	GATGTAACAG	AAAACACAGT	CTGCAACAAG	1740
	CAGGACTGTC	CAATGTATGG	ATGCTGTCTC	AATCCCTGCT	TTGCCGCGGT	GAAGTGTACT	1800
25	AGCTACCCCTG	ATGGCAGCTG	GAAATGTGGT	GCTTGTCCCC	CTGGTTACAG	TGGAAATGGC	1860
	ATCCAGTGCA	CAGATGTTGA	TGAGTGCAAA	GAAGTGCCCTG	ATGCTGCTCT	CAACCACAAT	1920
	GGAGAGCACC	GGTGTGAGAA	CACGGACCCC	GGCTACAAC	GCCTGCCCTG	CCCCCAACGC	1980
	TTCAACCGCT	CACAGCCCTT	CGGCCAGGGT	GTGAAACATG	CCACGCGCAA	CAAAACAGGTG	2040
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30	AACTACCTGG	GCCACTATAG	CGACCCCATG	TACCGCTGCG	AGTGCAAGCC	TGGCTACGCT	2160
	GGCAATGGCA	CAGATCTGGG	GGAGGACACA	GACCTGGATG	GCTGGCCCAA	TGAGAACCTG	2220
	GTGTGCGTGG	CCAATGCGAC	TTACCACTGC	AAAAAGGATA	ATTGCCCCAA	CCTTCCCAAC	2280
	TCAGGGCAGG	AAGACTATGA	CAAGGATGGA	ATTGGTGATG	CCTGTGATGA	TGACGATGAC	2340
	AATGATAAAA	TTCCAGATGA	CAGGGACAAC	TGTCCATTCC	ATTACAACCC	AGCTCAGTAT	2400
35	GACTATGACA	GAGATGATGT	GGGAGACCGC	TGTGACAACT	GTCCCTACAA	CCACAACCCA	2460
	GATCAGGCAG	ACACAGACAA	CAATGGGGAA	GGAGACGCCT	GTGCTGCAGA	CATTGATGGA	2520
	GACGGTATCC	TCAATGAACG	GGACAACCTG	CAGTACGTCT	ACAATGTGGA	CCAGAGAGAC	2580
	ACTGATATGG	ATGGGGTTGG	AGATCAGTGT	GACAATTGCC	CCTTGGAAAC	CAATCCGGAT	2640
	CAGCTGGACT	CTGACTCAGA	COGCATTGGA	GATACCTGTG	ACAACATCA	GGATATTGAT	2700
40	GAGATGCCCC	ACCAGAACAA	TCTGGACAAC	TGTCCCTATG	TGCCCAATGC	CAACCCAGGT	2760
	GACCATGACA	AAGATGGCAA	GGGAGATGCC	TGTGACCACG	ATGATGACAA	CGATGGCAAT	2820
	CCTGATGACA	AGGACAACATG	CAGACTCGTG	CCCAATCCCG	ACCAGAAGGA	CTCTGACGGC	2880
	GATGGTCCAG	GTGATGCCCTG	CAAGATGAT	TTTGACCATG	ACAGTGTGCC	AGACATCGAT	2940
	GACATCTGTG	CTGAGAAATG	TGACATCAGT	GAGACCGATT	TCCGCCGATT	CCAGATGATT	3000
45	CCTCTGGACC	CCAAAGGGAC	ATCCCAAAAT	GACCCTAAC	GGGTGTGACG	CCATCAGGGT	3060
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	AATGCTGTGG	ACTTTCAGTG	CACCTTCTTC	ATCAACACCG	AAAGGGACGA	TGACTATGCT	3180
	GGATTGTGCT	TTGGCTACCA	GTCCAGCAGC	CGCTTTTATG	TTGTGATGTG	GAAGCAAGTC	3240
	ACCCAGCTGT	CGTCTCTGTG	CAACCCCAAG	AGGGCTCAGG	GATACTCGGG	CCTTTCTGTG	3300
50	AAAGTTGTAA	ACTCCACCA	AGGGCCTGGC	GAGCACTGTC	GGAAACGCGT	GTGGCACACA	3360
	GGAAACACCC	CTGGCCAGGT	GGCAACCTG	TGGCATGACC	CTCGTCACAT	AGGCTGGAAA	3420
	GATTTCACCG	CCTACAGATG	GCGTCTCAGC	CACAGGCCAA	AGACGGGTTT	CATTAGAGTG	3480
	GTGATGTATG	AAGGGGAAGAA	AATCATGGCT	GACTCAGGAC	CCATCTATGA	TAAAACTTAT	3540
	GCTGTGTAAT	CGCTAGGGTT	GTTTGTCTTC	TCTCAAGAAA	TGGTGTCTCT	CTCTGACCTG	3600
55	AAATACGAAT	GTAGAGATCC	CTAATCATCA	AATGTGTGAT	TGAAAGACTG	ATCATAAACC	3660
	AATGCTGGTA	TTGCACTTTC	TGGAACATG	GGCTTGAGAA	AACCCCGAGG	ATCACTTCTC	3720
	CTTGGCTTCC	TTCTTTTCTG	TGCTTGATC	AGTGTGGACT	CCTAGAACGT	GCGACCTGCC	3780
	TCAGAAATAT	GCAGTTTTC	AAAACAGACT	CATCAGCAT	CAGCCTCCAA	TGAATAGAGC	3840
60	ATCTTCCAA	CAATATAACA	ATTGCTTTGG	TTTCCCTTTG	AAAAAGCATC	TACTTGTCTC	3900
	AGTTGGGAAG	GTGCCCATTC	CACCTGCTCT	TTGTACAGAA	GCAGGGTGCT	ATTGTGAGGC	3960
	CATCTCT						3967

Seq ID NO: C7 DNA Sequence

Nucleic Acid Accession #: NM_002192

Coding sequence: 86..1366

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	AAGTTGCTGG	ATTATAGTGA	GGAGTTCCCC	CACCCACAGGA	TCCAGAGGGC	ACAGCGCGGC	180
	CCCCGACTGT	CGCTCTGTG	CGCTGGCCGC	CCTCCCAAAG	GATGTACCCA	ACTCTCAGCC	240
	AGAGATGTGT	GAGGCCGTCA	AGAAGCAGAT	TTTAAACATG	CTGCACTTGA	AGAAGAGACC	300
	CGATGTCACC	CAGCCGGTAC	CCAAGGCGGC	GCTTCTGAAC	GCGATCAGAA	AGCTTCAATG	360
75	GGGCAAGTTC	GGGGAGAACG	GGTATGTGGA	GATAGAGGAT	GACATTGGAA	GGAGGGCAGA	420
	AATGAATGAA	CTTATGGAGC	AGACCTCGGA	GATCATCAGC	TTTGGCGAGT	CAGGAACAGC	480
	CAGGAGAGCG	CTGCTATTCG	AGATTTCCAA	GGAAGGCAGT	GACCTGTGAC	TGGTGGAGCG	540
	TGCAGAAGTC	TGCTCTTCCC	TAAAGTCCC	CAAGGCCAAC	AGGACCAGGA	CCAAAGTCAC	600
	CATCCGCTCT	TTCCAGCAGC	AGAAGCACCC	GCAGGGCAGC	TTGACACAG	GGGAAGAGGC	660
80	CGAGGAAGTG	GGCTTAAAGG	GGGAGAGGAG	TGAACCTGTT	CTCTCTGAAA	AAGTAGTAGA	720
	CGCTCGGAAG	AGGACCTGGC	ATGCTTCCC	TGCTCCAGC	AGCATCCAGC	GGTGTCTGGA	780
	CCAGGCGAAG	AGCTCCCTGG	ACGTTCCGAT	TGCTGTGAG	CAGTCCAGG	AGAGTGGCGC	840
	CAGCTTGGTT	CTCTCTGGCA	AGAAGAAGAA	GAAAGAAGAG	GAGGGGGAAG	GGAAAAAGAA	900
	GGGCGGAGGT	GAAGGTGGGG	CAGGAGCAGA	TGAGGAAAAG	GAGCAGTCGC	ACAGACCTTT	960
	CCTCATGCTG	CAGGCCCGGC	AGTCTGAAGA	CCACCCCTCAT	CGCCGGCGCT	GGCGGGGCTT	1020

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GGAGTGTGAT GGCAAGGTCA ACATCTGCTG TAAGAAACAG TTCCTTGCTA GTTTCAGGA 1080
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TGAGTGCCTCC AGCCATATAG CAGGCACGTC CGGTCTCTCA CTGTCCTTCC ACTCAACAGT 1200
CATCAACCAC TACCGCATGC GGGGCCATAG CCCCCTTGCC AACCTCAAT CGTGTGTGT 1260
GCCCCAACAG CTGAGACCCA TGTCCATGTT GTACTATGAT GATGGTCAAA ACATCATCAA 1320
AAAGGACATT CAGAACATGA TCGTGGAGGA GTGTGGGTGC TCATAGAGTT GCCCAGCCCA 1380
GGGGAAAGG GAGCAAGAGT TGTCCAGAGA AGACAGTGGC AAAATGAAGA AATTTTAAAG 1440
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TGGAGGGGAA AGGGAGAATG GTGTACCTTT TATTTCTTCT GAAATCACAC TGATGACATC 1680
AGTTGTTTAA ACGGGGTATT GTCTTTCCC CCCTTGAGGT TCCCTTGTA GCTTGAATCA 1740
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AGTTTGAAG GSCCATCAC AGGCATCTTC CTAGCCTAAT 1840

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Seq ID NO: C8 DNA Sequence
Nucleic Acid Accession #: NM_000055.1
Coding sequence: 26..2299

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GCAGATGCTT CCGGAACCTGC AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT 180
GGCGGAGCAG GTCAAGGAGA TCACGTTCCT GAAACACAGC GTGATGGAGT GTGACGCGTG 240
CGGGATGCAG CAGTCAGTAC GCACCGGCGT ACCCAGCGTG CGGCCCCCTG TCCAATGCGC 300
GCCCGGCTTC TGCTTCCCGG CGGTGGCCTG CATCCAGACG GAGAGCGGCG GCCGCTGCGG 360
CCCTTGCCTC GCGGCTTCA CCGGCACAGG CTGCACTGAC ACCGAGCTCA ACGATGTCAG 420
CGCCCCACCT TGCTTCCCTCC GAGTCCGCTG TATCAACACC AGCCCGGGGT TCCGCTGCGA 480
GGCTTGCCCG CCGGGGTACA GCGGCCCCAC CCACAGGGG GTGGGGCTGG CTTTCGCCAA 540
GGCCACACAG CAGGTTTGCA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAACCTCGT 600
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GTGCGTGTGT CCGGTGGGCT GGGCGGGCAA CGGATTCCTC TGTGGTCCG ACACCTGACCT 840
AGACGGCTTC CCGGACGAGA AGCTGCGCTG CCGGAGCCCG CAGTGCCTTA AGGACAACTG 900
CGTGACTGTG CCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCTG 960
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GAACCCAGAC CAGCGCAACA CGGACGAGGA CAAGTGGGGC GATGCGTGGC ACAACTGCGG 1080
GTCCCAAGAG AACGACGACC AAAAGGACAC AGACAGGAC GGCCGGGGCG ATGCGTGGCA 1140
CGACGACATC GACGCGGACC GATCCGCAAA CCAGGCGGAC AACTGCCCCA GGGTACCCAA 1200
CTCAGACCAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCA 1260
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TAACAGTGCC CAGGAGGACT CAGACCAAGA TGGCCAGGGT GATGCTGGG ACGACGACGA 1440
CGACAATGAC GAGTCCCTG ACAGTGGGGA CAACTGCCGC CTGGTGCTTA ACCCGGGCCA 1500
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GGTGTCAAC CAGGGAAGGG AGATCCGTGA GACATGAAC AGCGACCCAG GCTTGGCTGT 1740
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GGATGACGAG TATGCGGGCT TCATCTTTGG CTACCAAGAC AGCTCCAGCT TCTACGTGGT 1860
CATGTGGAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCCTTCCGTG CTGTGGCCGA 1920
CGCTGGCATC CACTCAAGG CTGTGAAGTC TTCCACAGGC CCGGGGGAAC AGCTGCGGAA 1980
CGCTCTGTGG CATAAGGAG ACACAGAGTC CCAGTGCAGG CTGCTGTGGA AGGACCCGCG 2040
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CTTGACACA ACCATGCGGG GTGGCGGCTT GGGGTCTTCT TGCTTCTCCC AGGAGAACAT 2220
CATCTGGGCC AACCTGCGTT ACCGCTGCAA TGACACCATC CAGAGGACT ATGAGACCCA 2280
TCAGCTGCGG CAGGCTAGG GACCAGGGTG AGGACCCGCG GATGACAGC CACCTCAC 2340
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AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGACGGG 2439

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Seq ID NO: C9 DNA Sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..874

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CGCTGCCCGG CAGCGGGGAG CCATGCGACC CCAGGGCCCC GCGGCTCTCC CGCAGCGGCT 180
CGCGGCGCTC TGCTGCTGCC GCTGCGCGCG CCGTGGAGCG CCTCTGAGAT 240
CCCCAAGGGG AAGCAAAAGG CGCAGTCCG CGAGAGGGAG GTGGTGGACC TGTAATATGG 300
AATGTGCTTA CAGGGCCAG CAGGAGTCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360
CATTCCGGGT ACACCTGGGA TCCCAGGTG GATGAGATT AAAGGAGAAA AGGGGGAATG 420
TCTGAGGAA AGCTTTGAGG AGTCCGTGAC ACCCAACTAC AAGCAGTGT CATGAGATT 480
ATTGAATTA GGCATAGATC TTGGGAAAT TGCGAGTGT ACATTACAA AGATGCGTTC 540
AAATAGTGT CTAAGAGTTT TGTTCAATGG CTCACTTCGG TAAATATGCA GAAATGCATG 600
CTGTACGGT TGGTATTCCA CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTG 660
AGCTATAATT TATTGGACC AAGGAAGCCC TGAAATGAAT TCAACAAATTA ATATTATCG 720

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Seq ID NO: C10 DNA Sequence

Nucleic Acid Accession #: NM_003225

Coding sequence: 41..295

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GACAGAGACG GTGACAGTGG CCCCCTGGA AAGACAGAAAT TGTGGTTTTC CTGGTGTAC 180
GCCCTCCAGC TGTGCAAATA AGGGCTGCTG TTTGACGAC ACCGTTCGTG GGGTCCCTCG 240
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Seq ID NO: C11 DNA Sequence

Nucleic Acid Accession #: NM_015419.1

Coding sequence: 1..8487

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CAGACCCCTC AGGGTCTCTC TAACTTAATG AGGCTGCACA TTGACCAACA CAAGATCGAG 420
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Nucleic Acid Accession #: AK001903
Coding sequence: none

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70 Seq ID NO: C13 Protein Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..5001

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	ACACCCGCGC	GGGCCCCAGA	ACAGCAGCCC	CCTCTCCCG	TGCCCACTC	CCAGCACCCAC	2640
	CGGGGACCCC	AGAGCAGAGA	CGCGGGTGGG	TCACTTCCCG	AGCCAGGCTC	CTCACTGACC	2700
	CAGGCCGCGG	GGCCCGCGCC	CAGTCCGAG	GGCCGCTCCC	ACTCTCTCTC	GGACCCCTAC	2760
40	ACGGCGAGCT	CCGAGGGGAT	GCTCCCGACG	GGCCCTCCAG	ACCAGGACGA	GGATGCCGAG	2820
	GGCAGCTACG	ACGACGACAG	CACAGAAGTC	GAGGCCACAG	ATGTGCGGGC	CCCGCGGCAC	2880
	GCAGCGCGCG	CCAAGGAGGC	AGCTGCGTCC	CTTCCCAAGC	ACCAGCAGGT	GGAGTCTCCC	2940
	ACAGGCGCAG	GGGACGGTGG	CGACCAACAG	TCCAGCGCGG	GACATGCGCG	CTCCCCCGCC	3000
	AGGCCCGAGC	GACCCGGCGG	CCGCCAGTCC	CGCGCCCGGG	TCCCGACGAG	GGCAGCGCGG	3060
45	GGGAAGTGGG	AGGCTCTCTC	CAAGCGGCCG	CTGTCTCTCA	AGTCCACGCA	GTGCTCTCA	3120
	GCGAGGAGCG	AGGAGGAGGA	GGACGCGGGG	TTTTTTAAAG	GCGGGAAGGA	AGACCTTCTG	3180
	TCTTCTCTCT	TGCCAAGATG	GCCCTCTTCC	TCCACTCCCA	GGGGGGGCAA	AGACGCGGAT	3240
	GGGAGCTCTG	CCAGGGAAGA	GAGGGAGCCT	GCCATCGCGC	TGCCCCCTCG	CGGAGGGAGC	3300
	CTGGCTCTCT	TGAAGCGAOC	TCTCCCCCA	CCTCCAGGCA	GCTCCCCCAG	GGCTTCCAC	3360
	GTCTCTTCCC	GACCGCCGCC	TGCGAGCGCT	GCCACCGTGA	GCCCGCTCGC	GGGCAACCCAC	3420
50	CCCTGGCGCG	GGTACACCCAC	GCGCGCCCCV	CCTGGCCACT	TCTCCACCAC	CCCGATGCTG	3480
	TTCTTGGCGC	AGAGGATGAT	GCATGCCAGA	TTCGGTAACC	CTCTCTCCCG	ACAGCCTGCC	3540
	AGACCTCTTT	ACAGCAAGGG	TTATAATGGC	AGACCAAATG	TAGAAGGGAA	AGTCTCTCTC	3600
	GGTAGTAATG	GAAACCGGAA	TGGACAGAGA	ATTATCAATG	GCCCTCAAGG	AACAAAGTGG	3660
	GTTGTGGACC	TTGATGTGGG	GTTAGTATTG	AATGCAGAAG	GAAGGTACCT	CCAAGATTCA	3720
55	CATGGAATTC	CTCTTGGGAT	TAAACTAGGA	GGAGATGGTC	GAACCATTTG	AGATCTGGAA	3780
	GGGACCCCGC	TGGTGTAGTCC	TGACGGCCTC	CCACTCTTTG	GGCAGGGGGG	ACATGGGACA	3840
	CCTCTGGGCA	AGGCGCAAGT	TGAGTCTTGG	GAGGAAAGCC	GCTGGTGGGC	GCTGGTGGGC	3900
	TTGGAGGTCA	TCAAAAAAAC	CAOCCATCCC	CCTACCACTA	CCATGCAGCC	CACCACTACT	3960
	AOGAGCCCCC	TGCTTACCC	TACAAACCCG	AGGCCCAACCA	CTGCCACCAC	CATGCAGCCC	4020
60	ACCACTACTA	CGAGGCCCCC	GCCTTACACT	ACACCGAGGC	CCACCACTGC	CACCAACCCG	4080
	CGCAOAGACA	CCAGGCGTCC	AACAACCA	GTCCGAACCA	CTAGCGGAC	AACCAACACC	4140
	ACCAACCCCA	AACCAACCA	TCCATCCCC	ACCTGTCCCC	CTGGGACCTT	GGAAACGGAC	4200
	GACGATGATG	GCAACCTGAT	AATGAGCTCC	AATGGGATCC	CAGAGTGCTA	CGCTGAAGAA	4260
	GATGAGTTCT	CAGGCTTGGG	GACTGACACT	GCAGTAOCTA	CGGAGAGGGC	CTAGTTTATA	4320
65	TATGATGAAG	ATTATGAATT	TGAGACGTCA	AGGCCACCAA	CCACCACTGA	GCCTTCGACC	4380
	ACTGCTACCA	CACGAGGGGT	GATCCAGAG	GAAGGCGCCA	TCAGTTCTCT	TCCTGAAGAA	4440
	GAATTTGATC	TGGCTGGAAG	GAAACGATTT	GTTGCTCTCT	ACGTGAAGTA	CCTAAATAAA	4500
	GACCCATCAG	CCCCGTGCTC	TCTGACTGAT	GCACTGGATC	ACTTCCAAGT	GGACAGCCTG	4560
	GATGAAATCA	TCCCAATGGA	CCTGAAGAAG	AGTGATCTGC	CTCCCCAGCA	TGCTCCCGCG	4620
70	AACATCACCG	TGGTGGCCGT	GGAAGGTTGC	CACTCATTTG	TCAATGTGGA	TTGGGACAAA	4680
	GCCACCCCGC	GAGATTGGT	CACAGGTTAT	TTGGTTTACA	GTGCATCTTA	TGAAGATTTC	4740
	ATCAGGAACA	AGTTTTCCAC	TCAAGCTTCA	TCAAGTAACT	ACTTGGCCAT	TGAGAACCTA	4800
	AAGCCCAACA	CGAGGTATTA	TTTTAAAGTG	CAAGCACAAA	ATCCTCATGG	CTAGGGACCT	4860
	ATCAGCCCTT	GGTCTCATTT	TGTCAACGAA	TCAGATAATC	CTCTGCTTGT	TGTGAGGCCC	4920
75	CCAGGCGGTC	GGAGGCTGTC	ATCCCATTTG	CTTTCAACAA	TGATCCAGC	TACAGGACTC	4980
	GCCATGGAGC	GCAATATGTC	AAGCGCACGT	GGTATCGAAA	GTTGCTGGGA	GTTGTTCTTT	5040
	GTAATTCACT	GAGGTATAAA	ATCTACCTCA	GTGACAACTT	GAAAGATACA	TTCTACAGCA	5100
	TTGGAGACAG	CTGGGGAAGA	GGTGAAGACC	ATTGCCAATT	TGTGAGTTCA	CACCTTGAATG	5160
	GAAGAACAGG	GCCTCAGTCC	TATGTAGAAG	CCCTCCCTAC	TATTAAGGCG	TACTATCGCC	5220
80	AGTATCGTCA	GGAGGCTGTC	AGGTTTGGGA	ACATCGGCTT	CGGAACCCCG	TACTACTATG	5280
	TGGGCTGGTA	CGAGTGTGGG	GTCTCCATCC	CTGGAAAGTG	GTAAATCAG	GACCGTCAATG	5340
	CTGCAAGCTT	GCCCTGCCCC	GCCCCACCAA	CTAAGTGGCA	CTAGGGGCTG	TGAGCAAGAA	5400
	CAGCCAGCAT	GCTCAGCCCC	GCTGCCCTAG	GTGCCAGGAA	GGTCAACAGT	GGACACTGGC	5460
	CATTCTGGTC	ATCTCAGTCT	GGAACTCAGT	CCCACTTCTT	GGCCTGGACA	ATGAACAGGA	5520
	TTCACTTTTG	CTGTTAACTT	TGCTTCTCTA	CTTTTTTTTG	TTTGTTTGTA	ATAGCACATC	5580

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CCAGAGACAT	CAGAAACAG	CAACTGATTC	AGTGTGATTT	CCCAGACTTT	TTAGGCATGA	5640
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TGCTACATGC	TTTCGTGTTT	TCTCATTTTG	GATTTCCTCA	AAACTAACTG	AATTTAAGCT	5760
TCAGTCCCT	TTGTATGCAG	TAGAAAGGAA	TTATTAATAA	CACCACCAA	GAAATAAAT	5820
ATATCCTACT	TGAAATTTAC	TCTATGGACT	TACCCACTGC	TAGAATAAAT	GTATCAAATC	5880
TTATTTGTAA	ATTCTCAATT	TTGATATATA	TATGTATATA	TGCATATACA	TATCCACACT	5940
TGCTGCAAG	AATATTGATT	AAAATTGCTA	AATTTGTACT	TGTTACACAA	AAAAAATAA	6000
AAAAAAA						6007

Seq ID NO: C14 DNA Sequence
Nucleic Acid Accession #: NM_003014
Coding sequence: 238..1278

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CGGAGCTCCG	CGGCGGGACC	CGCGGGCCCC	GCTTTGCTGC	CGACTGGAGT	TTGGGGGAAG	120
AAACTCTCCT	GGCOCACAGA	AGATTTCCTC	CTCGGCGAAG	GGACAGCGAA	AGATGAGGGT	180
GGCAGGAAGA	GAAGGGCTTT	TCTGTCTGCC	GGGGTGCAG	CGCGAGAGGG	CAGTGCCATG	240
TTCTCTCTCA	TCCTAGTGGC	GCTGTGCGTG	TGGCTGCACC	TGGCGCTGGG	CGTGCGCGGC	300
GGCGCCTGGG	AGGCGGTGGG	CATCCCTATG	TGCGGCGACA	TGCCCTGGAA	CATCAOGCGG	360
ATGCCCAACC	ACCTGCACCA	CAGCAOGCAG	GAGAACGCCA	TCCTGGCCAT	CGAGCAGTAC	420
GAGGAGCTGG	TGGAGCTGAA	CTGCAGCGCC	GTGCTGCGCT	TCTTCTTCTG	TGCCATGTAC	480
GGCGCCATTT	GCACCTTGA	GTCTCTGCAC	GACCCATCA	AGCCGTGCAA	GTGGGTGTGC	540
CAACGCGCGC	CGGACGACTG	CGAGCCCCCTC	ATGAAGATGT	ACAACCAAG	CTGGCCCGAA	600
AGCCTGGCCT	GGGACGAGCT	GCCTGTCTAT	GACCGTGGCG	TGTGCAATTC	GCCTGAAGCC	660
ATCGTCAACG	ACCTCCCGGA	GGATGTTAAG	TGGATAGACA	TCACACCAGA	CATGATGGTA	720
CAGGAAAGGC	CTCTTGATGT	TGACTGTAAA	CGCCTAAGCC	CCGATCGGTG	CAAGTGTAAA	780
AAGGTGAAGC	CAACTTTGGC	AACGTATCTC	AGCAAAACT	ACAGCTATGT	TATTCATGCC	840
AAAAATAAAG	CTGTGCAGAG	GAGTGGCTGC	AATGAGGTCA	CAACGGTGGT	GGATGTAAAA	900
GAGATCTTCA	AGTCTCATC	ACCCATCCCT	CGAATCTAAG	TCCCGCTCAT	TACAATTTCT	960
TCTTGCCAGT	GTCCACACAT	CCTGCCCCAT	CAAGATGTTT	TCATCATGTG	TTACGAGTGG	1020
CGTTCAAGGA	TGATGCTTCT	TGAAAATTGC	TTAGTTGAAA	AATGGAGAGA	TCAGCTTAGT	1080
AAAAGATCCA	TACAGTGGGA	AGAGAGGCTG	CAGGAACAGC	GGAGAACAGT	TCAGGACAAG	1140
AAGAAAACAG	CGGGGCGCAC	CAGTCTGAGT	AATCCCCCCA	AACCAAGGGG	AAAGCCTCCT	1200
GCTCCCAAC	CAGCCAGTCC	CAAGAAGAAC	ATTAAAACTA	GGAGTGCCTA	GAAGAGAACA	1260
AACCCGAAAA	GAGTGTGAGC	TAACTAGTTT	CCAAAGCGGA	GACTTCOGAC	TTCTTTACAG	1320
GATGAGGCTG	GGCATTTGCT	GGGACAGCCT	ATGTAAGGCC	ATGTGCCCTC	TGCCCTAACA	1380
ACTCACTGCA	GTGCTCTTCA	TAGACACATC	TTGCAGCATT	TTTCTTAAGG	CTATGCTTCA	1440
GTTTTCTTTT	TTAAGCCCAT	ACAAGCCATA	GTGGTAGGTT	TGCCCTTTGG	TACAGAAGGT	1500
GAGTTAAAGC	TGGTGGAAAA	GGCTTATTGC	ATTGCATTCA	GAGTAACCTG	TGTGCATACT	1560
CTAGAAGAGT	AGGAAAAATA	ATGCTTGTTA	CAATTGGACC	TAATATGTGC	ATTGTAAAAAT	1620
AAATGCCATA	TTTCAAAACA	AACACGTAAT	TTTTTTACAG	TATGTTTTAT	TACCTTTTGA	1680
TATCTGTGTG	TGCAATGTIA	GTGATGTTTT	AAAAATGTAT	GAAAAATATA	TGTTTTTAAG	1740
AAGGAACAGT	AGTGGAAATGA	ATGTTAAAG	ATCTTTATGT	GTTTATGGTC	TGCAGAAGGA	1800
TTTTTGATAT	GAAAGGGGAT	TTTTTGAAAA	ATTAGAGAAG	TAGCATATGG	AAAAATTATA	1860
TGTGTTTTTT	TACCAATGAC	TTTCTTTTCT	GTTTTATGCT	AGAACTTTAA	AAACAAAAAT	1920
AATAATAAAG	AAAAATAAAT	AAAAAGGAGA	GGCAGACAA	GTCTGGATTC	CTGTTTTTTG	1980
GTACCTGAT	TTCCATGATC	ATGATGCTTC	TTGTCAACAC	CCTCTTAAGC	AGCACCAGAA	2040
ACAGTGAATT	TGCTGTGACC	ATTAGGAGTT	AGGTACTAAT	TAGTTGGCTA	ATGCTCAAGT	2100
ATTTTATACC	CACAAGAGAG	GTATGTCACT	CATCTTACTT	CCCAGGACAT	CCACCTGAG	2160
AATAATTGA	CAAGCTTAAA	AATGGCCTTC	ATGTGAGTGC	CAAATTTTGT	TTTTCTTCAT	2220
TTAAATATTT	TCTTTGCCCTA	AATACATGTG	AGAGGAGTTA	AATATAAATG	TACAGAGAGG	2280
AAAGTTGAGT	TCCACCTCTG	AAATGAGAAT	TACTTGACAG	TTGGGATACT	TTAATCAGAA	2340
AAAAAGAACT	TATTTGCAGC	ATTTTATCAA	CAAAATTCAT	AATGTGGAC	AATTTGGAGG	2400
ATTTATTTTA	AAAAACAATT	TTATTGGCCT	TTTGCTAACA	CAGTAAGCAT	GTATTTTATA	2460
AGGCATTCAA	TAAATGCACA	ACGCCCAAG	GAAATAAAT	CCTATCTAAT	CCTACTCTCC	2520
ACTACACAGA	GGAATCACT	ATTAGTATTT	TGGCATATTA	TTCTCCAGGT	GTGTTGCTAT	2580
GCACATTATA	AATGATTTGA	ACAAATAAAA	CTAGGAACCT	GTATACATGT	GTGTTCAATC	2640
CTGCCCTCCT	TGCTTGGCCC	TTTATTGAGA	TAAGTTTTCC	TGTCAAGAAA	GCAGAAACCA	2700
TCTCATTTCT	AACAGCTGTG	TTATATTCCA	TAGTATGCAT	TACTCAACAA	ACTGTTGTGC	2760
TATTGGATAC	TTAGTGCTT	TCTTCACTGA	CAATACTGAA	TAAACATCTC	ACCGGAATTC	2820

Seq ID NO: C15 DNA Sequence
Nucleic Acid Accession #: NM_005940
Coding sequence: 23..1489

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CGCCCTCCTG	CGCCCGGATG	TGCTGCTGCT	GCTCCAGCCG	CGCGCGCTGC	TGGCCCGGGC	120
TCTGCGCGCG	GACGTCCACC	ACCTCCATGC	CGAGAGGAGG	GGGCCACAGC	CCTGGCATGC	180
AGCCCTGCCG	AGTAGCCCGG	CACCTGCCCC	TGCCACGCGG	GAAGCCCCCC	GGCCTGCCAG	240
CAGCCTCAGG	CCTCCCCGCT	GTGGCGTGCC	CGACCCATCT	GATGGGCTGA	GTGCCCGCAA	300
CCGACAGAA	AGGTTGCTGC	TTTCTGGCGG	GGCGTGGGAG	AAGAAGGACC	TCACCTACAG	360
GATCCCTCGG	TTCTTGGCTG	AGTTGGTGCA	GGAGCAGGTG	CGCAGACGCA	TGGCAGAGGC	420
CCTAAAGGTA	TGGAGCGATG	TGACGCCACT	CACCTTTACT	GAGGTGCAAG	AGGGCCGTGC	480
TGACATCATG	ATCGACTTGG	CCAGGTACTG	GCATGGGGAC	GACCTGCCGT	TGATGGGGCC	540
TGGGGGCATC	CTGGCCCATG	CCTTCTTCCC	CAAGACTCAC	CGAGAAGGGG	ATGTCCACTT	600
CGACTATGAT	GAGACCTGGA	CTATCGGGGA	TGACCCAGGC	ACAGACCTGC	TGCAGGTGGC	660
AGCCCTGAAA	TTTGGCCACG	TGCTGGGGCT	GCAGCACACA	ACAGCAGCCA	AGGCCCTGAT	720
GTCCGCTCTC	TACACCTTTC	GCTACCCACT	GAGTCTCAGC	CCAGATGACT	GCAGGGGCGT	780
TCAACACCTA	TATGGCCAGC	CTGGGCCAC	TGTCACTCCC	AGGACCCAG	CCCTGGGGCC	840
CCAGGCTGGG	ATAGACACCA	ATTGAGATTG	ACCGCTGGAG	CCAGACGCCC	CGCCAGATGC	900

5 CTGTGAGGCC TCCTTTGACG OGGTCTCCAC CATCOGAGGC GAGCTCTTTT TCTTCAAAGC 960
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 TCGCCACTGG CAGGGAAGTC CCAGCCCTGT GGAAGCTGCC TTCGAGGATG CCCAGGGCCA 1080
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 CCCCAGCACC CTCACGAGC TGGGCTTGGT GAGGTTCCCG GTCCATGCTG CTTTGGTCTG 1200
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 15 GGGACCCGCT ATCGAGGCTC TGGCAAACT GGCTGCCCTG TCTCATCCTT GTCCCTCAGG 1800
 GTAGCAACAT GGCAGGACTG GGGGAACTGG AGTGTCTTGT CTGTATCCTT GTTGTGAGGT 1860
 TCCTTCCAGG GGTGCGACT GAAGCAAGGG TGCTGGGGCC CATGGGCTT CAGCCCTGGC 1920
 TGAGCAACTG GGTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCTTGC 1980
 20 ATCTGTCTGC CTCTGGCTG ACAATCCTGG AAATCTGTTC TCCAGAAATC AGGCCAAAAA 2040
 GTTCACAGTC AAATGGGGAG GGGTATCTTT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG 2100
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 TTTTAAACT GAGGATTGTC ATTAAACACA GTTGTTTTCT 2260

25 Seq ID NO: C16 DNA Sequence
 Nucleic Acid Accession #: NM_024022
 Coding sequence: 202..1563

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 35 AGAGGTCCTG AAATAGTAC CATGGGGGAA AATGATCCCG CTGCTGTGTA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTGG CCTGTATGAT TTGAAAATAA GTCTCTGTGC ACCAGATGCA 300
 GATGCTGTGG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTCTTCC AATCATGCTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGATCCCA CTTCGATGTC 420
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 40 GGAATCTCGG ATTGCAAGA CCGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
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 45 TGTGCTCTGC GCCAGTGGT TAACCTGTCAG TGCACAGCCT GTGGTCATAG AAGGGGCTAC 840
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 ACTCGTTTAA GGCCTATTTT CATGATTTCT TTGTAGCATT TGGTGCTTGA CGTATTATTG 2400
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 AAAAA 2465

75 Seq ID NO: C17 DNA Sequence
 Nucleic Acid Accession #: NM_003220
 Coding sequence: 63..1376

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 GCACAGCAA CGGAGCGGCA CGGTTGCCCC AGCTGGGCAC TGTAGGTCAA TCTCCCTACA 180
 CGAGCGCCCC GCGCTGTGCC CACACCCCCA ATGCGGACTT CCAGCCCCCA TACTTCCCCC 240
 CACCCTACCA GCCTATCTAC CCCAGTGGC AAGATCCTTA CTCCCAAGTC AACGACCCCT 300

5 ACAGCCTGAA CCCCCTGCAC GCCCAGCCGC AGCCGAGCA CCCAGGCTGG CCGGCCAGA 360
 GGCAGAGCCA GGAGTCTGGG CTCCTGCACA CGCACCGGG GCTGCCTCAC CAGCTGTGG 420
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 TCAGCTCAG ACTCGGAGC CTCTCGATCC ACTCCTTACC TCAOGCCATC GAGGAGGTCC 540
 CGCATGTAGA AGACCGGGT ATTAACATCC CAGATCAAAC TGTAAATTAAG AAAGGCCCG 600
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 10 ATGGAGGAAG ATCTTTAAGA GAAAAACTGG ACAAATAGG ATTAATCTG CCTGCAGGA 900
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 15 GGAATCTAGC GGGCAACCCC ATCTGGAGC CGGCATCCA GAGCTGCTTG ACCCACTTCA 1200
 ACCTCATCTC CCAAGGCTTC GGCAGCCCG CGGTGTGTGC CGGCTCAAG CGCCTGCAGA 1260
 ACTATCTCAC CGAGGCCCTC AAGGCCATGG ACAAATGTA CCTCAGCAAC AACCCCAACA 1320
 GGCACAGCCG ACACACGCC AAAAGCAGTG ACAAAGAGGA GAAGCACAGA AAGTGAGGCT 1380
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 20 GTGACAGCTC CGGATCAGC AACCTTCTCT GCTGCTGCTA CTGCTGCTGC TGTGCGCGCC 1500
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 TGTGCCCCCG GAATTC 1636

25 Seq ID NO: C18 DNA Sequence
 Nucleic Acid Accession #: NM_002988
 Coding sequence: 71..340

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 CTGCTCCTGT GCACAAGTTG GTACCAACAA AGAGCTCTGC TGCTCTGCT ATACCTCTCTG 180
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 35 AGGTGTCTAT CTCTTAACCA AGAGAGGCGC GCAGATCTGT GCTGACCCCA ATAAGAAGTG 300
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Seq ID NO: C19 DNA Sequence
 Nucleic Acid Accession #: NM_004063
 Coding sequence: 121..2619

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Seq ID NO: C20 DNA Sequence
 Nucleic Acid Accession #: NM_004443
 Coding sequence: 28..3024

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Seq ID NO: C21 DNA Sequence
Nucleic Acid Accession #: NM_001804
Coding sequence: 82..879

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TACCCCGGCC CAGCCAGGCC AGCCAGCCTC GGCTTGGGCC CGGCAAACTA CGGCCCCCGC 180
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GCGCGCTACG GCGCGGGCCC CGCGGCCCTT GCGCCAGGCC CAGCTTCGCT GGCATTGGGG 360
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Seq ID NO: C22 DNA Sequence
Nucleic Acid Accession #: NM_021978
Coding sequence: 36..2603

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Seq ID NO: C23 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..2268

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 CAGGATGTGC CTGACCTGGT CTGAGGCTTC GATGGCATTG CCTTCCGTGG TGGCCCCACC 1260
 CTGACGGGCA GTGCTTGGC GCAGGCGGCA GAGCGTGGCT TCGGAGAGCG CACCAAGACA 1320
 65 GGCCAGGACC GGCCACGTAG AGTGGTGGTT TTGCTCACTG AGTCACACTC CGAGGATGAG 1380
 GTTGGCGGCC CAGCGCTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440
 GAGGCGGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC 1500
 TCGGATCCTC AGGATCTGTT CAACCAAATC CTTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
 CAGCGGCCAG GGTGCGGAC ACAAGCCCTG GACCTGTCTC TCAATGTTGA CACCTCTGCC 1620
 70 TCAATGAGGC CCGAGAAATT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680
 TTTGAGTGA ACCCTGACGT GACACAGTTC GGCTGTGGT TGTATGGCAG CCAGGTGAG 1740
 ACTGCTCTTG GGCTGACAC CAAACCCACC CCGGCTGOGA TGCTGCGGGC CATTAGCCAG 1800
 GCGGCTTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
 75 GTGATGACCG TCCAGAGGGG TGCCCGGCTT GGTGTCGCCA AAGCTGTGGT GGTGCTCACA 1920
 GCGCGGAGAG GCGCAGAGGA TGCGGCGGTT CCTGCCAGAG AGCTGAGGAA CAATGGCATC 1980
 TCTGTCTTGG TGTGGGGCTT GGGGCTGTCT CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040
 CCGGCGGATT CCTGATCCCA CGTGGCAGCT TACGCGGACC TGCGGTACCA CCAGGAGGTG 2100
 CTCAATGAGT GGTGTGTGG AGAAGCCAAG CCGCAGCTCA ACCTCTGCAA ACCAGCCCG 2160
 TGCATGAAAT AGGGCAGCTG CGTCTGACAG AATGGGAGCT ACCGCTGCAA GTGTGCGGAT 2220
 80 GGCTGGGAGG GCGCCACTG CGAGAACCGA TTCTTGAGAC GCCCTGTA 2268

Seq ID NO: C24 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..2424

80 1 11 21 31 41 51
 | | | | | |
 ATGCCCCCTT TCCTGTTGCT GGAGGCCGTC TGTGTTTTC TGTTTTCCAG AGTGCCCCCA 60
 TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120

5	AGCAAAATGA	TGTGGTGTCT	GGCTGCAGTG	GACATCATGT	TTCTGTTAGA	TGGGTCTAAC	180
	AGCGTCGGGA	AAGGGAGCTT	TGAAAGGTCC	AAGCACTTTG	CCATCACAGT	CTGTGACGGT	240
	CTGGACATCA	GGCCCGAGAG	GGTCAGAGTG	GGAGCATTC	AGTTCACTTC	CACTCCTCAT	300
	CTGGAATTC	CCTTGGATT	ATTTTCAACC	CAACAGGAAG	TGAAGGCAAG	AATCAAGAGG	360
	ATGGTTTTC	AAGSAGGCG	CACGGAGACG	GAACCTGTCT	TGAAATACCT	TCTGCACAGA	420
	GGGTGCGCTG	GAGGCAGAAA	TGCTTCTGTG	CCCCAGATCC	TCATCATCTG	CACTGATGGG	480
	AAGTCCCAAG	GGGATGTGGC	ACTGCCATCC	AAGCAGCTGA	AGGAAAGGGG	TGTCACTGTG	540
	TTTGCTGTGG	GGGTGAGGTT	TCCCAGGTGG	GAGGAGCTGC	ATGCACCTGG	CAGCGAGCCT	600
10	AGAGGGCAGC	ACGTGCTGTT	GGCTGAGCAG	GTGGAGGATG	CCACCAACGG	CCTCTTCAGC	660
	ACCTCTCAGCA	GCTCGGCCAT	CTGCTCCAGC	GCCACGCCAG	ACTGCAGGGT	CGAGGCTCAC	720
	CCCTGTGAGC	ACAGGACGCT	GGAGATGGTC	CGGAGTTTCG	CTGGCAATGC	CCCATGCTGG	780
	AGAGGATCGC	GGCGGACCTT	TGCGGTGCTG	GCTGCACACT	GTCCCTTCTA	CAGCTGGAAG	840
	AGAGTGTTC	TAACCCACCC	TGCCACCTGC	TACAGGACCA	CCTGCCCAGG	CCCCTGTGAC	900
15	TGCGAGCCCT	GCCAGAATGG	AGGCACATGT	GTTCAGAAAG	GACTGGACGG	CTACCACTGC	960
	CTCTGCCCG	TGGCCTTTGG	AGGGGAGGCT	AACCTGTGCC	TGAAGCTGAG	CCTGGAATGC	1020
	AGGGTCGACC	TCTCTTCTCT	GCTGGACAGC	TCTGCGGGCA	CCACTCTGGA	CGGCTTCCTG	1080
	CGGGCCAAAG	TCTTCTGTAA	GCGGTTTGTG	CGGGCCGTGC	TGAGCGAGGA	CTCTCGGGCC	1140
	CGAGTGGGTG	TGGCCACATA	CAGCAGGGAG	CTGCTGTGTG	CGGTGCTCTG	GGGGGAGTAC	1200
20	CAGGATGTGC	CTGACCTGGT	CTGGAGCCTC	GATGGCATTG	CCTTCCGTGG	TGGCCCCACC	1260
	CTGACCGGCA	TGGCCTTGGC	GCAGGCGGCA	GAGCGTGGCT	TGGGAGCGCG	CACCAAGACA	1320
	GGCCAGGACC	GGCCACGTAG	AGTGGTGGTT	TTGCTCACTG	AGTCACACTC	CGAGGATGAG	1380
	GTTCGCGGCG	CAGCGCGTCA	CGCAAGGGCG	CGAGAGCTGC	TCCTGCTGGG	TGTAGGCAGT	1440
	GAGGCCGTGC	GGGCAGAGCT	GGAGGAGATC	ACAGGCAGCC	CAAAGCATGT	GATGGTCTAC	1500
25	TGCGATCCTC	AGGATCTGTT	CAACCAATAT	CCTGAGCTGC	AGGGGAAGCT	GTGCAGCGCG	1560
	CAGCGGCGAG	GGTGGCGGAG	ACAAGCCCTG	GACCTGCTCT	TCATGTTGGA	CACCTCTGCC	1620
	TCAGTAGGGC	CGAGAAATTT	TGCTCAGATG	CAGAGCTTTG	TGAGAAGCTG	TGCCCTCCAG	1680
	TTTGAGGTGA	ACCCTGAGCT	GACACAGGTC	GGCCTGGTGG	TGTATGGCAG	CCAGGTGCAG	1740
	ACTGCTCTCG	GGCTGGACAC	CAAAACCCAC	CGGGCTGCGA	TGCTGCGGGC	CATTAGCCAG	1800
30	GGCCCTTACC	TAGGTGGGGT	GGGCTCAGCC	GGCACCGCCC	TGCTGCACAT	CTATGACAAA	1860
	GTGATGACCG	TCCAGAGGGG	TGCCCGGCTT	GGTGTCCCCA	AAGCTGTGGT	GGTGCTCACA	1920
	GGCGGGAGAG	GGCAGAGGGA	TGCAGCCGTT	CCTGCCCAGA	AGCTGAGGAA	CAATGGCATC	1980
	TCGTCTTGG	TGCTGGGCGT	GGGGCCTGTC	CTAAGTGAGG	GTCTGCGGAG	GCTTGCAGGT	2040
	CCCCGGGATT	CCCTGATCCA	CGTGGCAGCT	TACGCCGACC	TGCGGTACCA	CCAGGACGTG	2100
35	CTCATTTAGT	GGCTGTGTGG	AGAAGCCAAG	CAGCCAGTCA	ACCTCTGCAA	ACCCAGCCCG	2160
	TGCATGAATG	AGGGCAGCTG	CGTCTGTCAG	AATGGGAGCT	ACCCGTGCAA	GTGTGCGGAT	2220
	GGCTGGGAGG	GGCCCACTG	CGAGAACCGT	GAGTGGAGCT	CTTGCTCTGT	ATGTGTGAGC	2280
	CAGGGATGGA	TTCTTGAGAC	GGCCCTGAGG	CACATGGCTC	CGGTGCAGGA	GGGCGAGCAG	2340
	CGTACCCCTC	CCAGCAACTA	CAGAGAAGGC	CTGGGCACTG	AAATGGTGCC	TACCTTCTGG	2400
40	AATGTCTGTG	CCCCAGGTCC	TTAG				2424

Seq ID NO: C25 DNA Sequence
Nucleic Acid Accession #: XM_097386.3
Coding sequence: 142..795

45	1	11	21	31	41	51	
	CTCGCAGAAC	CACCTGGACT	CTGTCCGTGT	CTGTCCCCCG	GCCTCCAGGG	CTCCTCTCCC	60
	GGGACCCCCG	TCCACAGCCT	GGGCCCCGCG	CCGGGGGAAG	CGCTGTCTGC	CTATCTCTGT	120
	CTACCTCAGG	TCTGACTTTT	GATGCCAAAA	TCTGAGCCCC	TGGGGTGCCT	CTCCCCCGCC	180
50	TCCCGTGCAC	CAGGGTCTGC	AGCAGCCACT	GGGGCCTGGC	TGCCGTGTGC	ATCTGGCGGC	240
	CCTGACCCCG	TGGGGCCCCC	GTGCACCTGC	CCACCTCGGA	GCTTGGGGAG	GGGCGGTGCA	300
	GGGTGAGGGG	CTGGGTCTGT	TCCCTCGGGC	TGCGTGTGTG	TGTGCGGAAT	CCTGCGTGTG	360
	GTGTCTCTGG	GGGATCCGGC	CTCCCGGCGG	TGGGTGGACC	TGGATTCTAA	CTCAGAGGAC	420
55	TTGAGCCTGC	TGTTAACTCC	GATGATTGTA	GGGACAGGCG	GGGTGGGTGG	GGGGTGGGCG	480
	CGAGGCTGGG	TCCCGGCCCA	GGAGAAGGAA	GTGCGTGAAG	GCAGTGCCCA	TGCTGGCGGT	540
	GGAAATGGGA	GGGGGTGTGA	GAGGGTCTAT	GGGGCCCGGT	CCTGGATACT	CGGCGAGGAG	600
	CGGTGTCTGC	AGAGGCTCCT	CCCTGCCTCA	GGTGGCCCCG	TTCAACCCCA	CGCGTGCCCA	660
	TCCTCTGCGA	CGGCTGTGCG	GTGGGGGTTT	AAATTGCGTG	TGGCTTTCTG	GGGTGCGAGT	720
60	CAGCACCCCC	CCTTATGCAG	ACTGGGAGGG	GGTGGGCGAG	TCCCTCAGC	CACGAGGACC	780
	CTGATGGGTT	TCTAGTTTAC	TTGGGACCGT	GGGGCCTGGC	TGCGTACTGA	GTGGGTGCCC	840
	CACAGTCAAG	AGCAACGGGG	GCTCCCCCTG	CTCTGAGATG	TTGGGAGAAA	GGGCGCTTCT	900
	GGAACTTCC	GTGGGACCGG	TAAGTGGCTG	TCCAGAAAGG	CGGGAGGGTG	GGCACGGGCG	960
	ACGGGGGGCA	GCTGGGGTGG	TTGTTAAGGG	TCAAGCATCT	GTACAGTTGA	ATTTCCITTT	1020
65	TCTTATCATG	TTTTACCCAC	CTTGTCCCTT	TTTTCCCCAA	TGTGCTTTT	GCAATTTTTT	1080
	CCTTGGCAAA	TGTAACCTCA	GCCTTTCATT	CATGAAGTGT	GAAATTTTCA	TTTCTCTGGA	1140
	GTTTGTGAGA	CGGCGTGGGA	ACCACGCGTG	AAACTCAGGT	AATAGGAGGA	AAAAAAAAAA	1200
	AACTTAAAAA	AATTTTAAAA	AAACATAAAA	CTACTCTCTA	CCTCTGGCTG	GGCCAGCCT	1260
	GTCTCGCCCT	GGCGCGGCA	GGGTGGCGCT	TAACAATTTT	AGTTTTGCGA	GAACATTCAG	1320
70	GTATTAAAAA	GAAAAA					1337

Seq ID NO: C26 DNA Sequence
Nucleic Acid Accession #: Bos sequence
Coding sequence: 95..2128

75	1	11	21	31	41	51	
	GGGGTAGTTT	GTAGGGAGCG	AGCTCTCCAC	GTGGCGGACT	GGGAGGCTGG	AGGCTACGGG	60
	CTCCTGGAAA	GGAGAGACAC	CAGCAATTGC	CACAAATGCT	TCATCCACTG	ACTTTACATT	120
	TGCTTCTCGG	GAGCTTGTGG	TCCGCGTTGA	CCATCCCAAT	GAAGAGCAGC	AGAAAGACGT	180
80	CACACTGAGA	GTATCTGGAG	ACCTTTCATG	TGGAGGAGTG	ATGCTCAAGT	TAGTAGAACA	240
	GATCAATATA	TCCCAAGACT	GSTCAGACTT	TGCTTTTGG	TGGGAACAGA	AGCATTGCTG	300
	GCTTCTGAAA	ACCCACTGGA	CCCTGGACAA	ATATGGGGTC	CAGGCAGATG	CAAAGCTTCT	360
	CTTACCCCT	CAGCATAAAA	TGCTGGCGCT	TGCTCTGCGG	AATTTGAAGA	TGTTGAGGTT	420
	GCGAGTCAGC	TTCTCAGCTG	TGGTTTTTAA	AGCTGTCACT	GATATCTGCA	AAATCCTGAA	480

5	TATTAGAAGA	TCAGAAGAGC	TTTCCCTTGT	AAAGCCGTCT	GGTGACTATT	TTAAGAAGAA	540
	GAAGAAAAAA	GACAAAAATA	ATAAGGAACC	CATAATTGAA	GATATTCTAA	ACCTGGAGAG	600
	TTCTCCAAAC	GCTTCAGGTT	CATCAGTAAG	TCCTGGTTTA	TACAGTAAAA	CCATGACCCC	660
	TATATATGAC	CCCATCAATG	GAACACCAGC	ATCATCCACC	ATGACTTGGT	TCAGTGACAG	720
	CCCTTTGACG	GAACAAAAC	GCAGCATCCT	CGCATTTCAGC	CAACCCCCCC	AGTCCCCAGA	780
	AGCACTTGCG	GATATGTACC	AGCCTCGGTC	TCTGGTTGAT	AAAGCCAAGC	TCAATGCAGG	840
	TTGGCTAGAC	TCCTCACGCT	CCCTTATGGA	ACAAGGCATC	CAAGAGGATG	AGCAGCTGCT	900
	CTTAGCATTT	AAATATTATT	CTTTCTTCGA	CTTGAATCCT	AAATATGATG	CTGTCCGAAT	960
10	AAACCAACTC	TATGAGCAAG	CCAGGTGGGC	CAITCTCTTA	GAAGAAATTG	ATTGCACAGA	1020
	GGAAGAAATG	TTGATCTTTG	CAGCTCTACA	GTACCACATT	AGCAAACTGT	CGTTGTCTGC	1080
	TGAAACACAG	GATTTTGAGG	GCGAGTCCGA	GGTTGATGAA	ATAGAAGCGG	CGCTTTCTAA	1140
	TTTGGAAGTA	ACCCTAGAA	GTGGAAAAGC	GGACAGCCTT	TTGGAGGACA	TTACTGATAT	1200
	CCCTAAACTT	GCAGATAATC	TCAAAATTAT	TAGGCCCAAG	AAGTTACTAC	CAAAAGCTTT	1260
15	CAAAACATAT	TGGTTTATCT	TTAAAGACAC	ATCCATAGCA	TACTTTAAAA	ATAAGGAACT	1320
	TGAACAAGGA	GAACCACTAG	AAAAACTAAA	TCITTAGAGC	TGCGAAGTTG	TGCCCGATGT	1380
	AAATGTAGCA	GGAAGAAAAT	TTGGAATCAA	GTTACTAAATC	CCTGTTGCCG	ATGGTATGAA	1440
	TGAAATGTAT	TTGAGATGTG	ACCATGAGAA	TCAATACGCC	CAATGGATGG	CTGCTGTCAT	1500
	GTGGCATCG	AAGGGCAAAA	CCATGGCAGA	CAGCTCCTAC	CAGCCAGAGG	TCCTCAACAT	1560
20	CCTTTCATTT	CTGAGGATGA	AAAACAGGAA	CTCTGCATCT	CAGGTGGCTT	CCAGTCTCGA	1620
	AAACATGGAT	ATGAACCCAG	AATGTTTTGT	GTCAACACGG	TGTGCAAAAA	GACACAAATC	1680
	CAAAACAGCTG	GCCGCCCCGA	TCCTGGAGGC	GCACCAAGAC	GTGGCCCGCA	TGCCCTCGGT	1740
	CGAAGCCAAG	CTGGGTTTCA	TCCAGGGGTG	CCAGTCACTG	CCTGAGTTTG	GCCTCACCTA	1800
	CTACCTTGTC	AGATTTAAAG	GAAGCAAAAA	AGATGACATT	CTGGGAGTTT	CATATAACAG	1860
25	GTGATTAA	ATTGATGAG	CCACCGGGAT	TCCAGTGACA	ACATGGAGAT	TCACAAATAT	1920
	CAAAACAGTG	AATGTAAACT	GGGAAACCCG	GCAGGTGGTC	ATCGAGTTTG	ACCAAAACGT	1980
	CTTTACTGCT	TTCACTGCC	TGAGTGACGA	TTGCAAGATT	GTGCAAGAGT	ACATTGGCGG	2040
	CTACATTTT	TTGTCCACCC	GCTCCAAGGA	CCAGAATGAA	ACACTCGATG	AGGACTTGT	2100
	CCACAAATTG	ACCGGCGGTC	AGGATTGAAA	CAAGCACGGG	TGCTCGGCTC	ACACCAACAA	2160
30	GGCAAGCCAA	AGGCGCCCTT	CCCCAGAGGG	ATCCCTAACG	TGCCCGAGAT	GTAGATTCTG	2220
	GACTAACAGA	CAACATACAT	TCACCGCTGG	TCACCCAGAT	CCTCATTCAA	ACCCACTGCT	2280
	GGCAGATCCC	TTTCTTACT	TTGCCCTGTG	CTACCAGCCA	CGGAAGGAGC	CTCTCTTGTT	2340
	TTTTCTATA	AATGGGTAGG	CAGGAGAAAA	GCAGGTGCC	TAAGATTGCT	CTAAGGCCCA	2400
	GCATGTGGT	ACAGTTCTCT	GACTTGACGA	ACCTGCCAGG	TGTATGGCTA	CAAGTTATCC	2460
35	TGCTGCTGAT	CTGTCTCATT	ACTAAGTCAA	TGGAGAAGAC	AGAAAGGTAA	AAATCACGCTG	2520
	TAGCAAGAAC	AATCTTAT	TCACAACTC	AGGTATGAAA	CGAAACGCTT	GTCTCTCATG	2580
	GAATGCTTT	TAGCTCCTGT	CTTTTCAAAA	TGGCAGAGGG	AGTTCTCTACA	CACACTTTTT	2640
	CCCTGGAGGC	CAAGGTCTAG	GGGTAGAAAG	GGGAGGGGTG	GGGCTACCAG	GTAGCAGTTG	2700
40	ACAACCCAG	ATGACAGGAG	TGGCCCTCAG	TGTCTCTCTG	CCACAGTGAT	ACCTGCCAAG	2760
	ATGACCACTG	ACCCACATCT	GGTCTTAGTC	ATTGGTCTCC	TCAGATTCTT	GGGGCCACCT	2820
	CGAAGCCCCA	TTCCATTCTT	ACAGATCTCT	CAGCCACCTG	TAAGTCTCTT	GTGAAGATGT	2880
	GGGTGACACA	GGGGGACAGG	AAAACCCATT	TCTCAACCCA	GATCCATGTC	TCCACTGCTT	2940
	CTACTCTGGG	TTGGGATTCA	GGAGAGCAGG	CACAGTCCTC	TCTGTTTATA	GAACACCTG	3000
	CCAGTGTCAA	GGATTCCAGT	CAGGTGTCTA	TCCCAACTGG	TCAGGGAGAG	AAGGGCAGAC	3060
45	CCATTCTCAA	AGACCAACAT	GTCCAAGGTC	TGACAGCTCC	CACTGGCTG	CCCCCAGG	3120
	GGCTTAGGCG	TGGTCTGGGT	CATGGGGAAG	CGTCCCTCTT	ATCGCTGGTC	TGTGTTCTCC	3180
	TGGATTGGT	ATCTATGTTG	GTACGACTCC	TGGCCTTTTA	TCTAAAGGAC	TTTGGCTTTT	3240
	GTAAATCACA	AGCCAATAAT	AGACTTTTTT	CTCCCCCTCT	GTTTTTTGCT	GTGTCTCTCT	3300
	TGCTCTGAGA	CGCTCTGAG	ACAGTGCTTG	CCTTGAGAGA	GTGAGCCAAT	TAACAGCTGC	3360
50	CTGAATTGTC	ATTTTCCATT	TTGGTTTGT	AGAGGTGGGA	GGGTGGGTT	TTGAGAAGGT	3420
	CAAAAGCAAT	ACCAGAAGTA	AAGGGAAATA	TCAGACAATA	TTTTATTATT	TTTTTATAGA	3480
	TGTTCTGCCA	CACAAAGAAC	TTGGGGTGTA	AGGATAAGGC	AAAAGCTCCA	ATCCCATTTT	3540
	TCAGTTCTCC	TAGGATGCAC	CCCTCAGGGA	GCCTGGCCAG	AGTTCGAGG	CCCGTGAGCG	3600
	TCAGCTGTG	CTTTATTTC	CATCAAAGCC	CTCTGAGAAG	TGAGACCTCA	GCAATTCCGG	3660
55	GAGCCACATA	GAGACAGACT	TGGCAAGGGA	CCCCCTGGTT	CTGAGCCAGT	AGCTGCCATC	3720
	TGGAAATTC	TCCTTTAGCC	TCCTCTTAGA	GGTGAATGTT	AATGAAGCCT	CCCAGGCACC	3780
	CGCTGAATTT	CTGAGGCCTT	GCTTAAAGCT	CAGAAAGTGGT	TTAGGCATTT	GGAAAATCTG	3840
	GTTCACATCA	TAAAGAACTT	GATTTGAAAT	GTCTTCTATA	GAACCAAGTG	CTAAGTGATC	3900
	CGTATTATAC	TTGATGTTGG	TCATTTCTCA	GTCTATTTC	TCAGTCTTAT	TATTTTAGAA	3960
60	CCTAGTCAGT	TCCTTAAAGT	TATAACTGTT	CCTACATTAA	AATAATGCTT	CTGATGTCA	4020
	GATTTTACCT	GTGTTGCTGCT	GAGAACATCT	CTGCCTAATT	TACCAAGGCC	AGACCTTCAG	4080
	TTCAACATGC	TTCTTAGCT	TTTCATAGTT	GTCTGACATT	TCCATGAAAA	CAAGGGAACC	4140
	AACTTTGTTT	TAAACAAACT	TTGTTTGGTT	ACAGTTTTC	GGGGAGCGTT	TCTTCCATGA	4200
	CACACAGCAA	CATCCCAAG	AAATAAACAA	GTGTGACAAA	AAAAAATA	AACAAACCTA	4260
65	AATGCTACTG	TTCCAAAGAG	CAACTTGATG	GTTTTTTTTA	ATACTGAGTG	CAAAAGGTCA	4320
	CCCAAAATCC	TATGATGAAA	TTTTAAATTA	ATGGGCACCT	TTCAACATCA	TTTGCTTCCT	4380
	TATCTACAGT	TGATTGAGAA	ATCTGCATTT	TTTATTCTTT	TATATGACTT	TTAAGTAAAA	4440
	GATTTATATG	GATTTGAAAA	AAAAAATA	A			4471

Seq ID NO: C27 Protein Sequence
Protein Accession #: NP_005161.1

75	1	11	21	31	41	51	
	MDGGTLPRSA	PPAPFVPEVC	AARRRPASPE	LLRCSRRLRP	ATAETGGGAA	AVARRNERER	60
	NRVKLVNLGF	QALRHVPHG	GASKKLSKVE	TLRSAYEYIR	ALQRLAEHD	AVRNALAGGL	120
	RPQAVRPSAP	RGPPGTTPVA	ASPSRASSSP	GRGGSSEPGS	PRSAVSDDDS	CEGEGALSPAE	180
	RELLDPSSWL	GGY					193

Seq ID NO: C28 DNA Sequence
Nucleic Acid Accession #: NM_017763
Coding sequence: 169..2520

80	1	11	21	31	41	51	

5	AAAAA	AACTTTAGAG	AAAGGAAGGG	CCAAACTAC	GACTTGGCTT	TCTGAAACGG	60
	AAGCATAAAT	GTTCTTTTCC	TCCATTGTGC	TGGATCTGAG	AACCTGCAIT	TGGTATTAGC	120
	TAGTGGAGC	AGTATGTATG	GTTGAAGTGC	ATTGCTGCAG	CTGGTAGCAT	GAGTGGTGGC	180
	CACCAGCTGC	AGCTGGCTGC	CCTCTGGCCC	TGGCTGCTGA	TGGCTACCCCT	GCAGGCAGGC	240
	TTTGGACGCA	CAGGACTGGT	ACTGGCAGCA	GCGGTGGAGT	CTGAAAGATC	AGCAGAACAG	300
	AAAGCTGTTA	TCAGAGTGAT	CCCCTTGAAA	ATGGACCCCA	CAGGAAACT	GAATCTCACT	360
	TTGGAAGGTG	TGTTTGTCTG	TGTTGCTGAA	ATAACTCCAG	CAGAAGGAAA	ATTATGCGAG	420
	TCCCACCCAC	TGTACCTGTG	CAATGCCAGT	GATGACGACA	ATCTGGAGCC	TGGATTCAATC	480
10	AGCATCTGCA	AGCTGGAGAG	TCCTCGACGG	GCCCCCGGCC	CCTGCTCTGC	ACTGGCTAGC	540
	AAGGCTCGGA	TGGCGGTGTA	GCGAGGAGCC	AGTGTCTGTC	TCTTTGACAT	CACTGAGGAT	600
	CGAGCTGTCT	CTGAGCAGCT	GCAGCAGCCG	CTGGGGCTGA	CCTGGCCAGT	GGTGTGATC	660
	TGGGTAATG	ACGCTGAGAA	GCTGATGGAG	TTTGTGTACA	AGAACCAAAA	GGCCCATGTG	720
	AGGATTGAGC	TGAAGGAGCC	CCCAGCCTGG	CCAGATTATG	ATGTGTGGAT	CCTAATGACA	780
	GTGGTGGGCA	CCATCTTTGT	GATCATCTGT	GCTTCGGTGC	TGGCATCCG	GTGCGCGCCC	840
15	CGCCACGCA	GGCCGGATCC	GCTTCAGCAG	AGAACAGCCT	GGGCCATCAG	CCAGCTGGCC	900
	ACCAGGAGGT	ACCAGGCCAG	CTGCAGGCAG	GCCCGGGGTG	AGTGGCCAGA	CTCAGGGAGC	960
	AGCTGCAGCT	CAGCCCTGT	GTGTGCCATC	TGTCTGGAGG	AGTTCTCTGA	GGGGCAGGAG	1020
	CTACGGGTCA	TTTCTTGCCT	CCATGAGTTC	CATCGTAACT	GTGTGGACCC	CTGGTTACAT	1080
	CAGCATCGGA	CTTGCCCCCT	CTGCGTGTTC	AACATCAGAG	AGGGAGATTC	ATTTTCCCAG	1140
20	TCCTCGGAC	GCTCTCGATC	TTACCAAGAA	CCAGGTGAAA	GACTCCACCT	CATTGCGCAG	1200
	CATCCCGGCC	ATGCCCACTA	CCACCTCCCT	GCTGCTTACC	TGTTGGGCCC	TTCCCGGAGT	1260
	GCAGTGGCTC	GGCCCCCAGG	ACCTGGTCCC	TTCTTGCCAT	CCCAGGAGCC	AGGCATGGGC	1320
	CCTCGGCATC	ACCGCTTCCC	CAGAGCTGCA	CATCCCGGG	CTCCAGGAGA	GCAGCAGCGC	1380
25	CTGGCAGGAG	CCCAGCACCC	CTATGCACAA	GGCTGGGGAA	TGAGCCACCT	CCAATCCACC	1440
	TCACAGCACC	CTGCTGCTTG	CCCAGTGCCC	CTACGCGGG	CCAGGCCCCC	TGACAGCAGT	1500
	GGATCTGGAG	AAAGCTATTG	CACAGAACGC	AGTGGGTACC	TGGCAGATGG	GCCAGCCAGT	1560
	GACTCCAGCT	CAGGGCCCTG	TCATGGCTCT	TCCAGTGACT	CTGTGGTCAA	CTGCACGGAC	1620
	ATCAGCTTAC	AGGGGGTCCA	TGGCAGCAGT	TCTACTTTCT	GCAGCTCCCT	AAGCAGTGAC	1680
	TTTGACCCCC	TAGTGTACTG	CAGCCCTAAA	GGGGATCCCC	AGCGAGTGGG	CATGCAGCCT	1740
30	AGTGTGACCT	CTCGGCCTCG	TTCTTGGAC	TGCGTGGTGC	CCACAGGGGA	AACCCAGGTT	1800
	TCCAGCCATG	TCCACTACCA	CGCCACCGG	CACCACTACT	ACAAAAGCG	GTTCCAGTGG	1860
	CATGGCAGGA	AGCCTGGCCC	AGAAACCGGA	GTCCCCCAGT	CCAGGCCCTCC	TATTCTCTGG	1920
	ACACAGCACC	AGCCAGAGCC	ACCTTCTCCT	GATCAGCAAG	TCACCGGATC	CAACTCAGCA	1980
	GGCCCTTCGG	GGCGGCTCTC	TAAACCCAG	TGCCCCAGGG	CCCTCCCTGA	GCCAGCCCCCT	2040
35	GGCCCASTTG	ACGCTCCAG	CATCTGCCCC	AGTACCAGCA	GTCTGTTCAA	CTTGCAAAAA	2100
	TCCAGCCTCT	CTGCCCGACA	CCCACAGAGG	AAAAGGCGGG	GGGGTCCCTC	CGAGCCCCACC	2160
	CCTGGCTCTC	GGCCCCAGGA	TGCAACTGTG	CACCCAGCTT	GCCAGATTTT	TCCCCATTAC	2220
	ACCCCACTTG	TGGCATATCC	TTGGTCCCCA	GAGGCACACC	CCTTGATCTG	TGGACCTCCA	2280
40	GGCCTGAGCA	AGAGGCTGCT	ACCAGAAACC	CCAGGCCCTC	GTTACTCAA	TTCAAGGCCA	2340
	GTGTGGTTGT	GCCTGACTCC	TGCGCAGCCC	CTGGAACCC	ATCCACCTGG	GGAGGGGCTC	2400
	TCGTAATGGA	GTCTGACAC	CGCAGAGGGC	AGGCCATGCC	CTTATCCGCA	CTGCCAGGTG	2460
	CTGTGCGCCC	AGCCTGGCTC	AGAGGAGGAA	CTCGAGGAGC	TGTGTGAACA	GGCTGTGTGA	2520
	GATGTTTCCAG	CCTAGCTCCA	ACCAAGAGTG	TGCTCCAGAT	GTGTTTGGGC	CCTACCTGGC	2580
45	ACAGAGTCTT	GCTCTGGGA	AAGGAAAGGA	CCACAGCAAA	CACCATTCIT	TTTGCCTTAC	2640
	TTCTAGAAAG	CAGTGGGAAG	GGACTGTGTA	TGGTGGAGGG	TGAGAGGGTG	CCGTTTCTCT	2700
	CTCCAGCTCT	AGACCTTGTC	TGCAGAAAC	ATCTGCAGTG	CAGCAATACC	ATGTCCAGCC	2760
	AGGCACCCAG	CTGCTGCCTG	TGGCGTGTGT	GGGCTGGATC	CCTTGAAGGC	TGAGTTTITG	2820
	AGGGCAGAAA	AGGCAGATAT	GGTAGCCAGG	TGTTACAAAG	GTGCTGCTCC	TTCTCCAACC	2880
50	CCTACTTGGT	TTCCCTCACC	CCAAGCCTCA	TGTTCATACC	AGCCAGTGGG	TTCAAGCAGAA	2940
	CGCATGACAC	CTTATCACCT	CCCTCTCTGG	GTGAGCTCTG	AACACCAGCT	TTGGCCCTCT	3000
	CACAGTAAGG	CTGCTACATC	AGGGGCAACC	CTGGCTCTAT	CATTTCCTT	TTTTGCCAAA	3060
	AGGACCAAGTA	GCATAGGTGA	GCCTGAGCA	CTAAAGGAG	GGGTCCCTGA	AGCTTTCCCA	3120
	CTATAGTGTG	GAGTTCTGTC	CCTGAGGTGG	GTACAGCAGC	CTTGTTCTCT	CTGGGGGTTG	3180
55	AGAATAAGAA	TAGTGGGGAG	GGAAAAACTC	CTCCTTGAAG	ATTTCTCTGC	TCAGAGTCCC	3240
	AGAGAGGTAG	AAAGGAGGAA	TTTCTGCTGG	ACTTTATCTG	GGCAGAGGAA	GGATGGAATG	3300
	AAAGGTAGAAA	AGGCAGAAAT	ACAGCTGAGC	GGGGACAACA	AAGAGTTCTT	CTCTGGGAAA	3360
	AGTTTTGTCT	TAGAGCAAGG	ATGGAAAATG	GGGACAACAA	AGGAAAGCA	AAGTGTGAAC	3420
	CTTGGGTTTG	GACAGCCAG	AGGCCAGCT	CCCCAGTATA	AGCCATACAG	GCCAGGGACC	3480
60	CACAGGAGAG	TGGATTAGAG	CACAAGTCTG	GCCTCACTGA	GTGGACAAGA	GCTGATGGGC	3540
	CTCATCAGGG	TGACATTAC	CCCAGGCGAG	CCTGAOACT	CTTGGCCCTT	CAGGCATTAT	3600
	CCCATTTGGA	ATGTGAATGT	GGTGGCAAG	TGGGCAGAGG	ACCCCACTTG	GGAACTTTT	3660
	TCCTCATGTT	AGTGGGGAGA	CTAGCACCTA	GGTACCCACA	TGGGTATTTA	TATCTGAACC	3720
	AGACAGACGC	TTGAATCAGG	CATATGTGTA	AGAAATATAT	TTATTTGCTA	ATATATTTAT	3780
65	CCACAAAAAA	AAAAAAAAAA	AA				3802

Seq ID NO: C29 Protein Sequence
Protein Accession #: NP_004280.2

70	1	11	21	31	41	51	
	MNSSAHYHVN	FSQAISQDVN	LHEAILLCPN	NTFRRDPTAR	TSQSQEPFLQ	LNSHTNPEQ	60
	TLPGTNLTF	LSPVDNHNMR	LTSQDLYDL	DINIFDEINL	MSLATEDNFD	PIDVSQLPDE	120
	PDSDSLGLSD	SSHNNTSVIK	SNSSHSVDE	GAIGYCTDHE	SSSHDLEGA	VGGYYPEPSK	180
75	LCHLDQSDSD	PHGDLTFQHV	PHMHTYHLQ	TAPESTSEPF	PWPGKSQKIR	SRYLEDTDRN	240
	LSRDEQRARA	LHIPPVSVDEI	VGMPVDSFNS	MLSRYIYLDL	QVSLIRDIRR	RGNKRVAAQN	300
	CRKKLDIIL	NLEDDVCNLQ	AKKETLKRQ	AQCNKAINIM	KQKLHDLYHD	IFSRLEDDQ	360
	RPVNPVHYAL	QCTHDGSIIL	VPKELVASGR	KKETQKGRK			400

80 Seq ID NO: C30 DNA Sequence
Nucleic Acid Accession #: NM_004442
Coding sequence: 19..2982

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1216

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TTGCCATTCT AACTGGTGTG AGATGGTATC TCATTGTGGG TTTGATTGTC ATTTCCTCTAA 5040
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 GCTGAAAATG ACAGGGAGAA TGAACCCAGG TTGGAACAA CTCTTCAGGA TATTATCCAG 5340
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 AGCAGAGCTG GCAAAATGGT TAAAGAGTCA AGACTCATTG GTGTGCCGTA TTCAGGAGAC 6000
 CCATCTCAGC TGCAAGACA CACATAGGCT CAGAGTAAAA GGGATACAGG GGAATTC 6057

Seq ID NO: C31 DNA Sequence
 Nucleic Acid Accession #: NM_031942.1
 Coding sequence: 145..1260

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 GTAAAGAAAG ACTTAAGAAA ATTCAAGATG GTGAAGTTGA TTTCCATGGA AACCTCGTCA 240
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 GCGATGAAGT TTCCAGCGCG GAGTACCAGG GGAGCAACCA ACAAAAAGC AGAGTCCCCG 420
 CAGCCCTCAG AGAATTTCTG GACTGATTCC AACTCCGATT CAGAAGATGA AAGTGGAAAT 480
 AATTTTTTGG AGAAAAGGGC TTTAAATATA AAGCAAAACA AAGCAATGCT TGCAAAACTC 540
 ATGCTGAAT TAGAAGCTT CCCTGGCTCG TTCGTTGGA GACATCCCCC CCCAGGCTCC 600
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 CCTGAACCGA GAGCTCGTCC TCTTACCAGG TCAAGGTCCT GGATCTCTGG GTCCCTTGAC 720
 GCTCTACCCA TGGAGGAGGA GGAGGAAGAG GATAAGTACA TGTGTGTGAG AAAGAGGAAG 780
 ACCGTGGATG GCTACATGAA TGAAGATGAC CTGCCAGAA GCCGTGCTC CAGATCATCC 840
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 TATGAAGACA TATTTTATTT ACTTGTGTTT GAAATAGCCC TCATAAAACC TAAGCACTTG 1620
 GAACACAAAT AATAGTATTA ACTAAGTAGA TCTATTGAAT TTCAGAGAAG AGCCTCTTAA 1680
 CTGTGTTTACA CAATAACGAG TATGATTAG CACTCATACT AGTTGAAAT TTTAATAGAA 1740
 TCAAGGCAACA AAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT 1800
 CTCTCAATCC CATGCTTGGC GCCTATGTTA CAAGTTGTTG TCACAGTTGA GACTTAATTT 1860
 CTCTTAATTT CTCTGCCC GAGGTAAGT GGTGCGTCCA GCTTACACGA TCATAATTCA 1920
 AAGGTTGGTG GGCAGTGA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGGAGATT 1980
 ATGAGTAAAG TGATTTGAAT TTTCAATATA AAACCTTAGT ATAATTGTAG TTTGCAAGT 2040
 TTATTTCAGT TCATATGTA GGTATTGCAA ATAAATTCCT GGACAATTT GTATGGAAC 2100
 TTGATATTAA AAACATGCT GTGGTTCTTT GCAGTTTCTT GTAAATTTAT AAACCAAGCA 2160
 CAAGGTTCAA GTTTAGATT TAAGCACTTT TATAACCAATG ATAAGTGCCT TTTTGGAGAT 2220
 GTAACTTTTA GCAGTTTGTT AACCTGACAT CTCTGCCAGT CTAGTTTCTG GGCAGGTTTC 2280
 CTGTGTGAGT ATTTCCCTCT CTCTTGCAT TAATCAAGGT ATTTGGTAGA GGTGGAATCT 2340
 AAGTGTGTTT ATGTCCAATT TACTTGATA TGTAAACCAT TGCTGTGCCA TCTAATGTTT 2400
 GATGCATAAT TGAACCTTGA ATCGATAAGT GTAAATACAG CTTTGTATCT GTAATGCTTT 2460
 TATACAAAG TTTATTTTAA TAATAAAATG TTTGTTCTAA AAAAAAATA 2510

Seq ID NO: C32 DNA Sequence
 Nucleic Acid Accession #: NM_012445.1
 Coding sequence: 276..1271

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 TCTCGCTGGA GCGCAGGCGG TGCAGCATCG AAGACAGGAG GAACCTGGAGC CTCATTGGCC 180
 GCGCGCGGGC GCGCGCTCGG GGTCTAAATA GGAGCTCCGG GCTCTGGCTG GGAACCGACC 240
 GCTGCGCGCC CGCTCCCGG TGTCTCTGCC GGGTGTGGA AAAACCCAGC CGCGCGCGCG 300
 CCTGCGGCAA GGCCTCTGCG GCTCTCTCTC TGSCCACTCT CCGCGCGGCC GGCAGGCTC 360
 TTGGGGGAGA GTCCATCTGT TCGGCCAGAG CCGCGGCCAA ATACAGCATC ACCTTCAGCG 420
 GCAAGTGGAG CCAAGCGGCC TTCCCAAGC AGTACCCCTT GTTCCGCCCC CTTGCGCAGT 480
 GGTCTTGGCT GCTGGGGGCC GCGCATAGCT CCGACTACAG CATGTGGAGG AAGAACCACT 540
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AGATCGAGGC GGC GGCGGAG GCGCTGCAGA GCGTGCACGC GGTGTTTTCG GCGCCCGCCG 660
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TCTCGTTTGT GGTGGGCATC GTGCCAGCC CCGACTGGTT CGTGGGCGTG GACAGCCTGG 780
ACCTGTGGGA CGGGGACOGT TGGCGGGAAC AGCGGGCGCT GGACCTGTAC CCCTACGACG 840
CGGGGACGGA CAGCGGCTTC ACCTTCTCCT CCCCAACTT CGCCACCATC CCGCAGGACA 900
CGGTGACCGA GATAACGTCC TCCTCTCCCA GCCACCGCGC CAACTCTCTC TACTACCCGC 960
GGCTGAAGGC CCTGCTCCG ATCGCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCCA 1020
GGGCCTTCAT CCTCCCGCC CAGTCTCTGC CCAGCAGGGA CAATGAGATT GTAGACAGCG 1080
CTCAGTTCC AGAAACGCG CTGSACTGCG AGGTCTCCCT GTGGTCTGTC TGGGACTGT 1140
GCGGAGGCCA CTGTGGGAGG CTGGGACCA AGAGCAGGAC TCGCTAOGTC CGGGTCCAGC 1200
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GGAAACGTCA GTGTTCCAT GTTATGGATC TCTCTGCGTT TGAATAAAGA CTATCTCTGT 1800
TGCTCAC 1807

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Seq ID NO: C33 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1314

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TACTTCTCTT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGAAGGAGAG 240
CTGGACTGTC CCTTGGGGGA GAGCGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGGCT 300
GCAGTGGGAG TCCGCTCTC CAAGGACCGA TCCACACTGC AGGTGTCTGA CTCGGCCACA 360
GGGAACCTGT TCTCTGCTG TTTCGACAA TCCACAGAAG CTCTCGCTGA GACAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAACCCACTT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTGCGATGCG GAACTCAAGT 540
GGGCCCTGTC TCTCAGGCTC CTGCTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
AAGACCCCCC GTGTGGTGGG TGGGAGGAGG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGAACC CCACTGGGTC 720
CTCAGCGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
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GACACCTGCG AGGGTATAGC TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
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Seq ID NO: C34 DNA Sequence
Nucleic Acid Accession #: NM_003045.1
Coding sequence: 148..2037

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CAGATGCTGC GCGGGAAGGT GGTGACTGT AGCGGGGAGG AGAOCGGGCT GTCTCGCTGC 240
CTGAACACTT TTGATCTGGT GGCCTCGGG GTGGGCAGCA CACTGGGTGC TGGTGTCTAC 300
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CCCAAGACGG GCTCAGCTTA CCTCTACAG TATGTACCG TTGGAGAGCT CTGGGCCCTC 480
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5 TCTGGGCTAA TTGTGAACAT TTCAACCAGC CTTATAGCTG TTCTCATCAT CACCTTCTGC 1680
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 TTCTGTAACG TCTATCTCAT GATGCAGCTG GACCAGGGCA CCTGGGTCOG GTTTGCTGTG 1920
 TGGATGCTGA TAGGCTTCAT CATCTACTTT GGCTATGGCC TGTGGCAGAG CGAGGAGGCG 1980
 TCCCTGGATG CGGACCAAGC AAGGACTCCT GACGGCAACT TGGACCACTG CAAGTGACGC 2040
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 10 CACCCACCC TCCCACCAG TGCAACAGAA ACCACCTGGG TCCACACCT CACTGCA 2157

Seq ID NO: C35 DNA Sequence

Nucleic Acid Accession #: NM_002776.1

Coding sequence: 82..912

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 20 GCCCGGGCTC TGGCGAAGCT GCTGCCGCTG CTGATGGCGC AACTCTGGGC CGCAGAGGGC 180
 GGCTGTCTCC CCGAAAACGA CACGCGCTTG GACCCGGAAG CCTATGGCGC CCGGTGCGCG 240
 CGCGCTCGCG AGCCCTGGCA GGTCTGCTTC TTCAACGGCC TCTGTTCCA CTGCGCGGGT 300
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 25 CGCTCTGTG TCCATCCCAA GTACCAACAG GGTCTAGGCC CCATCTCGCC AAGCGAAAG 480
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 30 GTCTGTGACG AGACCTCCCA AGGCATCCTC TCGTGGGGTG TTTACCCCTG TGGCTCTGCC 840
 CAGCATCCAG CTGTCTACAC CCAGATCTGC AAATACATGT CCTGGATCAA TAAAGTCATA 900
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 CAGATGCCCA GAGGCTCCAT CGTCCATCCT CTCTCTCCCG AGTGGCTGTA ACTCTCCCT 1020
 35 TGTCTGCACT GTTCAAACTC CTGCGCCCTC CCACACTCTT AAACATCTCC CCTCTCACT 1080
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 AGTGCCCTCT CTGAACCTCA GTTTCTCTAT CTGCAAAATG GGAACAATGA CGTGCCCTACC 1320
 40 TCTTAGACAT GTTGTGAGGA GACTATGATA TAACATGTGT ATGTAAATCT TCATGTGATT 1380
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Seq ID NO: C36 DNA Sequence

Nucleic Acid Accession #: XM_095088

Coding sequence: 1..4074

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 GAGCTGCCAA GCGGGGTGCT GGAGGGCCTG AGCCAGCGGC GCGGGCCGCA GCGGGAGCA 240
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 55 TGCGCTGGAA CCGAGACCGG GCGCGGACGC AGGTGCGAGC GCCTGCGAGC CCTTGGAGGC 360
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 75 ATGTTAGAGA ACTACAGAAA CCTGTTCTCC CTGGGTATGA CTGCTCTAA GCCAGACTTG 1560
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 GATTCACTCC AAAAAGTAAT ACCAAGAAC TAATGAAAAT GTGGACATGA GAATTTACAA 1740
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Seq ID NO: C37 DNA Sequence

Nucleic Acid Accession #: NM_032044

Coding sequence: 182..658

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Seq ID NO: C38 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 52..3042

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35	CAAGTTGTGC	CCATCCCTGT	GGTGAAGAAG	AAGAAGTTGT	GAGGACAGCT	GCCGCCCGGT	3060
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Coding sequence: 322.1338

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 GATGTTGAAA CTATACCCAT GAAAAATATG GAAAAATGTA ATAAATGTTA TCATAAGAT 2520
 CATGTATATG GTATTACAAA TCCTGTTATG ACAAGCCCAT CACAACATTG A 2571

Seq ID NO: C41 DNA Sequence

Nucleic Acid Accession #: NM_033049
Coding sequence: 28..1566

5	1	11	21	31	41	51	
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	CTCCTTTCTG	TAAACACAGC	CACCAACCAA	GGCAACTCAG	CTGATGCTGT	AACAACCCACA	120
	GAAACTGCGA	CTAGTGGTCC	TACAGTAGCT	GCAGCTGATA	CCACTGAAAC	TAATTTCCCT	180
10	GAAACTGCTA	GCACCACAGC	AAATACACCT	TCTTTCCCAA	CAGCTACTTC	ACCTGCTCCC	240
	CCCATAACTA	GTACACATAG	TTCTCCACA	ATTCTACAC	CTGCTCCCC	CATAATTAGT	300
	ACACATAGTT	CCTCCACAAT	TCCTATACCT	ACTGCTGCAG	ACAGTAGAGT	AACCACAAAT	360
	GTAATTCAT	TAGCTACCTC	TGACATAATC	ACCGCTTCAT	CTCCAAATGA	TGGATTAAATC	420
	ACAATGGTTC	CTTCTGAAAC	ACAAAGTAAC	AATGAAATGT	CCCCACCAC	AGAAGACAAT	480
	CAATCATCAG	GGCCTCCAC	TGGCACCCT	TTATTGGAGA	CCAGCACCTC	AAACAGCACA	540
15	GGTCCACAG	AATCTGCCA	AGATGATCCC	TGTGCAGATA	ATTGCTTATG	TGTTAAGCTG	600
	CATAATACAA	GTTTGTGCT	GTGTTTAGAA	GGGTATTACT	ACAACCTCTC	TACATGTAAG	660
	AAAGGAAAGG	TATTCCTGG	GAAGATTTC	GTGACAGTAT	CAGAAACATT	TGACCCAGAA	720
	GAGAAACATT	CCATGGGCTA	TCAAGACTTG	CATAGTGAAA	TTACTAGCTT	GTTTAAAGAT	780
20	GTATTGGCA	CATCTGTTTA	TGGACAGACT	GTAAATCTTA	CTGTAGCAC	ATCTCTGTCA	840
	CCAAGATCTG	AAATGCGTGC	TGATGACAAG	TTTGTTAATG	TAACAATAGT	AACAATTTTG	900
	GCAGAAACCA	CAAGTGACAA	TGAGAAGACT	GTGACTGAGA	AAATTAATAA	AGCAATTAGA	960
	AGTAGCTCAA	GCACTTTCT	AAACTATGAT	TTGACCCCTC	GGTGTGATTA	TTATGGCTGT	1020
	AACGAGACTG	CGGATGACTG	CCTCAATGGT	TTAGCATGCG	ATTGCAAAATC	TGACCTGCAA	1080
25	AGGCTTAACC	CACAGAGCCC	TTTCTGCGTT	GCCTCCAGTC	TCAAGTGTCC	TGATGCGCTG	1140
	AACGCAAGC	ACAAGCAATG	CTTAATAAAG	AAGAGTGGTG	GGGCCCTGGA	GTGTGGGTGC	1200
	GTGCCCGGCT	ACCAGGAAGA	TGCTAATGGG	AACTGCCAAA	AGTGTGCATT	TGGCTACAGT	1260
	GGACTCGACT	GTAAAGGCAA	ATTTGAGCTG	ATCCTCACTA	TTGTGGGCAC	CATCGCTGGC	1320
	ATTGTCACTG	CGGATGACTG	AATTTGCATTG	ATTGTCACAG	CAAGATCAAA	TAACAAAACG	1380
30	AAGCATATTG	AAGAGAGAA	CTTGATGAC	GAAGACTTTC	AAAATCTAAA	ACTGCGGTGC	1440
	ACAGGCTTCA	CCAATCTTGG	AGCAGAAGGG	AGCGTCTTTC	CTAAGGTGAG	GATAACGGCC	1500
	TCCAGAGACA	GCCAGATGCA	AAATCCCTAT	TCAAGACACA	GCAGCATGCC	CCGCCCTGAC	1560
	TATTAGAAAT	ATAAGAATGT	GGAAACCGCC	ATGGCCCCCA	ACCAATGTAC	AAGCTATTAT	1620
	TAGAGTGTG	TAGAAAGACT	GATGGAGAAG	TGAGCACCAG	TAAAGATCTG	GCCTCGGGG	1680
35	TTTTCTTCC	ATCTGACATC	TGCCAGCCTC	TCTGAATGGA	AGTTGTGAAT	GTTTGCACAG	1740
	AATCCAGCTC	ACTTCTCTAA	TAAAGATCTA	TGACATTAAA	TGTAGTAGAT	GCTATTAGCG	1800
	CTTGTACAG	AGGTGGTTTT	CTTCAATCAG	TACAAAGTAG	TGAGACAATG	GTTAGGGTTG	1860
	TTTTCTTAAT	TCTTTTCTCT	GTAGGGCAAC	AAGAACCAAT	TCCAATCTAG	AGGAAAGCTC	1920
	CCCAGACTCG	CTTGCTCTCT	GGCAACACTT	GCTCTTGAGT	TAAGTGACCT	AATTCCTCTG	1980
40	GGAGACATAC	GCATCAACTG	TGGAGGTCCG	AGGGGATGAG	AAGGGATACC	CACCACCTTT	2040
	CAAGGTCAC	AAGCTCACTC	TCTGACAAAT	CAGAAATGGG	ACACTGCTTC	TATCCCTCCA	2100
	ATGGAGTGT	TCTGGCAACC	TTTGAACAGC	CCAGAGCTTG	CAACCTAGCC	TCACCAAGA	2160
	AGACTGGAAA	GAGACATATC	TCTCAGCTTT	TTGAGGAGGC	GTGCTGGGGA	ATCCAGGAAC	2220
	TTTTGTGTC	TAAATAGAAAG	GCCTGGACTA	AAAATGTCCA	CTATGGGGTG	CACCTCTACG	2280
45	TTTTTGAAAT	GCTAGGAGGC	AGAAGGGGCA	GAGAGTAAAA	AACATGACCT	GGTAGAAGGA	2340
	AGAGAGGCAA	AGGAACTTGG	GTGGGGAGGA	TCAATTAGAG	AGGAGGCACC	TGGGATCCAC	2400
	CTTCTTCTTT	AGGTCCCTCT	CTCCATCAGC	AAAGGAGCAC	TTCTCTAATC	ATGCCCTCCC	2460
	GAAGACTGGC	TGGGAGAAAG	TTTAAAAACA	AAAAATCCAG	GAGTAAGAGC	CTTAGGTTCAG	2520
	TTTGAATTG	GAGACAAACT	GTCTGGCAAA	GGGTGCGAGA	GGGAGCTTGT	GCTCAGGAGT	2580
50	CCAGCCGTCC	AGCCTCGGGG	TGTAGGTTC	TGAGGTGTGC	CATTGGGGCC	TCAGCCTTCT	2640
	CTGTGTGACG	AGGCTCAGCT	GTGGCCACCA	ACACACAACC	ACACACACAC	AACACACAC	2700
	ACAAATGGGG	GCAATCCACAT	CCAGTACRAAG	CTTTTACAAA	TGTTATTAGT	GTCTTTTCTT	2760
	ATTTCTAATG	CCTGTCTCTC	TTAAAGTTA	TTTATTATTG	TATTATTATT	TGTTCTTGAC	2820
	TGTTAATTGT	GAATGGTAAT	GCAATAAAGT	GCCTTTGTTA	GATGGTGAAA	AAAAAAAAAA	2880
55	AAAAAA						2887

Seq ID NO: C42 DNA Sequence
Nucleic Acid Accession #: NM_001432.1
Coding sequence: 167..676

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	TGACAGCGCG	TCTCCAGCCA	CTGCCGCGAG	CCCGTCTGCT	CCCGCCCTGC	CCGTGCACTC	120
	TCCGAGCGCG	CCCTCCGCCA	AGCCCCAGCG	CCCGCTCCCA	TGCGCGATGA	CCGCGGGGAG	180
65	GAGGATGGAG	ATGCTCTGTG	COGGCAGGGT	CCCTTGCGCTG	CTGCTCTGCC	TGGGTTTCCA	240
	TCTTCTACAG	GCAGTCCCTCA	GTACAACCTGT	GATTCCATCA	TGTATCCGAG	GAGAGTCCAG	300
	TGATAACTGC	ACAGCTTTAG	TTTACAGAGA	AGACAATCCA	CGTGTGGCTC	AAGTGTCAAT	360
	AACAAAGTGT	AGCTCTGACA	TGAATGGCTA	TTGTTTGCAT	GGACAGTGCA	TCTATCTGGT	420
	GGACATGAGT	CAAACTACT	GCAGGTGTGA	AGTGGGTTAT	ACTGGTGTCC	GATGTGAACA	480
70	CTTCTTTTAA	ACCGTCCACC	AACTTTAAG	CAAGAGTAT	GTGGCTTTGA	CCGTGATTCT	540
	TATTATTITG	TTTCTTATCA	CAGTCTGCTG	TTCCACATAT	TATTTCTGCA	GATGGTACAG	600
	AAATCGAAAA	AGTAAAGRAC	CAAGAGAGGA	ATATGAGAGA	GTACTCTCAG	GGGATCCAGA	660
	GTGCGCGCAA	GTCTGAATAT	GAGAGAGTTA	CCTCAGGGGA	TCCAGAGTTG	CCGCAAGTCT	720
	GAATGGCGCC	ATCAAACTTA	TGGGCAGGGA	TAAACAGTGT	CCTGGTTAAT	ATTAATATTC	780
75	CATTTTATTA	ATAATATTTA	TGTTGGGTCA	AGTGTAGGT	CAATAACACT	GTAATTTAAT	840
	GTACTTGAAA	AATGTTTTTA	TTTTTGTTTT	ATTTTGTGAC	GACTATTTGC	TAAATGTATA	900
	TGTGCGAGAA	ATATTTAATA	TCAAAAGAAA	ATTGATATTT	TTATACAAGT	AATTTCTGTA	960
	GCTAAATGCT	TCATTTGAAAG	CTTCAAGTT	TATATGCTCT	GTGCACAGTG	CTTAGAAGTA	1020
	AGCAATTGCC	AGGTCAATAG	TCAAGAAATG	TAGCAAAATG	ACAGATTCTT	GTAAGCCTAT	1080
80	ATATATAGTC	AAATCGATT	AGTAAGTAG	TTTTTTATGT	TCTTCAAATC	AGTGATAATT	1140
	GGTTTGACTG	TACCATGGTT	TGATATGTAG	TGGGCACCAT	GGTATCATAT	ATTAACACAA	1200
	TAAATGCAAT	AGAAATTTGG	AGAAGCAAAAT	ATAGGTCTCT	TGTTAAACAC	TACACATTTG	1260
	AAACAGCTTA	ACCTGGGGGA	GTCTATGGTC	TCTTCACTCA	GGTCTCAGCT	ATAATCTGT	1320
	TATATGAGGG	GCAGTGGACA	GTTCCTCTATG	CCAATCTACG	ACTCTACAG	GTACTAGTCA	1380

5	CTCATCTACC	AGATTCTGCC	TATGTAAAA	GAATTGAAAA	ACAATTTTCT	GTAATCTTTT	1440
	ATTTAAGTAG	TGGGCATTTC	ATAGCTTCAC	AATGTTCCCT	TTTTGTATAT	TACAACATTT	1500
	ATGTGAGGTA	ATTATTGCTC	AACAGACAAT	TAGAAAAAAG	TCCACACTTG	AAGCCTAAAT	1560
	TTGTGCTTTT	TAAGAAATATT	TTTAGACTAT	TTCTTTTAT	AGGGGCTTGG	CTGAATTCTA	1620
	ACATTAAATC	ACAGCCCAAA	ATTTGATGGA	CTAATTATTA	TTTTAAATA	TATGAAGACA	1680
	ATAATTCTAC	ATGTTGTCTT	AAGATGGAAA	TACAGTTATT	TCATCTTTTA	TTCAAGGAAG	1740
	TTTTAACTTT	AATACAGCTC	AGTAAATGGC	TTCTTCTAGA	ATGTAAAGTT	ATGTATTTAA	1800
	AGTTGTATCT	TGACACAGGA	AATGGGAAAA	AACCTAAAAA	TTAATATGGT	GTATTTTCC	1860
10	AAATGAAAAA	TCTCAATTGA	AAGCTTTTAA	AATGTAGAAA	CTTAAACACA	CCTTCCTGTG	1920
	GAGGCTGAGA	TGAAAAC TAG	GGCTCATTTT	CCTGACATTT	GTTTATTTTT	TGGAAGAGAC	1980
	AAAGATTTC	TCTGCATCT	GAGCCCATAG	GTCTCAGAGA	GTTAATAGGA	GTATTTTGG	2040
	GCTATTGCA	AAGGAGCCAC	TGCTGCCACC	ACTTTTGGAT	TTTATGGGAG	GCTCCTTCAT	2100
	CGAATGCTAA	ACCTTTGAGT	AGAGTCTCCC	TGGATCAGAT	ACCAGGTGAG	GGAGGATCTG	2160
15	TTCTTCTCT	ACGTTTATCC	TGGCATGTGC	TAGGGTAAAC	GAAGGCATAA	TAAGCCATGG	2220
	CTGACCTCTG	TGCCAGGACT	TGCTCCTCAT	TGTATCCATG	TGTATCCATG	CATTATATAC	2280
	CCTGGTGCAA	TCACACGACT	GTACTCTAAA	GTCTGCGCCC	TGGCCCTTAC	TATTAGGAAA	2340
	ATAAACAGAC	AAAAACAAGT	AAATATATAT	GGTCTTATAC	ATATTGTATA	TATATTCTA	2400
	TACAAACATG	TATGTATACA	TGACCTTAAT	GGATCATAGA	ATTGCAGTCA	TTTGGTGCTC	2460
20	TGCTAACCAT	TTATATAAAA	CTTAAAAACA	AGAGAAAAGA	AAAATCAATT	AGATCTAAAC	2520
	AGTTATTTC	GTTCCTTATT	TAATATAGCT	GAAGTCAAAA	TATGTAAAGA	CACATTTTAA	2580
	ATACTCTACT	TACAGTTGGC	CCTCTGTGGT	TAGTTCACCA	TCTGTGGATT	CAACCAACCA	2640
	AGGACGGAAA	ATGCTTAAAA	AATAATACAA	CAACAACAAA	AAATACATTA	TAACACTTAT	2700
	TTACTTTTTT	TTTTTCTTTT	TTGAGATGGA	GTCTCGCTCT	GTGCCCAGG	TTGGAGTGCA	2760
25	GTGGCAGCAT	CTCGGCTCAC	TGCAACCTCA	CCTCCCGGGT	TCAAGAGACT	CTCCTGCCTC	2820
	AGCCTCCTGA	GCAGCTGGGA	CTACAGGCGC	ATGCCACCAT	GCCACGCTAA	TTTTTGTATT	2880
	TTTAGTAGAG	CGCGGGTTTC	ACCATGTTGG	CCAGGATGGT	CTCAATCTCC	TAACCTTGAG	2940
	ATCCACCTCT	CACAGCTCC	CAAACTGCTG	GGATTACAGG	CGTAGGCCAC	CGCACGTAGC	3000
	ATTTACATTA	GGTATTACAA	GTAATGTAAA	GATGATTTAA	GTATACAGGA	GGATGTGAAT	3060
30	AGGTTATATG	CAAGCAGTAT	GCCCTTTTAT	ATAAGTGACT	TGAACATCTG	TGCCCGATT	3120
	TAGTATGTGC	AGGGGGGCGA	TCTGGGAATC	AGTCCCTGT	GGATACCAAG	GTACAACTGT	3180
	ATTTATTAAC	GCTTACTAGA	TGTGAGGAGA	GTCTGAATAT	TTTCAGTGAT	CTTGGCTGTT	3240
	TCAAAAAAT	CTATTGACTT	TTCAATAAAT	CAGCTGCAAT	CCATTTTATT	CATTTACAAA	3300
	AGATTTATTT	TAAGCCCTCT	AATCTTGGTT	TTTCAGTTGA	TCTTAAAGCAT	GTCAATTCAT	3360
35	AAAAACAAGT	CATTTTGTGA	TTTTTCTATC	TTAAGAAATG	TTAAAAAGC	TAATCCCTAA	3420
	AATAGTTAGA	TCTTTGTAAA	TGCATATTAA	ATAATAAAGT	ATGACCCACA	TTACTTTTAA	3480
	TGGGTGAAAA	TAAGACAAAA	ATAATAGTTT	TAGTGAGGAT	GGTGCTGAGT	AAACATAAAA	3540
	ACTGATTTTC	TCTCAGCTGA	TGTGTCTGT	ACACAGTGGG	AAGATTTTAG	TTTCACTTAA	3600
40	GTCTAACTCC	CCCATTTTAC	AGAATTTCTA	CTATATATAT	TTCTAGAAGG	GGCTATGCAT	3660
	ATTCAATGTA	TGAGAAACCA	AAGCAACACC	AAATGCATAA	ATGCATAATT	TATGGTCTTC	3720
	AACCAAGGCC	ACATAATAAC	CCAGTTAACT	TACTCTTTAA	CCAGGAATAT	TAAGTTCTAT	3780
	AACTAGTACT	CAAGGTTTAA	CCTTAAAAAT	AAGATTTCTT	TAACCTTAA	CTTAAAAATT	3840
	ATATTATATT	AAACATACAT	AATCAATAGT	AACTCCACTG	TTCTCTGAA	TATTTTGTGC	3900
45	TCTAATCTCT	CTGCCGAAAG	TCAAAGTGAT	GGGAGAAATT	GTATACTGGT	ATGACTACGT	3960
	CTTAAGTCAG	ATTTTATTTT	ATGAGTCTTT	GAGACTAAAT	TCAATCACC	CCAGGTATCA	4020
	AATCAACTTT	TATGCAGCAA	ATATATGATT	CTAGTGTCTG	ACTTTTGTGA	AAITCAGTAA	4080
	TGCAGTTTTT	AAAAACCTGT	ATCTGACCCA	CITTTGTAAT	TTTGCTCCAA	TATCCATTCT	4140
	GTAGACTTTT	GAATAAAAG	TTTTTAATTT	GATGCCCAAT	ATATTCTGAC	CGTTAAAAAA	4200
50	TTCTTGTCT	TATGGGAGAA	GGGGGAGTAA	TGACTTGATC	AAACAGTATT	TCTGGTGTAT	4260
	ATTTTAATGT	TTTTAAAAAG	AGTAATTTCA	TTTAAATATC	TGTTATTCAA	ATTGTATGAT	4320
	GTAAATGTA	ATATAATGTA	TTTTCTTTTT	ATTTTGCATC	CTGTAATTGC	ACTTTTAAAG	4380
	TTTGAAGAGC	CATTTTGTGA	AACGGTTTTT	ATTAAGATG	CTATGGAAAC	TAAAGTTGTA	4440
	TTGCATGCAA	TTTAAAGTAA	CTTATTGTAC	TATGAATATT	ATCGGATTAC	TGAATTGTAT	4500
	CAATTTGTTT	GTGTTCAATA	TCAGCTTTGA	TAATGTGTGA	CCTTAAGATA	TTGAAGGAGA	4560
55	AAATAGATAA	TTTACAGAT	ATTATTAATT	TTTATTATT	TTTCTTGGGA	ATTGAAAAAA	4620
	ATTGAAATAA	ATAAAAAATG	ATTGAACATC	TTGCATTCAA	AATCTTCACT	GAC	4673

Seq ID NO: C43 DNA Sequence
Nucleic Acid Accession #: AF011468.1
Coding sequence: 257..1468

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	CAAGTCCCCT	GTCCGTTTCT	CCGTCCCTGA	GTGTCTTGG	CGTGCCTTGG	TGCCCGCCCA	180
	GCGCCTTTGC	ATCCGCTCCT	GGGCACCGAG	GCGCCCTGTA	GGATCTGCT	TGTTACTTAT	240
	TACAGCTAGA	GGCATCATGC	ACCGATCTAA	AGAAAACTGC	ATTTTCAGGAC	CTGTTAAGGC	300
70	TACAGCTCCA	GTTGGAGGTC	CAAAAAGTGT	TCTCGTGACT	CAGCAAAATC	CTTGTGAGAA	360
	TCCATTACCT	GTAAATAGTG	GCCAGGCTCA	GCGGGTCTTG	TGTCCTTCAA	ATTCTTCCCA	420
	GCGGTTTCT	TGCGAAGCAC	AAAAGCTTGT	CTCCAGTCAC	AAGCGGTTCT	AGAATCAGAA	480
	GCAGAAGCAA	TTGCAGGCAA	CCAGTGTACC	TCTCTCTGTC	TCCAGGCCAC	TGAATAACAC	540
	CCAAAAGAGC	AAGCAGCCCC	TGCCATCGGC	ACCTGAAAT	AATCCTGAGG	AGGAACCTGC	600
75	ATCAAAACAG	AAAAATGAAG	AATCAAAAAA	GAGGCAGTGG	GCTTTGGAAG	ACTTTGAAAT	660
	TGGTCCGCTT	CTGGGTAAAG	GAAAGTTTGG	TAATGTTTAT	TTGGCAAGAG	AAAAGCAAAG	720
	CAAGTTTATT	TGGCTCTTTA	AAGTGTATT	TAAAGCTCAG	CTGGAGAAAG	CCGAGTGGGA	780
	GCATCAGCTC	AGAAGAGAA	TAGAAATACA	GTCCACCTT	CGGCATCTTA	ATATTCTTAG	840
	ACTGTATGGT	TATTTCCATG	ATGCTACCAG	AGTCTACCTA	ATTCTGGAAT	ATGCACCACT	900
80	TGGAACAGCT	TATGAGAAAC	TTCAAGAACT	TTCAAGTTT	GATGAGCAGA	GAACCTGCTAC	960
	TTATATAACA	GAATTTGGCA	ATGCCCTGTC	TTACTGTCT	TGGAAGAGAG	TTATTCTATG	1020
	AGACATTAA	CCAGAGAACT	TACTTCTTGG	ATCAGCTGGA	GAGCTTAAAA	TTGCAGATTT	1080
	TGGGTGGTCA	GTACATGCTC	CATCTTCCAG	GAGGACCACT	CTCTGTGGCA	CCCTGGACTA	1140
	CTGCCCCCT	GAAATGATTG	AAGGTCCGAT	GCATGATGAG	AAGGTGGATC	TCTGGAGCCT	1200
	TGGAGTTCTT	TGCTATGAAT	TTTTAGTTGG	GAAAGCTCCT	TTTGAGGCCA	ACACATACCA	1260

	AGAGACCTAC	AAAAGAATAT	CACGGGTGGA	ATTCACATTC	CCTGACTTTG	TAACAGAGGG	1320
	AGCCAGGGAC	CTCATTTCAA	GACTGTTGAA	GCATAATCCC	AGCCAGAGGC	CAATGCTCAG	1380
	AGAAGTACTT	GAACCCCCCT	GGATCACAGC	AAATTCATCA	AAACCATCAA	ATTGCCAAAA	1440
5	CAAGAATCA	GCTAGCAAAC	AGTCTTAGGA	ATCGTGACGG	GGGAGAAATC	CTTGAGCCAG	1500
	GGTGCCATA	TAACCTGACA	GGAACATGCT	ACTGAAGTTT	ATTTTACCAT	TGACTGCTGC	1560
	CCTCAATCTA	GAACGCTACA	CAAGAAATAT	TTGTTTTACT	CAGCAGGTGT	GCCTTAACCT	1620
	CCCTATTTCAG	AAAGCTCCAC	ATCAATAAAC	ATGACACTCT	GAAGTGAAAG	TAGCCACGAG	1680
	AATTGTGCTA	CTTATACTGG	TTCATAATCT	GGAGGCAAGG	TTCGACTGCA	GCCGCCCCGT	1740
10	CAGCCTGTGC	TAGGCATGGT	GTCTTCACAG	GAGGCAAAATC	CAGAGCCTGG	CTGTGGGGAA	1800
	AGTGACCACT	ATGCCCTGAC	CCCGATCAGT	TAAGGAGCTG	TGCAATAAACC	TTCCTAGTAC	1860
	CTGAGTGAGT	GTGTAACTTA	TTGGGTGGCG	GAAGCCTGGT	AAAGCTGTGT	GAATGAGTAT	1920
	GTGATTCTTT	TTAGGTATGA	AAATAAAGAT	ATATGTACAG	ACTTGTATTT	TTTCTCTGGT	1980
	GGCATTCCCT	TAGGAATGCT	GTGTGTCTGT	COGGCACCCC	GGTAGGCCCTG	ATTGGGTTC	2040
15	TAGTCTCCT	TAACCACTTA	TCTCCCATAT	GAGAGTGGA	AAAATAGGAA	CACGTGCTCT	2100
	ACCTCCATT	AGGGATTTCG	TTGGGATACA	GAAGAGGCCA	TGTGTCTCAG	AGCTGTTAAG	2160
	GGCTTATTTT	TTTAAACAT	TGGAGTCATA	GCATGTGTGT	AAACTTTAAA	TATGCARAATA	2220
	AATAAGTATC	TATGTCTAAA	AAAAAAAAAA	AAA			2253

Seq ID NO: C44 DNA Sequence
Nucleic Acid Accession #: NM_013372
Coding sequence: 63..617

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	AA	CC	GC	GC	GC	GC	780
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40	CC	AT	GC	GC	GC	GC	900
	CT	CA	GC	GC	GC	GC	960
	GG	GC	GC	GC	GC	GC	1020
	GA	CT	GC	GC	GC	GC	1080
	CT	TT	GC	GC	GC	GC	1140
45	AT	CT	GC	GC	GC	GC	1200
	TT	TT	GC	GC	GC	GC	1260
	TG	GA	GC	GC	GC	GC	1320
	GA	CA	GC	GC	GC	GC	1380
	TT	TT	GC	GC	GC	GC	1440
50	AT	TA	GC	GC	GC	GC	1500
	AC	CA	GC	GC	GC	GC	1560
	CC	CA	GC	GC	GC	GC	1620
	AA	AC	GC	GC	GC	GC	1680
	TC	CA	GC	GC	GC	GC	1740
55	GC	CT	GC	GC	GC	GC	1800
	TT	TT	GC	GC	GC	GC	1860
	RA	GA	GC	GC	GC	GC	1920
	GG	GT	GC	GC	GC	GC	1980
	AG	GA	GC	GC	GC	GC	2040
60	CT	AC	GC	GC	GC	GC	2100
	TC	TA	GC	GC	GC	GC	2160
	AG	GG	GC	GC	GC	GC	2220
	TT	TT	GC	GC	GC	GC	2280
	AG	TC	GC	GC	GC	GC	2340
65	TC	GC	GC	GC	GC	GC	2400
	TC	CA	GC	GC	GC	GC	2460
	AC	CA	GC	GC	GC	GC	2520
	CT	AG	GC	GC	GC	GC	2580
	CC	AA	GC	GC	GC	GC	2640
70	AC	CA	GC	GC	GC	GC	2700
	AT	GA	GC	GC	GC	GC	2760
	TT	GT	GC	GC	GC	GC	2820
	AG	CA	GC	GC	GC	GC	2880
	CA	AG	GC	GC	GC	GC	2940
75	TA	AA	GC	GC	GC	GC	3000
	GA	CT	GC	GC	GC	GC	3060
	TT	TT	GC	GC	GC	GC	3120
	TT	AT	GC	GC	GC	GC	3180
	TG	AA	GC	GC	GC	GC	3240
80	GT	CT	GC	GC	GC	GC	3300
	TG	GA	GC	GC	GC	GC	3360
	AT	TT	GC	GC	GC	GC	3420
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	TA	AG	GC	GC	GC	GC	3540
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Seq ID NO: C45 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 200..2932

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1 11 21 31 41 51
| | | | |
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Seq ID NO: C46 DNA Sequence
Nucleic Acid Accession #: NM_000584.1
Coding sequence: 75..374

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5 CAAAAACAA CAAATRAATT TTAATATATA GGATTTTCT AGATATTGCA CGGGAGAATA 660
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Seq ID NO: C47 DNA Sequence

Nucleic Acid Accession #: NM_005603.1

Coding sequence: 1..3756

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Seq ID NO: C48 DNA Sequence
 Nucleic Acid Accession #: XM_044533
 Coding sequence: 238..2751

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Seq ID NO: C49 DNA Sequence
 Nucleic Acid Accession #: NM_007019.1
 Coding sequence: 41..580

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Seq ID NO: C50 DNA Sequence
Nucleic Acid Accession #: NM_014584.1
Coding sequence: 227..1633

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GTTCTAAGCT TCTCAACTA GCGTTTATG TAATAATATG TAATAATAAT AAAACTATGG 1980
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TTGTATTTTA TCTGGCAATC CTAAAATACA TTGGTATGAA ACAAATCACT TTAGAAGTA 2280
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TTAAAATTTT TTTTAGAGAC AAGGTTTTCG TGTGTTGCCC AAGCTGGAAC TTGAACGACT 2880
GGGCTGAAGT GATCTTCCCA CCTCAGCCTC CCAAGTAGCT GGGATACAG GTGTCTGCCA 2940
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AAAACTGTGC CCTCTTTACA TATGCTTAT CAGGTATAAC ATGTTGAAAT GTCACATTAG 3180
TAGTAAAGTG GGGTTTATTT ATATAGTGTG TAAGAAATGT CAGTTTACAC TGCTGTATAC 3240
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ATATTGTTG GATGAAAAA AAAAAAAA AAAA

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Seq ID NO: C51 DNA Sequence
Nucleic Acid Accession #: NM_002888.1
Coding sequence: 37..723

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CTGTTGCTCG CCCCGGTGGC GGGGCGCGCG GGGTCCGGGG GCCCGGACGA CCTCGGGCAG 180
CCTCAGGATG CTGGGGTCCC GCGCAGGCTC CTGCAGCAGA AGCGCGCGGC GCGCTTCAC 240
TTCTTCAACT TCGGGTCCGG CTGCGCCAGC GCGCTGCGAG TGCTGGCCGA GGTGCAGGAG 300
GGCGCGCGGT GGATTAATCC AAAAGAGGGA TGTAAAGTTC ACCTGGTCTT CAGCACAGAG 360
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CAGGTGTGAC ACTACTACTT GGCACAGCTC ACTAGTGTGA GGCAGTGGGT AAGAAAAACC 720
TGAAAAATTA CTGTGCCAC AAGAGTTACA ATCAAAGTGG TCTCCTTAGA CTGAATTCT 780
GTGAACCTCT AATTTCATAT CAAGAGTTGT AATCACAATT ATTTCAATAA ATATGTGAGT 840
TCCTGC 846

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Seq ID NO: C52 DNA Sequence
Nucleic Acid Accession #: NM_005409.3
Coding sequence: 94..378

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TGTCTTTGCA TAGGCCCTGG GGTAAAAACA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
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GAAAGAAAGA ATTTTAAAA ATATCAAAAC ATATGAAGTC CTGGAAAAGG GCATCTGAAA 420
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GGTTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTGTATT ATACATTCTAT 720
GCATTTCTAG GCTAGAGAAC CTCTAGATT TGATGCTTAC AACTATTCTG TTGTACTAT 780
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CATCTATGTC TCGTAAAGCA TTCTCAAAAC ATTTTTCAT GCAAAACAC ACITCTTTCC 960
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Seq ID NO: C53 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..609

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CACAGCCTGG CCAAGATCGA GCGCAGCCTG GCCAGCAGCC TTTTCCCTCC GGACCACTGC 240
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TCCCAACGCG GGGCAATAT TTTGCTCCAG GCTGAGGGGA TCTGCGAGC CCACCGAGCC 360
GTGCTGGAAA TGAAGGTGAA CCACAAGGCG TATAATTATA CTTTTTCCCA TCTGTGTGTG 420
TTGAGAAATC AGGATAAGAA ATGOGTGCTG GATGATATTA TTTCACTGCT AGAGGATCTC 480
AGGCAGGCTG CCGTCTCCAA TAAGACAACA GCCAGGGTGC AAGTGAGGTA TCCCAACACT 540
AAATTAAAGG TATGCTCCTT CTGCATGCTT CTGCCAATTA AAGAGGCAGC ACTTCATTTT 600
TTGCCCTAA 609

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Seq ID NO: C54 DNA Sequence
Nucleic Acid Accession #: NM_002438.1
Coding sequence: 104..4474

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GCCCTCCTGT CCATCAGGAG AAGGAAAGGA TAAACCTCG GCCATGAGGC TACCCCTGCT 120
CCTGTGTTTT GCCTCTGTCA TCCGCGGTGC TGTTCTCTTA CTGACACCA GGCAATTTTT 180
AATCTATAAT GAAGATACCA AGCGCTGCGT GGATGCAAGT AGTCCCAAGT CCGTCCAAAC 240
CGCAGCTTGC AACCAAGGAT CCGAATCACA GAAATTCGA TGGGTGTCG AATCTCAGAT 300
TATGAGTGTG GCATTTAAAT TATGCCCTGG AGTGCCATCA AAAACAGACT GGGTTGCTAT 360
CACTCTCTAT GCCTGTGACT CAAAAAGTGA ATTTAGAAA TGGGAGTGCA AAAATGACAC 420
ACTTTTGGGG ATCAAGGAG AAGATTATTT TTTTAACAC GGCAACAGAC AAGAAAAGAA 480
TATTATGCTC TACAAGGAT CGGTTTATG GAGCAGGTGG AAGATCTATG GAACCAAGA 540
CAATCTGTGC TCAGAGGTT ATGAAGCCAT GTATACGCTA CTAGGCAATG CCAATGGAGC 600
AACCTGTGCA TTCCCGTTCA AGTTTGAAGA CAAAGTGGTAC GCAGATTGCA CGAGTGCTGG 660
GCGGTGCGAT GAGTGGCTCT GGTGCGGAAC CACTACTGAC TATGACACAG ACAAGCTATT 720

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5	TGGATATTGT	CCATTGAAAT	TTGAGGGCAG	TGAAAGCTTA	TGGAATAAAG	ACCCGCTGAC	780
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	CTGCCAACAA	CAGAACGCTG	AGCTCTCTGAG	CATCACAGAG	ATACATGAGC	AAACATACCT	900
	GACAGGATTA	ACCCAGTTCT	TGACCTCAGG	ACTCTGGATT	GGACTTAACA	GTCTGAGCTT	960
	CAACAGCGGT	TGGCAGTGG	GTGACCCGAG	TCCTTTCCGA	TATTTGAACT	GGTTACCAGG	1020
	AAGTCCATCA	GCTGAACCTG	GAAAAAGCTG	TGTGTCACTA	AATCCTGGAA	AAAAATGCTAA	1080
	ATGGGAAAAAT	CTGGAATGTG	TTCAGAAACT	GGGCTATATT	TGCAAAAAGG	GCAACACCAC	1140
	TTTAAATCTCT	TTTGTATTTC	CCTCAGAAAG	TGATGTGCCT	ACTCACTGTC	CTAGTCAGTG	1200
10	GTGGCCGTAT	GCCGCTCACT	GTTACAAGAT	TCACAGAGAT	GAGAAAAAAA	TCCAGAGGGA	1260
	TGCTCTGACC	ACCTGCAGGA	AGGAAGGCGG	TGACCTCACA	AGTATCCACA	CCATCGAGGA	1320
	ATTGGACTTT	ATTATCTCCC	AGCTAGGATA	TGAGCCAAAT	GACGAATTGT	GGATCGGCTT	1380
	AAATGACATT	AAGATTCAAA	TGTACTTTGA	GTGGAGTGAT	GGGACCCCTG	TAAAGTTTAC	1440
	CAAAATGGCTT	CGTGAGAAAC	CAAGCCATGA	AAACAACAGA	CAGGAGGATT	GTGTGGTGAT	1500
15	GAAAGGCAAG	GATGGTACT	GGGCAGATCG	GGGCTGTGAG	TGGCCTCTTG	GCTACATCTG	1560
	CAAGATGAAA	TCACGAAGCC	AAGGTCCAGA	AATAGTGGAA	GTGCAAAAAG	GCTGCAGGAA	1620
	AGGCTGGAAA	AAACATCACT	TTTACTGCTA	TATGATTGGA	CATACGCTTT	CAACATTGTC	1680
	AGAAGCAAAAC	CAAGACTGTA	ATAATGAGAA	TGCTTATTTA	ACAACTATTG	AAGACAGATA	1740
	TGAACAGGCC	TTCTGAGCTA	GTTTCGTGGG	CTTAAGGCCCT	GAAAAATATT	TCTGGACAGG	1800
20	ACTTTCAGAT	ATACAAACCA	AAGGGACTTT	TCAGTGGACC	ATCGAGGAAG	AGGTTTCGGTT	1860
	CACCCACTGG	AATTTCAGATA	TGCCAGGGCG	AAAGCCAGGG	TGTGTTCCCA	TGAGAACCOG	1920
	GATTGCAAGG	GGCTTATGGG	ATGTTTGAAG	ATGTGATGAA	AAGGCAAAAT	TTGTGTGCAA	1980
	GCACGTGGGA	GAAGGAGTAA	CCCAACCACC	GAAGCCACG	ACGACTCCCG	AACCCAAATG	2040
	TCGGGAGGAT	TGGGCGGCCA	GCAGTAGAAC	AAGCTTGTGT	TTCAAGCTGT	ATGCAAAAAG	2100
25	AAAAACATGAG	AAGAAAAAGT	GGTTTGAATC	TCGAGATTTT	TGTCGAGCTC	TGGGTGGAGA	2160
	CTTAGCTAGC	ATCAATAACA	AAGAGGAACA	GCAAAACAATA	TGGCGATTAA	TAAACAGTAG	2220
	TGGAAGCTAC	CACAAACTGT	TTTGGTTGGG	ATTGACATAT	GGAAAGCCCTT	CAGAAGGTTT	2280
	TACTTGAAGT	GATGGTCTCT	CTGTTTCATA	TGAAAACTGG	GCTTATGGAG	AACCTAATAA	2340
	TTATCAAAAT	GTGAAATACT	GTGGTGAGCT	GAAAGGTGAC	CCTACTATGT	CTTGGAAATGA	2400
30	TATTAATTTGT	GAACACCTTA	ACAACTGGAT	TTGCCAGATA	CAAAAAGGAC	AAACACCCAA	2460
	ACCTGAGTAC	ACACCAAGCTC	CTCAAGACAA	TCCACCAAGT	ACTGAAGATG	GGTGGGTTAT	2520
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	GTTTTCGAAG	AGGAATTTTG	GTGATCTTGT	TTCTATTCAA	AGTGAAGAGT	AAAAGAAAGT	2640
	TCTATGGAAA	TATGTAAACA	GAAATGATGC	ACAGTCTGCA	TATTTTATTG	GTTTATTGAT	2700
35	CAGCTTGGAT	AAAAAGTTTG	CTTGGATGGA	TGGAAGCAAA	GTGGATTACG	TGCTCTGGGC	2760
	CACAGGATGA	CAAGAACTTTG	CAAAATGAAGA	TGAAAACTGT	GTGACCATGT	ATTCAAAATC	2820
	AGGGTTTGGG	AATGACATTA	ACTGTGGCTA	TCCAAACGCC	TTCAATTTGCC	AGCGACATAA	2880
	CAGTAGTATC	AATGCTACCA	CAGTTATGCC	TACCATGCCC	TCGGTCCCCT	CAGGGTGCAA	2940
	GGAAGGTTGG	AATTTCTACA	GCAACAAGTG	TTTCAAAATC	TTTGGATTTA	TGGAAGAAGA	3000
40	AAGAAAAAAT	TGGCAGAGGG	CAGGAAAAGC	TTGTATAGGC	TTTGGAGGGA	ATCTGGTCTC	3060
	CATACAAAGT	GAAACAGAGC	AAGCAATTCT	TACCTATCAC	ATGAAGGACT	CCACTTTCAG	3120
	TGCTTGGACT	GGGCTGAATG	ATGTCAATTG	AGAACACACG	TTCTTTTGGG	CGGATGGACG	3180
	AGGAGTCCAT	TACACAAACT	GGGGGAAAGG	TTACCTTGGT	GGGAAGAGAA	GCAGTCTTTC	3240
	TTATGAAGAT	GCTGACTGTG	TTGTTATTAT	TGGAGGTGCA	TCAAAATGAAG	CAGGAAAATG	3300
45	GATGTGATGAT	ACCTCGGACA	GTAACAGGAG	CTACATATGC	CAGACACGAT	CCGACCCCTC	3360
	CTTGACTAAT	CCTCCAGCAA	CGATTCAAAC	AGATGGCTTT	GTTAAATATG	GCAAAAGCAG	3420
	CTATTCACTC	ATGAGACAAA	AATTTCAATG	GCATGAAGCG	GAGACATACT	GCAAGCTTCA	3480
	CAATTCCTCT	ATAGCCAGCA	TTCTGGATCC	CTACAGTAAT	GCATTGTGGT	GGCTGCAGAT	3540
	GGAAACATCT	AATGAACGTT	TGTGGATCGC	CCTGAACAGT	AACCTTGACTG	ATAATCAATA	3600
50	CACCTGGACT	GATAAGTGGG	GGGTGAGGTA	CACCTAAGTG	GCTGCTGATG	AGCCCAAATT	3660
	GAAATCAGCA	TGTGTTTATC	TGGATCTTGA	TGGCTACTGG	AAGACAGCAC	ATTGCAATGA	3720
	AAGTTTTTAC	TTTCTCTGTA	AAAGATCAGA	TGAAATCCCT	GCTACTGAAC	CCCCACAATC	3780
	GCCTGGCAGA	TGCCCGGAGT	CAGATCACAC	AGCATGGATT	CCTTTCCATG	GTCACTGTTA	3840
	CTATATTAGT	TCTCATATTA	CAAGAAACTG	GGGCCAAGCT	TCTCTGGAAT	GTCTTCGAAT	3900
55	GGGTTCCTCT	CTGGTTTCCA	TTGAAAGTGC	TGCAGAAATC	AGTTTCTCTG	CATATCGGGT	3960
	TGAGCCACTT	AAAAGTAAAA	CCAATTTTGT	GATAGGATTG	TTCAAGAAATG	TTGAAGGGAC	4020
	GTGGCTGTGG	ATAAATAACA	GTCCGGTCTC	CTTTGTCAAC	TGGAACACAG	GAGATCCCTC	4080
	TGGTGAACGG	AATGATTGTG	TAGCTTTACA	TGCGTCTTCT	GGGTTTGGGA	GTAATATTCA	4140
	CTGTCTCTCC	TACAAAGGAT	ATATTGTGAA	AAGACCAAAA	ATTATTGATG	CTAAACCTAC	4200
60	TCATGAATTA	CTTCAACCAA	AAGCTGACAC	AAGGAAGATG	GACCCCTCTA	AACCGTCTTC	4260
	CAACGTGGCC	GGAGTAGTCA	TCATTGTGAT	CCTCCTGATT	TTAACGGGTG	CTGGCCTTGC	4320
	CGCCTATTTC	TTTTATAAGA	AAAGACGTGT	GCACCTACCT	CAAGAGGGCG	CCTTTGAAAA	4380
	CACTCTGTAT	TTTAAACAGT	AGTCAAGCCC	AGGAACATAGT	GATATGAAG	ATCTCGTGGG	4440
	CAATATTGAA	CAGAATGAAC	ACTCGGTCA	CTAGTACCTC	AATGCGATTG	TGAGATATTT	4500
65	GAATTTTATA	AAATTGTAA	TGAAATTTAA	AATTTTATG	TCAATGTGAT	TGTTTCTTTT	4560
	AAATGAGTA	CTGAATTGTA	CTGGTCTGTC	CTTTTCTCT	TTGCCTAATT	GAAGAAATAA	4620
	TTGCTTGTTT	TCTAGCTGGG	CAAGATATTT	TCATAAAAGA	GGGATAACAA	TGCTGATTAC	4680
	TACCTTTTAA	AATATTTTAG	ATRAATGCAC	AGCACCACAG	CACCACATCT	AAGCAATTAG	4740
	GATGGGTAGC	TGATGTCAGC	TTTCAATGGA	TTTAAAGCAC	TCTAGAAACA	ATGAAGCTTC	4800
70	TTGSCATATT	TTAAGGAGCT	CCCAAAATGT	GTTACCTATT	AAATTGTAAC	TCAGCAAGTA	4860
	GAAGACCAT	TGAAAAGTCA	GGTACAAAT	TCCTCAAGTG	GCAATAAAAT	GTAGTCAGTT	4920
	TTCTCTTTTC	CCGCTTTTAA	TTTCCACTCC	AATTATTTAG	AACCTTATTT	GTACATGTGC	4980
	AGAAGAATAA	GGCAGCTGAG	AATCTGTGTT	CCCCCAAGAG	AGTTTACAG	GCTGAGTGTT	5040
	GCAAAATGTT	TCITTTGCTT	GTTATATGTA	TATCAGGAAT	ACAAGGATGT	GAATAAATAC	5100
75	TGTAATTTTG	CATAACTGGA	TGTACTTAGA	TAATGTGAAA	TAAACATTAA	AGACAAAGTC	5160
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Seq ID NO: CS5 DNA Sequence
Nucleic Acid Accession #: NM_024574.2
Coding sequence: 424..2130

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5	CGCTGCCCGG	GGATTCCCCA	GCCCCGCGCG	GCTCCCTACT	CCACTTGGCA	GCAACTTGGG	180
	CGACCGCGCG	CGCCCCGCCC	TGCCCCGCGT	TTGAAGTTTG	CTGTGCGGAC	CGCAAAGTTG	240
	GGACACTTCA	GGCGATTGAA	TTTTTCTCTT	TTATCTGCGT	CGTCCCCGCG	CCTCCAGGCT	300
	TCTCGTTCCCT	GGATATTGGT	GCTTAGCATC	TTGGCAGGGT	CGGGGAAGT	GGACTATTTC	360
	GCACACCACA	CCACGGGGAG	GGATTTTTTT	CTATTTTCCC	TACGAAAAAC	AGATCTTTTT	420
	AAGGATGGTG	CTGCTCCACT	GGTGCCCTGT	GTGGCTCCTG	TTTCCACTCA	GCTCAAGGAC	480
	CCAGAAGTTA	CCCACCGGGG	ATGAGGAAC	TTTTCAGATG	CAGATCOGGG	ACAAAGGCATT	540
	TTTTCATGAT	TGGTCAGTAA	TTCCAGATGG	AGCTGAAATT	AGCAGTTATC	TCTTTAGAGA	600
10	TACACCTAAA	AGGTATTCTT	TTGTGGTTGA	AGAAGACAAT	ACTCCATTAT	CAGTCACAGT	660
	GACGCGCTGT	GATGCGCCTT	TGGAGTGGAA	GCTGAGCCTC	CAGGAGCTGC	CAGAGGACAG	720
	GAGCGGGGAA	GGCTCAGGTG	ATCTGGAACC	TCTTGAGCAG	CAGAAGCAGC	AGATCATTAA	780
	TGAGGAAGGC	ACTGAGTTAT	TCTCCTACAA	AGGCAATGAT	GTTGAGTATT	TTATATGCTC	840
	TAGTTCCCCA	TCCGGTTTAT	ATCAGTTGGA	TCTTCTTTCA	ACAGAGAAAG	ACACACATTT	900
15	CAAAGTATAT	GCCACCACAA	CTCCAGAAATC	TGATCAGCCA	TACCCTGAGT	TACCCTATGA	960
	CCCAAGAGTA	GATGTGACCT	CACCTGGGCG	CACCACGGTC	ACTTTGGCCT	GGAAACCAAG	1020
	CCCCACTGCC	TCTTTGCTGA	AAACAACCAT	TCAGTACTGT	GTGGTCATCA	ACAAAGAGCA	1080
	CAATTTCAAA	AGTCTCTGTG	CAGTGGAAAG	AAAACTGAGT	GCAGATGATG	CTTTTATGAT	1140
	GGCACCGAAA	CCTGGTCTGG	ACTTCAGCCC	CTTTGACTTT	GCCACTTTTG	GAITTCCTTC	1200
20	TGATAATTCA	GGTAAGAAC	GCAGTTTCCA	GGCAAGCCT	TCTCCAAAAC	TGGGGCGTCA	1260
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	CACCGTCTCT	GATCTGAAAC	CCGACACGCA	GTACTACTTT	GACGTATTTG	TGGTCAACAT	1380
	CAACAGCAAC	ATGAGCAACG	CTTATGTAGG	TACCTTTGCC	AGGACCAAGG	AAGAAGCCAA	1440
	ACAGAAGACA	GTGAGCTCA	AAGATGGGAA	GATAACAGAT	GTATTTGTGA	AAAGGAAGGG	1500
25	AGCAAAGTTT	CTACGGTTTG	CTCCAGTCTC	TTCTCACCAG	AAAGTCACCT	TCTTTATTCA	1560
	CTCTGTGCTG	GATGCTGTCC	AAATCCAAGT	GAGAAGAGAT	GGGAAACTTC	TTCTGTCTCA	1620
	GAATGTGGAA	GGCATTCAGC	AGTTTCAGCT	TAGAGGAAAA	CCTAAAGCTA	AATACCTCGT	1680
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30	CCGTACCTGT	TCCTCGGCCA	CGGTGGCTTG	GCTAGGCAC	CAGGAAAGGA	ACAAGTTTTG	1860
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	CCAATGTCTA	GGACACAGTA	TAAGGAAGAA	GTCAAGAAAG	GTCTCTGTA	AATATTTC	1980
	CAGTCAAAAC	CTGCAGAAAG	CAGTGACCAC	AGAAACAATT	AAAGTCTTTC	AGCTGGCCAA	2040
	ATCTTACCTG	CTGGATGTTT	ATGTCATAGG	ACATGGGGGG	CACCTCTGTA	AGTATCAGAG	2100
35	TAAGGTGTGT	AAAACTAGAA	AGTTCTGTGA	GTTACCTTCT	TATAGAGATA	TATTATGTAG	2160
	AACTCCAGGA	GGGACATTAA	ATCACTTTAA	GTATAAATCT	ACTACTCCCA	CAGTTGAGAG	2220
	AAGTTGTGAC	CTGTACTTGT	ACTATGGAAG	GAAGGATATC	AACGTGTGTA	TATTGATGTT	2280
	TATATAAGTA	ACTCTTGAAG	GAGACTTGTT	CTAGCGTGCC	CCATGGTACC	TAGTGTGTGT	2340
	CTGATGCCGG	TTGGTGTCAA	AGATAGAGGG	CTTCTTGAA	GAACCTGCCA	TTCTTGCTT	2400
40	TGACCACCTG	ATGAACTGCT	TCTAAATTAT	TTTATTACCT	AAAAATTAA	AAATATGCCAT	2460
	TCATTGCACA	CACCCACAAA	TGCAAAATCAT	TCCTCTCTAT	AGATGCTAGG	ATATATATAA	2520
	ATTATTTTAT	AAATCTCTGT	TTTAAATGTC	AGTGTCTCTA	TGATTGTAAA	CTATTAAATT	2580
	CTTTTCTTAT	TAAAGTACAG	ATCTAATCTA	AGTATTATTA	AGTTGATAGC	CCTCTAGTCA	2640
	GTTATATTGC	TATTGTAAAT	TCTTGTTTGT	TGAGTAAAT	GTTTAAATAC	TATATGTATC	2700
45	TCATGTACAA	AGTTGACATA	CATTATATTC	ATGTACATAA	AATTAAGAG	ATTAGATTAT	2760
	ATACTGTATA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAA		2808

Seq ID NO: C56 DNA Sequence

Nucleic Acid Accession #: BC034229.1

Coding sequence: 373..1422

50	1	11	21	31	41	51	
	ATCCGGCGGT	GGTGACGCGA	GAGGCTGGGG	TCTCCAGGAC	CAACTCCTCT	TCATCTTCGT	60
55	CTTCTCAGC	CTGCTCAATG	TGAAGCCCTT	GATCATGATT	CACCTCCACT	TAATAAATAA	120
	AGTGTTTACA	AATCAGAATA	ACTTTTAGAC	AATATTAAGG	TGGTAATCAT	GAACAGAAAA	180
	GATTTGTAGT	TTCTTCCATG	GGGAAAACCT	GGAAATCTG	TAAAGCTAAA	ATATAGCAAT	240
	GTAATAATTA	AAACAAAAGT	CTAAGATTG	AAGAGATAAT	TTGCTTCAGG	ATTTTGTATG	300
60	AAGGCAATG	CTAACTTTAA	AAACCAGATT	TCCGAGAAAT	ACAAAAGMAA	TAGAAATGCT	360
	CAAGAACTGC	GAATGGAGAA	AGTACAGTTA	GAGTTTGAGA	ACCAAGAGAT	GGAGAAGAAA	420
	CTGCAAGAA	TCCGATCCAC	AAGAAACRAA	GAAAAGGAAG	ATAGAGAGTC	AAGCGAGTAT	480
	TACTGGAAAT	CTGGAAAAGT	GGGCAAAATG	GTCAATCAAT	CATATATGAT	GTCACAAAAT	540
	AAAGGAAATG	TTGTTAAGTT	TTCTGCTGGA	AAAGTGAAAT	TAAAATTGCT	GAAGGAACAG	600
65	ATTCAAGAGC	CAGTGAAACC	AACAGTTAAT	TATAAAATGG	CAAATCTCTT	AGAATGTGAA	660
	AAACCCAAGA	TAAATGGGAA	AGTTTGTGGA	CAGTGTGAGA	ACAAAGCTGC	TCTACTGGTA	720
	TGCTTGAAT	GTGGAGAAGA	TTATTGTTCA	GGATGCTTTG	CTAATGTTCA	CCAGAAAGGG	780
	GCACTAAAGC	TCCACAGAAC	AACTCTTTTG	CAGGCAAGAT	CTCAATATT	ATTCAATGTA	840
	TTGGATGTTG	CCCATCAGTT	TATAAAGGAT	GTTAATCCAG	ATGAACCCAA	AGAGGAGNAAT	900
70	AATTCTACAA	AGGAAACCCAG	TAAAATTCAA	CATAAACCCA	AATCTGTACT	TCTCCAGAGG	960
	AGCAGCTCTG	AGGTAGAAAT	TACAACGATG	AAAAGAGCAC	AACGTACAAA	ACCAAGAAAG	1020
	AGTCTGTTGT	GTGAAGGGTC	ATTGATGAA	GAAGCTTCTG	CACAGTCTCT	TCAGGAAGTG	1080
	TTAAGTCAAT	GGAGAACCGG	AAATCATGAT	GACAACAAGA	AACAGAAATT	ACATGCAGCA	1140
	GTAAAAGACT	CATTGGAAGA	ATGCGAAGTA	CAGACTAATC	TGAAAATTTG	GAGAGAACCA	1200
75	CTTAATATTG	AACTTAAAGA	AGACATTCTA	TCCTATATGG	AAAAATTATG	GCTTAAAAAA	1260
	CACAGGAGAA	CTCCACAAGA	GCAACTTTTT	AAATGCTACC	AGATACGTTT	CCACATCCAC	1320
	ATGAAACCA	TGGTGATGCA	CAGTGTCTC	AAAATGAAAA	CGATGAAGAT	AGTGATGGTG	1380
	AGGAGACCAA	AGTACACAC	ACAGCTCTTT	TATTGCCAGT	AGAAACATTA	AACATAGAGA	1440
	GACCTGAACC	ATCTCTGAAG	ATAGTGAAC	TGGATGATAC	TTATGAAGAG	GAATTTGAAG	1500
80	AAGCAGAAAA	TATTGTGCTT	TACAAAGTTA	AATTAGCTGA	TGCAGACAGT	CAAGAAAGTT	1560
	GTGCTTTTCA	TGATTGTGAG	AAGAATAGCT	TTCCATATGA	AAATGGCATC	CATCAACATC	1620
	ATGTTTTTGA	TAAAGGAAAG	AGAGACTTCT	TAAATCTTTG	TCTGAGAAAC	AGCTCTACTT	1680
	ATTATAAAGA	TAATTCAAAA	GGAGAACTTT	CAACACAGA	TTTTGACAAC	ATCGTGGATC	1740
	CTGATGTGTA	TTCTTCTGAC	ATTGAAAAAA	TTGAGGAAAG	CACCTCTCTT	GAAGAAATTT	1800
	TAAAGGAGAA	AAATATAGST	TTAGAAAGTA	ATCAAAAGTC	TGATGATTCC	TGTGTATCAC	1860

5 TTGAAAGCAA GGACACTTTG CTAGGTAGAG ATTTAGAAAA AGCTCCCAT T GAGGAGAAAT 1920
 TATCTCAAGA CATCAAGAGAA TCCTTGGAAAT TGAGCAATCT GTATAAGAGG CCAAGCTTTG 1980
 AAGAATCAAA AACTACAAAG TCATCACTGT TGTACAAGA AATAGCCTGC AGAAGTAAGC 2040
 CTATAACAAA ACAATATCAA GGACTTGAGA GATTCTTTAT TTTTGATACA AATGAAAGAC 2100
 TCAACTTACT TCCTTCTCAT CGTTTAGAAT GCAACAATTC CAGTACTAGG ATTACACTTG 2160
 CAGGTCAGAA ATCAGAGAGA CCTTCAACAG CAAATTTTCC ACTTTCCAC TCTGTTAAAG 2220
 AAAGCTCCAG TTGCCTTTCA TCCTCTCATC CTGATCAAG AAGTGCAGCT GCTCAATCAT 2280
 CATCTAGAGC TGCTTCTGAA ATTTAGAAA TTGAATATAT TGATATTACT GACCAGAATG 2340
 10 AGCTTTCTCT AGATGACACT ACTGATCAAC ATACTTTAGA CAATTTGGAA AAAGAATTAC 2400
 AAGTGCTGAG ATCTCTTGCA GATACTTCAG AAAAGCTTTA CAGCTTAACC TCAGAAGAGT 2460
 TCCAGATTTC CAGCAGCCAA TCACTGAATA TAAGTCAGAT TTCCACAGAT TTCCTTAAGA 2520
 CCTCACATGT GAGGGGTCCC TGTGGAGTTG AGGAATTGAG CTGTTCTGGA AGAGATACCA 2580
 AAATTGAGTC TTGCTGTGCA CTTTCTGAGA GCAGTACAGA TGAGGAGGAG GAAGATTTTC 2640
 TCAACAAGCA ACATGTCATC ACACCTACCG GTTCAAAGAG TACTTAAAGA TTATTTGTTT 2700
 15 ATTACTGTTT CCATTTTGTA CCCAGAGTAA AGCAAAACAC TGAGAAAAGT AACCAAGTGA 2760
 TTACCTATCC AAGTGTGGA GATTTTGATT ACTAATGTCT TTGATGTTTC AAGGCTACAA 2820
 ACTAATAAAA GTAAAATTAT AAGTTCAAAA AAATTTTATA AAAAAAAAT AAAAAA 2876

20 Seq ID NO: C57 DNA Sequence
 Nucleic Acid Accession #: NM_024687.1
 Coding sequence: 138..1706

25 1 11 21 31 41 51
 AAAAAACATGA TGACAACAAG AAACAGAAAT TACATGCAGC AGTAAAAGAC TCATTGGAAG 60
 AATGCGAAGT ACAGACTAAT CTGAAAATTT GGAGAGAACC ACTTAATATT GAACCTTAAAG 120
 AAGACATTTT ATCCTATATG GAAAAATTTT GGCTTAAAAA ACACAGGAGA ACTCCACAAG 180
 30 AGCAACTTTT TAAATATGCTA TCAGATACGT TCCACATCC ACATGAAACC ACTGGTGATG 240
 CACAGTGTTC TCAAAATGAA AACGATGAAG ATAGTGATGG TGAGGAGACC AAGTACAAC 300
 ACACAGCTCT TTTATTGCCA GTAGAAACAT TAAACATAGA GAGACCTGAA CCATCTCTGA 360
 AGATAGTCGA ACTGGATGAT ACTTATGAAG AGGAATTTGA AGAAGCAGAA AATATTGTGC 420
 CTTACAAAGT TAAATTAGCT GATGCAGACA GTCAACGAAG TTGTGCTTTT CATGATTGTC 480
 AGAAGATAG CTTTCCATAT GAAAATGGCA TCCATCAACA TCATGTTTTC GATAAGGGAA 540
 35 AGAGAGACTT CTTAAATCTT TGTCTGAGAA ACAGCTCTAC TTATTATAAA GATAATTCAA 600
 AAGGAGAAAC TTCAACACA GATTTTGACA ACATCGTGGA TCCTGATGTG TATTCTCTG 660
 ACATTGAAAA AATTGAGGAA AGCACCTCCT TTGAAAGAAA TTTAAAGGAG AAAAAATAG 720
 GTTTAGAAAG TAATCAAAAG TCTGATGATT CCTGTGTATC ACTTGAAAGC AAGGACACTT 780
 40 TGCTAGGTAG AGATTTAGAA AAAGCTCCCA TTGAGGAGAA ATTATCTCAA GACATCAAAG 840
 AATCCTTGGA ATTGAGCAAT CTGTATAAGA GGCCAAGCTT TGAAGAATCA AAAACTACAA 900
 AGTCATCACT GTTGTACAA GAAATAGCCT GCAGAAGTAA GCCTATAACA AAACAATATC 960
 AAGGACTTGA GAGATTCTTT ATTTTGATA CAAATGAAAG ACTCAACTTA CTCTCTCTC 1020
 ATCGTTTGA ATGCAACAAT TCCAGTACTA GGATTACACT TGCAGAGAC AGAGAATGGA 1080
 45 TTCCAGACCA TAGCTTAAGT GAATATGCTG ATAATGCAAT TGTCTTGGGT GTTCTGCAGG 1140
 GTGCTCAGAG TCCATCATCA AGTAGAAAAC AGCAAAAGAT GGGTCAGAAA TCACAGAGAC 1200
 CTTCAACAGC AAATTTTCCA CTTTCCAAC CTGTTAAAGA AAGCTCCAGT TGCCCTTCAT 1260
 CCTCTCATCC TCGATCAGAA AGTGCAGCTG CTCATCATC ATCTAGAGCT GCTTCTGAAA 1320
 TTTCAAGAA TGAATATATT GATATTACTG ACCAGAATGA GCCTTCCCTA GATGACACTA 1380
 50 CTGATCAACA TACTTTAGAC AATTTGGAAG AAGAATTACA AGTGCTGAGA TCTCTTGAG 1440
 ATACTTCAGA AAAGCTTTAC AGCTTAACCT CAGAAGAGTT CCCGATTTC AGCAGCCAAAT 1500
 CACTGAATAT AAGTCAGATT TCCACAGATT TCCTTAAGAC CTCACATGTG AGGGGTCCCT 1560
 GTGGAGTTGA GGAATTGAGC TGTTCTGGA GAGATACCAA AATTCAGTCT TTGCTGTGAC 1620
 TTTCTGAGAG CAGTACAGAT GAGGAGGAGG AAGATTTTCT CAACAAGCAA CATGTCATCA 1680
 55 CACTACGCTG GTCAAAGAGT ACTTAAAGAT TATTTGTGTA TTACTGTTTC CATTTGTGAC 1740
 CCAGAGTAAA GCAACAACCT GAGAAAAGTA ACCAAGTGAT TACCTATCCA AGTGCTGGAG 1800
 ATTTTGATTA CTAATGTCTT TGATGTTTCA AGGCTACAAA CTAATAAAG TAAATTTATA 1860
 AGTTCAAAAA AAAAAAATA AAAA 1884

60 Seq ID NO: C58 DNA Sequence
 Nucleic Acid Accession #: NM_005408.1
 Coding sequence: 76..372

65 1 11 21 31 41 51
 AAAAGGCCGG CGGAACAGCC AGAGGAGCAG AGAGGCCAAG AAACATGTGT AAATCTCCAA 60
 CTCTTAACCT TCAACATGAA AGTCTCTGCA GTGCTTCTGT GCCTGCTGCT CATGACAGCA 120
 GCTTTCAACC CCCAGGAGCT TGCTCAGCCA GATGCACTCA ACGTCCCATC TACTTGCTGC 180
 70 TTCACTTTA GCAGTAAGAA GATCTCCTTG CAGAGGCTGA AGAGCTATGT GATCACCACC 240
 AGCAGGTGTC CCCAGAAGGC TGTCTCTCTC AGAACCAAAC TGGGCAAGGA GATCTGTGCT 300
 GACCCAAAGG AGAAGTGGGT CCAGAATTAT ATGAAACACC TGGGCGGAAA AGCTCACACC 360
 CTGAAGACTT GAATCTGCTC ACCCTACTG AAATCAAGCT GGAGTACGTG AAATGACTTT 420
 TCCATCTCCC TCTGGCTCTC TCTTCTATGC TTTGGAATAC TTCTACCATA ATTTTCAAAT 480
 AGGATGCATT CGGTTTGTG ATTCAAAATG TACTATGTGT TAAGTAATAT TGGCTATTAT 540
 75 TTGACTTGTG GCTGGTTTGG AGTTTATTTG AGTATTGCTG ATCTTTTCTA AAGCAAGGCC 600
 TTGAGCAAGT AGGTGTGCTG CTCTAAGCCC CCTTCCCTTC CACTATGAGC TGCTGGCAGT 660
 GGGTTGTAT TGGTTTCCCA GGGGTTGAGA GCATGCCTGT GGGAGTCATG GACATGAAGG 720
 GATGCTGCAA TGTAGGAAGG AGAGCTCTTT GTGAATGTGA GGTGTTGCTA AATATGTTAT 780
 80 TGTGGAAAGA TGAATGCAAT AGTAGGACTG CTGACATTTT GCAGAAAATA CATTTTATTT 840
 AAAATCTCCA AAAAAAATA

Seq ID NO: C59 DNA Sequence
 Nucleic Acid Accession #: AK097746.1
 Coding sequence: 185..2224

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1      11      21      31      41      51
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      CTTTCATGAC AGTAACAAAT CCAAGATTTT GGAAAAGGCG CTACGATATT TAAATGACCA 60
      CTTTCACATAC AACTTATATG GTAATATATG CCGATCAGTA TTTGAGAAGG ACAAGCTGTT 120
      ATTTTCCTTT TTATTATGTG CCAATCTTCT TCTGGCAAGG AAAGAGATTG AATACCAGGA 180
      ACTGATGTTT CTTTAACTG GAGGAGTAAG TCTTAAAGT GCTGAGAAAA ATCCTGATCC 240
      AACTTGGCTA CAGGACAAAA GCTGGGAGGA AATCTGTGCG GCAAGTGAAT TTCCTGCCTT 300
      CAGAGGACTC AGGCAACATT TTTGTGAACA TATATATGAA TGGCGAGAAA TCTATGACAG 360
10     TAAAGAGCCA CATAATGCTA AATTTCCAGC ACCAATGGAT AAGAACCTAA ATGAATACA 420
      GAAAATAATA ATTCTTCGGT GTTTAAGACC TGATAAGATA ACCCCAGCTA TAACAAACTA 480
      TGTAACTGAC AAAC TAGGGA AAAAGTTTGT AGAGCCTCCA CCATTGATT TGACAAAGAG 540
      TTACTTGGAT TCAAAATTGCA CCATTCCCTT AATTTTGTGTT CTATCTCCAG GAGCAGATCC 600
      TATGGCCAGC CTGCTGAAAT TTGCAAAATGA TAAATCTATG TCTGGAAATA AGTTTCAAGC 660
15     TATTTCACTG GGACAGGGAC AAGGACCGAT TGCAGCAAAA ATGATTAAAG CAGCAATTGA 720
      AGAAGGAACCT TGGGTGTGCC TACAGAATTG CCATCTTGCA GTGTCTCGGA TGCCCATGTT 780
      GGAAAAAATA TTGGAAGATT TTACCTCTGA AACCTGTAAC TCATCCTTTA GGCTTTGGCT 840
      GACAAGCTAT CCATCTTCAA AATTCOCAGT AACAACTCTA CAGAATGGAG TAAAAATGAC 900
      TAATGAACCT CCCACGGGTC TTCCGCTGAA TCTCCTTCAA TCATATCTCA CTGATCCAGT 960
20     TTCTGATCCT GAGTTTTCAT AGGGATGCGG TGGAAAGGAA CTGTTATTTA TCAATGAATA 1020
      TGATACAAAT CCATTGGAAG CTATATCTTA CCTGACTGGG GAGTGTAAAT ATGGAGGAAG 1080
      AGTGACAGAC GATTGGGACA GACGTCTTCT ATTAACCATG CTGGCTGACT TTTATAATCT 1140
      GTACATAGTT GAAAACCCCTC ATTATAAGTT TTCTCCAGT GGAACCTATT TTGCACTCC 1200
25     TAAAGGCAC TATGAGGACT ACATTGAATT CATTAAAGAA CTTCCTTTA CTCAACACCC 1260
      TGAGATATTT GGATTACATG AAAACGTTGA CATCTCCAAG GATCTTCAAC AAACAAAAAC 1320
      CCTCTTTGAG TCCTTGTCTC TCAACCCAGG AGGCTCCAAA CAGACAGGAG CCTCAGGAAG 1380
      TACTGATCAG ATTCTGTTAG AAATTACCAA AGATATCCTC AACACGCTCC CTAGTGATTT 1440
      CGACATTGAA ATGGCACTAC GGAAGTATCC TGTGAGATAT GAAGAAAGCA TGAATACTGT 1500
      GTTAGTACAA GAAATGGAAA GATTTAACAA TTTAATTATA ACTATAAGTA AACTCTACG 1560
30     GGACCTTGAA AAGCTTATTA AGGGTGTGGT TGTGATGGAT TCTGCATTGG AGGCATCTCT 1620
      CAGTAGCTTA CTGTGTGGA AGGTTCCAGA AATATGGGCC AAACGTTTAT ACCCAAGCCT 1680
      TAAGCCCTCG GGAAGTTACA TCACAGATT TCTAGCCCGG TTGAAGTTT TACAGCACTG 1740
      GTATAATTCA GGAACACCTT GTGTGTTTGG GCTGTCAAGT TTCTTTTTC CACGAGCCTT 1800
      TTTAACTGGA GCTATGCGA ATATATGCCAG AAAATATACC ACCCCTATTG ATTTGCTAGG 1860
35     ATATGAATTT AATAAGTATC CATCTGATAC ATCTGACACA TCACCAGAA AGTGTGTTTA 1920
      TATCCACGGA CTGTATCTCG ATGGCGCAGC CTGGGACCGA GAAAGTGGAT TGCTTGTCTGA 1980
      ACAATATCCC AAACCTTCTGT TTGACCTGAT GCCCATCATA TGGATAAAAC CAACTCAAAA 2040
      ATCTCGGATT TAAAGTCCG ATGCCCTATGT CTGTCCCTC TACAAGACAA GTGAACGTAA 2100
      AGGAACCTCT TCCACTACGG GACATCTTAC TAACTTTGTC ATTGCAATGT TGTTAAAAAC 2160
40     AGACCAACCT ACTCGGCACT GGATCAAGCG CGGGGTGCT TTGCTTTGTC AGTTGGATGA 2220
      CTAATTTGGA CAAATTTATA AAACATCCAA AAGTTT 2256

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Seq ID NO: C60 DNA Sequence
Nucleic Acid Accession #: J02761.1
Coding sequence: 14..1159

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1      11      21      31      41      51
50     |      |      |      |      |
      GAATTCGGGT GCCATGGCTG AGTCACACCT GCTGCACTGG CTGCTGCTGC TGCTGCCAC 60
      GCTCTGTGGC CCAGGCACTG CTGCCCTGGAC CACCTCATCC TTGGCCTGTG CCCAGGGGCC 120
      TGAGTTCCTG TGCCAAAGCC TGGAGCAAGC ATTGCACTGC AGAGCCCTAG GGCATTGCC 180
      ACAGGAAGTC TGGGACATCG TGGGAGCCGA TGACCTATGC CAAGAGTGTG AGGACATGTT 240
      CCACATCCTT AACAAAGATG CCAAGGAGGC CATTTTCCAG GACACGATGA GGAAGTTCT 300
      GGAGCAGGAG TGCAAGCTCC TCCCTTGAA GCTGCTCATG CCCAGTGCA ACCAAGTGCT 360
55     TGACGACTAC TTCCCTCTGG TCATCGACTA CTTCAGAAC CAGACTGACT CAAACGGCAT 420
      CTGTATGCAC TTGGGCTGTG GCAAAATCCG GCAGCCAGAG CCAGAGCAGG AGCCAGGGAT 480
      GTCAGACCCC CTGCCCAAAC CTCTGCGGGA CCCTCTGCCA GACCTCTGCT TGGACAAGCT 540
      CGTCTCCTCT GTGCTGCGCG GGGCCCTCCA GGGGAGGCTT GGGCTCACA CACAGGATCT 600
      CTCGAGCAGC CAATTCCCCA TTCTCTGCC CTATTGCTGG CTCTGACGG CTCTGATCAA 660
60     GCGGATCCAA GCCATGATTC CCAAGGGTGC GCTAGCTGTG GCAGTGGCCC AGGTGTGCG 720
      CGTGGTACCT CTGGTGCGCG GCGGCATCTG CCAGTGCTCG GCTGAGCGCT ACTCCGTCAT 780
      CCTGCTCGAC ACGCTGCTGG GCGGCATGCT GCCCAGCTG GTCTGCGGCC TCCTCCTCG 840
      GTGCTCCATG GATGACAGCG CTGGCCCAAG GTGCGCGACA GGAGAATGGC TGCCGCGAGA 900
      CTCTGAGTGC CACCTCTGCA TGTCCGTGAC CACCCAGGCC GGGAACAGCA GCGAGCAGGC 960
65     CATACCACAG GCAATGCTCC AGGCCTGTGT TGGCTCTGCG CTGACAGGG AAAAGTGCAA 1020
      GCAATTTGTG GAGCAGCACA OGCCCCAGCT GCTGACCTCG GTGCCAGGG GCTGGGATGC 1080
      CCACACACCT TGCCAGGCC TCGGGGTGTG TGGGAACATG TCCAGCCCTC TCCAGTGTAT 1140
      CCACAGCCCC GACCTTTGAT GAGAACTCAG CTGTCCAGCT GCAAGGAAA AGCCAAGTGA 1200
      GAGGGCTCTT GGGACCATGG TGACCAAGCT CTTCCTCTGC TCCCTGGCCC TCGCCAGCTG 1260
70     CCAGGCTGAA AAGAAGCCTC AGCTCCACCA CCGCCCTCCT CACCTCCCTT CCTCGGCAGT 1320
      CACTCCACTT ATGAAAGGCG GGGCCCCCAG CCCTGTGTG CGCTTGTCTG TCTCAGCTCA 1380
      ACCACAGTCT GACACAGAG CCCACTTCCA TCCTCTCTGG TGTGAGGCAC AGCGAGGGCA 1440
      GCATCTGGAG GAGCTCTGCA GCCTCCACAC CTACCAAGAC CTCCAGGGC TGGGCTCAGG 1500
75     AAAAAACGAG CACTGCTTTA CAGGACAGGG GGTGAAGCT GAGCCCGGCC TCACACCCAC 1560
      CCCCATGCA CAAAGATTG GATTTTACAG CTACTTGCAA TTCAAAATTC AGAAGATAA 1620
      AAAAAAGGAA CATACAGAAC TCTAAAGAT AGACATCAGA AATTGTTAAG TTAAGCTTTT 1680
      TCAAAAAATC AGCAATTCCC CAGGTAGTC AAGGTGAGC ACTGCAGCT CTGGCATGAT 1740
      GGGATGGCGA CCGGGCAAGC TTTCTTCTC GAGATGCTCT GCTGCTTGAG AGCTATTGCT 1800
80     TTGTTAAGAT ATAAAAAGG GTTTCTTTT GTCTTCTGT AAGGTGGACT TCCAGATTTT 1860
      GATTGAAAGT CCTAGGGTGA TTCTATTCT GCTGTGATTT ATCTGCTGAA AGCTCAGCTG 1920
      GGGTGTGCA AGCTAGGGAC CCATTCTGT GTAATACAAT GTCTGCACCA ATGCTAATAA 1980
      AGTCTATCTC TCTTTTAAAA AAAAAAAGG AAAAAAACG GAATTC 2026

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Seq ID NO: C61 DNA Sequence

Nucleic Acid Accession #: NM_139172.1
Coding sequence: 19..552

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5      1      11      21      31      41      51
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GGGCTCTGGG GAGGTGACAT GTTGGGCTGT GGGATCCCAG CGCTGGGCTT GCTCCTGCTG 60
CTGCAGGGCT CGGCAGACGG AAATGGAATC CAGGGATTCT TCTACCCATG GAGCTGTGAG 120
GGTGACATAT GGGACCGGGA GAGCTGTGGG GGCCAGGCGG CCATCGATAG CCCCAACCTC 180
TGCTGCGTCT TCGGTGCTG CTACCGCAAT GGGGTCTGCT ACCACCAGCG TCCAGACGAA 240
10    AACGTGCGGA GGAAGCACAT GTGGGCGCTG GTCTGSAAGT GCAGGCGCTT CCTCTCTCTG 300
AGCTGCAGCA TCTGCTTGTG CTGGTGGGCC AAGCGCCGGG ACGTGTCTGA TATGCCCGGT 360
TTCTTGGCGG GTCCGTGTGA CATGTCCAAG TCCGTCTCGC TGCTCTCCAA GCACCGAGGG 420
ACCAAGAAGA CGCCGTCCAC GGGCAGCGTG CCAGTCCGCC TGTCCAAGA GTCCAGGGAT 480
GTGGAGGGAG GCACCGAGGG GGAAGGGAGG GAGGAGGGTG AGGAGACAGA GGGCGAGGAA 540
15    GAGGAGGATT AGGGGAGTCC CCGGGGGACT GCTCAATACA GATACGGTGG ACG 593

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Seq ID NO: C62 DNA Sequence
Nucleic Acid Accession #: NM_054023.2
Coding sequence: 98..379

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20      1      11      21      31      41      51
|      |      |      |      |      |
GGGGACACTT TGTATGGCAA GTGGAACCCAG TGGCTTGGTG GATTTTGCTA GATTTTCTG 60
ATTTTAAAC TCCTGAAAAA TATCCAGAT AACTGTCAAT AAGCTGGTAA CTATCTTCTT 120
GCTGGTGACC ATCAGCCTTT GTAGTTACTC TGCTACTGCC TTCTCATCA ACAAGTGGC 180
CCTTCTCTGT GACAAGTTGG CACCTTTACC TCTGGACAAC ATTCTTCCCT TTATGGATCC 240
ATTAAGCTTT TCTTGAAAAA CTCTGGGCAT TTCTGTGAG CACCTTGTGG AGGGGCTAAG 300
GAAGTGTGTA AATGAGCTGG GACCAGAGGC TTCTGAAGCT GTGAAGAAAC TGCTGGAGGC 360
GCTATCACAC TTGGTGTGAC ATCAAGATAA AGAGCGGAGG TGGATGGGGA TGAAGATGA 420
TGCTCCTATC TCCTCTGCCT GAAACCTGTT CTACCAATTA TAGATCAAAAT GCCCTAAAAA 480
GTAGTGACCC GTGAAAAGGA CAAATAAAGC AATGAATACT AAAAAAATAA AAAAAAATAA 540
AAAAAATAA 550

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Seq ID NO: C63 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..2874

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35      1      11      21      31      41      51
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ATGCCCTCTG CCTATGCCTA TAAAAACGCT GAGACCCTAG CAGGCAGACA CACAAGCAGC 60
TGGATGTCGA GAGGAGCATA TCAGCGGAGG AACACACGGG CAGCTGGAGC TCCAGAGGAA 120
TGCACTGACA GAAACTGGCA TGCTGGCAGA ACACGTGGAA TTTGGCTGGG GCAGTTGGAG 180
GAGAGATGTT GAGATGTGTT CGGAGTTTCT TTCTTCTGTT GGGTTCTGGT TCTCGCTGGC 240
TCAGGAGCGA AGCTCGAGAC CTTCACGCCA GCCCAGGAAG GGGCTCCCACT AGTGCAGCGG 300
CAGGCTGAAG CGCTCTCAAA GTGCCGCCAG AGTGGGCGTC CAGGCAGAGG AGGCGCCGAG 360
AGCGAGCGAG CGAGGGATGC CAGCATGCTG TCACCTCTCA GTGCTGCCAT GCGAAACTAC 420
CCAAAGTCTT CTACCATCCC TCCAAGAAGA TCCTACTCTC CAACGAAAT TGCTCACAAG 480
AGTTACTCCT GCAGCCTTCC AGACATGAAA ATCTCCATGG CAGAATCTGG CCCCTCCTTG 540
GATAGCCTTG ACATTCTGGA GGATGGCGAG TCTGGGTAC CATTCTTGT GACTCATTTG 600
TACTTTCTGG GGGTGTCTAC CACTGGGATG GAACAAC TAGTATTGAA AGGACCAAA 660
ATATTGTGAT TGCAGATTTA TGTGAAGGAT GAGGTGGTGG TCACAGACCT GCAAGTCTCT 720
ACTGTCCAGG TAACAGATGT GAACGAGCCA CCTCAGTTTC AAGGCAACTT GGCAGAAGAT 780
CATCTCCGTT CAGACCCAGC ACATTTCAAT GCTCATAGTC ACACGTACGT GAGGGTAGTG 840
GCTACTGCTG TGGCCAGGCA CAGGCTTAGA TCTAGCAATT GTTCCCTCTT CCTGGGCACC 900
TTCTGTGTTG TGGTGGGCAT GCAGTATTTT CTGATTTCTC CCCCAAGAG CTTCAGAATG 960
TCTGCTAATG GCACCTCTT CTCCACAACA GAATTGGACT TTGAAGCAGG ACACAGAAGT 1020
TTCCATCTCA TCGTGGAGGT GAGGGACAGT GGAGGCCCTA AAGCCTCCAC AGAGCTCCAG 1080
GTGAACATCG TGAACCTCAA CGACGAAATC CCTCGCTTTA CCAGCCCGAC ACGAGTGTAC 1140
ACAGTCTCTG AGGAACTGAG TCCAGGAACC ATCGTGGCCA ATATCACAGC GGAGGATCCT 1200
GATGATGAAG GTTTTCCAG CCACCTCCTC TACAGCATTA CCACTGTTAG CAAATATTTC 1260
ATGATAAATC AGTTGACTGG TACAATCCAA GTGGCCCAA GATAGACCG AGATGCAGGT 1320
GAATTGAGAC AAAATCCAC CATTTCCCTG GAAGTCTTAG TGAAGGACAG ACCATATGGG 1380
GGTCAGGAGA ATCGCATCCA GATAACCTTC ATTGTGGAAG ACGTCAACGA CAATCCTGCC 1440
ACATGCCAAA AGTTACCTT CAGATCCAGT CTCACCCCTG CTCTGTGCTC CAAGAAGCTG 1500
ACCTGGATGG ATACCGTATT AGACTGTTT CATGCTGCTG ATAAAGATAT ACCTGTGACT 1560
GGGCGATTTA CAAAAGAAAG AGGTTTAATT GGACTTACAG TTCCACATGG CTGGGGAAGC 1620
CTCACAAATCA TGGCAGAAGG CAAGGAGGAG CAAGTCAAT CTTACATGGA TGGCAGCAGG 1680
CAAGAGATA GAGCTTGTGT AGGGAAACTC CTCCTTATAA AGCCATCAGA TCTCATGAGA 1740
CTTAGTCACT ATCACGAGAA CAACTCAGGA AAGACTTGCC CCCATGATTC CATTTCTCTC 1800
TACCAGGTCC CTCOCACAA ATGTAGGAAT TCAAGAAATC AGGCCACCAA CAACGAAGAC 1860
ACAAGCTCTG TCACTGTTAC TGTGAATC CTGAAGAAA ATGATGAAAA GCCAATTGTG 1920
ACTCCAACCT CTATTCTCTT GGCCTCCCA GTGGATCTGA AAGTTGGCAC AAATATTTCAG 1980
AATTTCAAGC TGACATGTAC CGAOCCTGAT TCCAGCCCA GATCTTTCCG TTATTCCATT 2040
GGCCAGGTA ACGTCAACAA TCATTTCACC TTCTCTCCCA ATGCTGGTTC CAATGTACA 2100
CGCTGCTGCG TTACTCTCG CTTTGACTAT GCTGGTGGGT TTGATAAGAT CTGGGACTAC 2160
AAGCTACTTG TCTACGTAA TCATGACAAC TGATGTCTG ACAGGAAGAA AGCGGAGGCT 2220
CTTGTGTAGA CAGGAACAGT GACTCTGAGT ATTAAGATCA TTCCCAACCC AACCACTATC 2280
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CTGTGTATCC TGGTGTCTCT ATTGGCCAAA GCCATCCACA GACTCTGCC CTGCAAGACT 2460
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GAGCAAGCTT CACTCGAGCT CTATGCCCTG CTGCCAGCT GCTGCGACCC TAGTCCAGTA 2640
ACCTTAAGAA AGGTCCAGGT GTGTGGGAG AGTGAAGAGA CCGTTCAGTG TTCCGGCCAC 2700

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ATCACACTTC CCGGCAAGAT TCCAGTGGAT GACCCAAGGA AACAGGAAAC AGGCCTGCAG 2760
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5

Seq ID NO: C64 DNA Sequence
 Nucleic Acid Accession #: XM_168571.1
 Coding sequence: 155..988

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 15 GGTGAATTGA GACAAAATCC CACCAATTCC CTGGAAGTTC TAGTGAAGGA CAGACCATAT 240
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 GCCACATGCC AAAAGTTCAC CTTCAGCATT ATGGTGCCGG AAAGAACAGC CAAGGGGACG 360
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 40 AAGTCACTC AAATCTTCTT CAAAAGAAGC AGAACAGTGA AAAAAACAGA TGAGTAAGTT 1800
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 GGTGTCOOGA TCAGCATCTC GCATGTGAGA TTCATCCACG TTGTCTGTCT TAGCAGTAGT 1920
 TCAGTTCTCT TCATGGTTAT GTCTGGTTTC ATTCTATGAT TATATCACAA TTTATCTATT 1980
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 45 ACTACAGAAAT GTGCTGATG GCTCATGCCT GTAATGCCAG CACTTTGGCA AGGTGGGCAG 2100
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 TAAAAAATAC AAAAATTAGC TTGGTGTGGT GGTGGGCACA TGTAATCCCA GCTACTTGGG 2220
 AGGCTGAGGT AGGGAAGACT GCTTAAACCT GAGAGGTGGA GGTTACAGTG AGTTGAGATT 2280
 50 GTGCCACTGC ACTCTAGCCT GGGTGACAAA GCAAGACTCC ATCTCAGAAA AAAAAAATAA 2340
 AAGTGAATTA CAACACT 2357

Seq ID NO: C65 DNA Sequence
 Nucleic Acid Accession #: NM_005266.3
 Coding sequence: 122..1198

55

1 11 21 31 41 51
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 60 GATGGGCGAT TGGAGCTTCC TGGGAAATTT CTTGGAGGAA GTACACAAGC ACTGACCGT 180
 GGTAGGCAAG GTCTGGCTCA CTGTCTCTTT CATATTCCGT ATGCTCGTGC TGGGCACAGC 240
 TGCTGAGTCT TCCTGGGGGG ATGAGCAGGC TGATTTCCGG TGTGATACGA TTCAGCCTGG 300
 CTGCCAGAAAT GTCTGCTACG ACCAGGCTTT CCCCATCTCC CACATTGCT ACTGGGTGCT 360
 65 GCAGATCATC TTGCTCTCCA CGCCTCTCT GGTGTACATG GGCCAAGCCA TGCACACTGT 420
 GGCATGACAG GAGAGCGCA AGCTACGGGA GGCCGAGAGG GCCAAGAGG TCCGGGGCTC 480
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 TGGAAAGGAT GCCTCCAGG GCACTCTGCT CAACACCTAT GTGTGACGCA TCCTGATCCG 600
 CACCACCATG GAGGTGGGCT TCATTGTGGG CCAGTACTTC ATCTACGGAA TCTTCTTGAC 660
 70 CACCCTGCAT GTCTGCGCA GAGTCCCTG TCCCACCGG GTCAACTGTT ACGTATCCCG 720
 GCCCAGAGAG AAGAATGTCT TCATTGTCTT TATGCTGGCT GTGGCTGCAC TGTCCCTCT 780
 CCTTAGCCTG GCTGAACCTC ACCACCTGGG CTGGAAGAAG ATCAGACAGC GATTGTCTAA 840
 ACCCGGGCAG CACATGGCTA AGTGCCAGCT TTCTGGCCCC TCTGTGGGCA TAGTCCAGAG 900
 CTGCCACACA CCCCCTGACT TTAATCAGTG CTGGAGAAAT GGCCCTGGGG GAAATTTCTT 960
 75 CAATCCCTTC AGCAATAATA TGGCTCCCA ACAAAACACA GACAACCTGG TCACCGAGCA 1020
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5 AAAGTTCOCA GCCAATAGAC AGCATGAATC AAGGAACTTG CATTATATGT GCTCTTGAAT 1680
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 CTCTCTCTCC CTCTACTCAG CCTTAAAAAG GGCTTCTTGG AACTTTTACCA GCAGCCTCAG 1800
 CTTTACAAAT GCCTTGGTAT GTACCTCTGG CAAATGCCCT GGTATGTACC TCTGGCAAAAT 1860
 GCCCCACCTT GGTGATGTTG CAACCTTTCC TTCTGCTAGG GTGTACACCT AGCCTGTGCA 1920
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 10 GCTGTGTGCC TCTCTCGAAC CCTGACCAGA TCATCAGCCA CTGAGGCCAG TGAATTTTCC 2160
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Seq ID NO: C66 DNA Sequence
 Nucleic Acid Accession #: NM_014459.2
 Coding sequence: 738..3407

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 ACCTCCCTGC TCCTTCCTCC ACTCGATGTG AAGAGTATTG CGAGTCTCC GGGCGGGAGT 300
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 25 CTCTCCCAAG CGAGATTTC TTCTTATGCG CTGCCCTATC GCTCAAGTTT GAGCCTTCCG 420
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 TGCTCCAGAG CCTCGAGCT CTGCTGCACC GCAGCTTCTC ACCAGTGGG GATGCTGTAG 540
 ATCAACAGGT TCAGGAACT TGAGCAGAAAT AAGGAGAGAC CACCGGGTGC CGCAGCTCGG 600
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5 TCCGATCAG ATGGCAAGGG TCTTTGCAGA TGTGCATTCC AGAGCCAGCC GGGATTCCAG 4080
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 AAAGACCAAT GCTGCTTTAA GGCTTTTAGT GAACATCTGA AGTGCCCAAC AGTATGTTCT 4380
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 10 GAAAAAGGAG GATGAGGAGA AGAATTACCT TTTGACAATC TGTAGGAAAG GTATGCAGTG 4560
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 CACCAAAAT TAACACATAT TTGTGGTAAA CATTTCTGTA TAAAGTTACC TGACACACAT 4800
 15 ATAAACACAA GGAACATTCC ATATCATTAG TCGAAAACAA AAACAAAAAA AAAACCTTTG 4860
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Seq ID NO: C67 DNA Sequence

Nucleic Acid Accession #: NM_005601.2

Coding sequence: 101..598

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 GGCCCTGCTG GGGGGCTCCC TGGGCTGAT GTTCTGCTGT ATTGCTTTGA GCACCGATT 180
 CTGTTTGGAG GCTGTGGGTG CCACCCACTC AGCTCACTCG GGCCCTCTGGC CAACAGGGCA 240
 TGGGACATCT ATATCAGGCT ACATCCACGT GACGCGAGCC TTCAGCATTA TGGCTGTTCT 300
 30 GTGGGCGCTG GTGTCCGTGA GCTTCTCTGT CCTGTCTCTG TCCCTCTCAC TGTTCCTCCC 360
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 CTCTCTCTCC TGGTCTCTCT ACCTGGGCTG GGTCTCAGCT ATCCTCTTGC TCTGTACAGG 540
 TGCCCTGAGC CTGGGTGCTC ACTGTGGCGG TCCCGTCTCT GGCTATGAAA CCTTGTGAGC 600
 35 AGAAGGCAAG AGCGGCAAGA TGAGTTTGA GCGTTGTATT CCAAGGCCCT CATCTGAGC 660
 CTCGGGAAAG TCTGTCTCTA CATTTGCCCG CCCTTCCAGC CCTTCCCTCT CCCCCTCTCT 720
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 AAA 783

Seq ID NO: C68 DNA Sequence

Nucleic Acid Accession #: NM_006433.2

Coding sequence: 129..566

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 50 GTCTGTCTCT CTCTGCTCTG AGCCCTGAGT ACTACGACCT GGCAAGAGCC CACTGCGGTG 240
 ATGAGGAGAA ATCTCGCCCG TGCTGGGCC AGGAGGGGCC CCAGGGTGAC CTGTTGACCA 300
 AAACACAGGA GCTGGGCCGT GACTACAGGA CCTGTCTGAC GATAGTCCAA AAAGTGAAGA 360
 AGATGTGGA TAAGCCCAAC CAGAGAAGTG TTTCCAATGC TGCGACCCCG GTGTGTAGGA 420
 CGGGAGGCTC ACCATGGGCG GACGTCTGCA GAAATTTCT GAGGAGGTAT CAGTCTAGAG 480
 55 TTACCCAGGG CCTGTGGGCC GGAGAACTG CCCAGCAGAT CTGTGAGGAC CTCAGGTTGT 540
 GTATACCTTC TACAGGTCCC CTCTGAGCCC TCTCACCCTT TCCTGTGGA GAAGCACAGG 600
 CTCCTGTCTC CAGATCCCGG GAACCTCAGC AACCTCTGCC GGCTCTCTGC TTCTCTGATC 660
 CAGAATCCAC TCTCCAGTCT CCCTCCCTCT ACTCCCTCTG CTGTCTCTCC CTCTCAGAG 720
 AATAAAGTGT CAAGCAAG 738

Seq ID NO: C69 DNA Sequence

Nucleic Acid Accession #: NM_002985.2

Coding sequence: 69..344

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 65 1 | 11 | 21 | 31 | 41 | 51
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 CAGGTACCAT GAAGGTCTCC GGGCAGGCC TCGCTGTCAT CCTATTGCT ACTGCCCTCT 120
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 TTGCCCGCCC ACTGCCCGGT GCCACATCA AGGAGTATTT CTACACCAGT GGCAAGTGCT 240
 CCACCCAGC AGTCTGCTTT GTCAACCGAA AGAACCGCCA AGTGTGTGCC AACCCAGAGA 300
 AGAAATGGGT TCGGGAGTAC ATCAACTCTT TGGAGATGAG CTAGGATGGA GAGTCTCTGA 360
 75 ACCTGAATCT ACACAAATT GCCTGTTTCT GCTTGTCTCT GTCTAGCTT GGGAGGCTTC 420
 CCTCACTAT CCTACCCAC CGCTCTCTTG AAGGGCCAG ATTCTACAC ACAGCAGCAG 480
 TTACAAAAAC CTTCCTCCAG CTGGAAGTGG TGGCTCAAGC CTGTAATCCC AGCACTTTGG 540
 GAGGCCAAGG TGGGTGGATC ACTTGAGGTC AGGAGTTOGA GACCAGCCTG GCCAACATGA 600
 TGAACCCCA TCTCTACTAA AAATACAAAA AATTAGCCGG GCGTGGTAGC GGGCGCTGT 660
 AGTCCAGCT ACTCGGAGG CTGAGGCAGG AGAATGGCT GAACCCGGGA GCGGAGCTT 720
 80 GCAGTGAGCC GAGATCGCGC CACTGCACTC CAGCCTGGGC GACAGAGCGA GACTCCGTCT 780
 CAAAAAAA AAAAATAAAA AAATACAAA AATTAGCCGG GCGTGGTGGC CCACGCTGT 840
 AATCCAGCT ACTCGGAGG CTAAGGCAGG AAAATTGTTT GAACCCAGGA GGTGGAGGCT 900
 GCAGTGAGCT GAGATTGTGC CACTTCACTC CAGCCTGGGT GACAAAGTGA GACTCCGTCA 960
 CAACACAC AACAAAAAGC TTCCCAACT AAAGCCTAGA AGAGCTTCTG AGGCGCTGTCT 1020
 TTGTCAAAAG GAAGTCTCTA GGTCTGAGC TCTGGCTTGT CCTTGGCTTT GCCAGGGCTC 1080

TGTGACCAGG AAGGAAGTCA GCATGCCTCT AGAGGCAAGG AGGGGAGGAA CACTGCACTC 1140
 TTAAGCTTCC GCCGTCTCAA CCCCTCACAG GAGCTTACTG GCAAACATGA AAAATCGGCT 1200
 TACCATTAAA GTTCTCAATG CAACCATAAA AAAAAA 1237

5

Seq ID NO: C70 DNA Sequence
 Nucleic Acid Accession #: NM_022154.2
 Coding sequence: 1381..1722

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CATATGTACG	CAAACTCTGG	GGCGTTTGCA	AACCCGGATC	CGGGGCGTCT	GGCCCCATGC	120
CCGGCCGGGC	GTATTGAGGC	TACTGCCACG	CAGCGTTTCT	GGAGCCTGCC	GGCTGGTGCC	180
CTGGTGGCCT	TATCTCTGTG	CCCCCTTTGT	CCTCTTTATC	TCAGGCTCTC	CAGGAGGCCG	240
GGGGGCCAC	TCCGCCTATC	GCTCCCTCG	GCTACGCTGC	CACTCCAATG	CCCCGCAGGT	300
GGGAGCTCG	TGTTCTTTTG	AAGGCGCCGG	AGAACCCAGG	GGTCCCGCG	CCACCTCTGA	360
CTCGAGCAG	GGCGAGCAC	TGACGCTCCC	GGCCTTGGGC	AAGGACGCCA	GTGCGCCCGC	420
GGCGTCCCT	CTGGCGGGCA	GGCCGTCCGG	GGCCCTCAAG	GGGAAGCCCA	GGCCAGGATG	480
GCCCGGGTC	GGCGGTGGGC	CGGGCTCCTG	TTGCTGGCGG	CGCCCGGCT	CGGAGGAGTG	540
GGGAGGGGC	CAGGGCTAGC	CTTCAGCGAG	GATGTGCTGA	GGTGTTCGG	CGCGAATCTG	600
AGCCTGTCCG	GGCGCAGCT	CCAGCACTTG	CTGGAGCAGA	TGGGAGCCGC	CTCCCGCGTG	660
GGCGTCCCG	AGCCTGGCCA	GCTGCACCTC	AACCACTGTT	TAACTGCTGA	AGAGATCTTT	720
TCCCTTCATG	GCTTTTCAAA	TGCTACCCAA	ATAACCAAGT	CCAAATTCCT	TGTCATCTGT	780
CCAGCAGTCT	TACAGCAATT	GAACCTTCAC	CCATGTGAGG	ATCGGCCCAA	GCACAAAAAC	840
AGACCAAGTC	ATTGAGAAAT	TTGGGGATAT	GGATTCTCTG	CAGTGACGAT	TATTAACTCTG	900
GCATCTCTCC	TGGGATTGAT	TTTGAATCCA	CTGATAAAGA	AATCTTATTT	CCCAAGAGTT	960
TTGACCTTTT	TTGTGGGGCT	GGCTATTGGG	ACTCTTTTTT	CAATGCAAT	TTTCCAACTT	1020
ATTCCAGAGG	CATTGTGATT	TGATCCCAAA	GTGACAGATT	ATGTTGAGAA	GGCAGTTGCT	1080
GTGTTTGGTG	GATTTTACCT	ACTTTTCTTT	TTTGAAGAGG	TGCTAAAGAT	GTTATTAAGA	1140
ACATATGGTC	AGAATGTGCA	TACCCACTTT	GGAAATGATA	ACTTTGGTCC	TCAAGAAAAA	1200
ACTCATCAAC	CTAAAGCATT	ACCTGCCATC	AATGGTGTA	CATGCTATGC	AAATCCTGCT	1260
GTACAGAAAG	CTAATGAGCA	TATCCATTTT	GATAATGTCA	GTGTGGTATC	TCTACAGGAT	1320
GGAAAAAAG	AGCCAAAGTC	ATGTACCTGT	TTGAAGGGGC	CCAACTGTGC	AGAAATAGGG	1380
ACGATTCGCT	GGATGATAAC	GCTCTGGGAT	GGCCTCCACA	ATTTCATCGA	TGGCCTGGCG	1440
ATTGGGGCTT	CCTGCACCTT	GTCTCTCTCT	CAGGGAATCA	GTACTTCCAT	AGCAATCCTA	1500
TGTGAGGAGT	TTCCCCACGA	GTTAGGAGAC	TTTGTGATCC	TACTCAATGC	AGGGATGAGC	1560
ACTCGACAAG	CCTTGCTATT	CAACTTCCTT	TCGTCATGTT	CCTGCTATGT	TGGGCTAGCT	1620
TTTGGCAATT	TGGTGGGCAA	CAATTTGCTG	CCAAATATTA	TATTGCACT	TGCTGGAGGC	1680
ATGTTCTCTT	ATATTTCTCT	GGCAGATATG	TTTCCAGAGA	TGAATGATAT	GCTGAGAGAA	1740
AAGGTAACCTG	GAAGAAAAAC	CGATTTCACC	TTCTTCATGA	TTGAGAATGC	TGGAATGTTA	1800
ACTGGATTCA	CAGCCATTCT	ACTCATTACC	TTGTATGCAG	GAGAAATCGA	ATTGGAGTAA	1860
TAGAAATAGG	AAGATGGTGT	TGTTAATAAA	GGCATTTAAT	AGATAAAAAAC	ATCTCCAAAA	1920
AGGATTTTGA	AGCTGATCCT	ATTAGTTAA	AAAGATAATT	TTGCTTTCAA	CTGTAGGTCC	1980
AGAAAACTAA	TATTGTGATC	CAGTCTGTGA	AATAGTCCAT	TATTTGTTGT	TAAAAATGCT	2040
TCAAAAGGTT	TTCAAGTGCA	GTCTGAGATG	CCTGGTATAT	AGGAGCCTTT	GGGAAATACT	2100
TATTTTTCAG	TATTCATGTC	ATATTAGATA	TCACCATGAA	GCAAGAGACA	TGCAATCTAT	2160
AATCATGTAG	CACCTCAGAC	TCAGGGGAAA	ATACAAGTTA	TATCCTGAAA	GCCTTTAAAA	2220
CTCTATGGTA	GGATCAAGAA	TTCAATAGGT	TTGAGAGAGG	TTTTATTCTA	ATTAATTTGT	2280
TCTAGTGCTT	TCAGAGGCAA	GTACATCAAA	ATGTAGAAGG	TAAAAATGAT	GCAACACTAA	2340
TATAAATTAT	TCCAAGTCTT	TAAGGAGCCA	AAGAAAAAAA	AGATTTCTCA	CAGCTTTTGT	2400
TTCTGTTTGT	TATTTCAATT	AGGAACCTGC	AGTATTATTT	TGAAAAACAT	TCTAAAAATA	2460
TAGGAGTTAG	AGAAATAAATA	AAGTTTGTCT	AGCCCTGCTA	AGTTCAAGCT	TAGAGGCTTA	2520
TCGCTAAGTN	TAACTCTCAC	CAGATTCCAC	GAAAGCTGG	ATAGCTTTTT	TTCTGACTTA	2580
TGTTGTGGTT	GCACCCCTCA	CAATGGCAG	AACAGTATGT	AAAGCTGGTA	ACACCTCGGT	2640
TTCACTGCAC	CATGTGTTTG	CTTTGTGAAG	GTGAAGAATA	TGTTGGTTTA	GAGAAAGAAA	2700
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TTTTATAAAA	TGCAAAACAA	CAGCTGGACT	GCTGTACATC	AAGGACAGAT	TAACTGGAAA	2820
ACATATGTTC	CTTATGTGTG	ATTGAGAGCC	ATTGAGAAAA	GACTTCCTTT	GTGTTCAAGC	2880
TATACTTTTC	CATATGGTAT	ACCTTGAAAA	AAATTAGCAC	ACCATGGTTA	TTTTTCTACC	2940
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GAACATCCTA	GATTCACACT	CCCAAGTCAC	TTAAGGTGAT	TTGATGGTGA	GGAAATGAT	3060
TGACAAAGCC	CAACAATGAT	CTCAGGAATT	ACATTTTCCA	ACAGACCAAA	AAATGTTTTT	3120
ATGTAGCAGC	AATGCAAGAT	TGGTGAATAT	TTAATATATA	TTTTAGTATG	TATTTCACTT	3180
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70

Seq ID NO: C71 DNA Sequence
 Nucleic Acid Accession #: NM_004184.2
 Coding sequence: 188..1603

75

80

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CTCAACTGCC	CAGCGTGACC	AGTGCCACCC	TCTGCACTGT	CTTCCACAA	CTGGTCTTGA	120
CTGCTCTGCT	GAACAAATCC	TCTGACCTCA	GGCCGGCTGT	GAACGTAGTT	CCTGAGAGAT	180
AGCAAAACATG	CCCAACAGTG	AGCCCGCATC	TCTGCTGGAG	CTGTTCAACA	GCATCGCCAC	240
ACAAGGGGAG	CTCGTAAGGT	CCCTCAAAGC	GGGAAATGCG	TCAAAGGATG	AAATTGATTC	300
TGCAGTAAAG	ATGTTGGTGT	CATTAAAAAT	GAGCTACAAA	GCTGCCGCGG	GGGAGGATTA	360
CAAGGCTGAC	TGTCTCCAG	GGAACCCAGC	ACCTACCACT	AATCATGGCC	CAGATGCCAC	420
AGAAGCTGAA	GAGGATTTTG	TGGACCCATG	GACAGTACAG	ACAAGCAGTG	CAAAAGGCAT	480
AGACTACGAT	AAGCTCATTG	TTCGGTTTGG	AAGTAGTAAA	ATTGACAAAG	AGCTAATAAA	540
CCGAATAGAG	AGAGCCACCG	GCCAAAGACC	ACACCACTTC	CTGGCGCAGG	GCATCTTCTT	600

5	CTCACACAGA	GATATGAATC	AGGTTCTTGA	TGCCTATGAA	AATAAGAAGC	CATTTTATCT	660
	GTACACGGGC	CGGGGCCCTT	CTTCTGAAGC	AATGCATGTA	GGTCACCTCA	TTCCATTAT	720
	TTTCACAAAG	TGCTCCAGG	ATGTATTATA	CGTGCCTTGG	GTACATCCAGA	TGACGGATGA	780
	CGAGAAGTAT	CTGTGGAAGG	ACCTGACCCCT	GGACCCAGGCC	TATGGCGATG	CTGTTGAGAA	840
	TGCCAAGGAC	ATCATCGCCT	GTGGCTTTGA	CATCAACAAG	ACTTTCATAT	TCTCTGACCT	900
	GGACTACATG	GGGATGAGCT	CAGGTTTCTA	CAAAAATGTG	GTGAAGATTG	AAAAGCATGT	960
	TACCTTCAAC	CAAGTGAAAG	GCATTTTTCG	CTTCACTGAC	AGCGACTGCA	TGGGAAGAT	1020
	CAGTTTTCCT	GCCATCCAGG	CTGCTCCCTC	CTTCAGCAAC	TCATTTCCAC	AGATCTTCCG	1080
10	AGACAGGACG	GATATCCAGT	GCCTTATCCC	ATGTGCCATT	GACCAGGATC	CTTACTTTAG	1140
	AATGACAAGG	GAGTTCGCC	CCAGGATCGG	CTATCTCTAA	CCAGCCCTGT	TGCACTCCAC	1200
	CTTCTTCCCA	GCCTTCGAGG	GCGCCAGAC	CAAAATGAGT	GCCAGCGACC	CAAACTCCTC	1260
	CATCTTCTTC	ACCGACACGG	CCAGCAGAT	CAAAACCAAG	GTCAATAAGC	ATGCGTTTTC	1320
	TGGAGGGAGA	GACACCATCG	AGGAGCACAG	GCAGTTTGGG	GGCAACTGTG	ATGTGGACGT	1380
15	GTCTTTCATG	TACCTGACCT	TCTTCTCTGA	GGACGACGAC	AAGCTCGAGC	AGATCAGSAA	1440
	GGATTACACC	AGCGGAGCCA	TGCTCACCGG	TGAGCTCAAG	AAGGCACTCA	TAGAGGTTCT	1500
	GCAGCCCTTG	ATCGCAGAGC	ACCAGGCCCG	GCGCAAGGAG	GTCAAGGATG	AGATAGTGAA	1560
	AGAGTTCTAG	ACTCCCCGGA	AGCTGTCTCT	CGACTTTCAG	TAGCACTCGT	TTTACATATG	1620
	CTTATAAAAG	AAGTGATGTA	TCAGTAATGT	ATCAATAATC	CCAGCCCACT	CAAGCACCAG	1680
20	CCACCTGTAT	GCTTCTGTCT	CATGTAAT	ACTGGCCTG	GCCTCTGTAA	GCCTGTGTAT	1740
	GTATATCAAT	CTGTTTCTTC	CTGTGAGTTC	CAITATTCTT	ATCTCTTATG	GGCAAAAGCAT	1800
	TGTGGTAAAT	TGGTGTCTGG	TAACATTGCA	TGGTCCGATA	GAGAAGTCCA	GCTGTGAGTC	1860
	TCTCCCAAAA	GCAGCCCCAC	AGTGGAGCCT	TCCGCTGGAA	GTCCATGGGC	CACCCGTGTC	1920
	TGTTCATGAG	AGGACTTCCG	AGGGTTCCAA	GTATACTCTT	AAGACCCACT	CTGTTTAAAA	1980
25	ATATATATTC	TATGATGCG	TATATGGAAT	TGAAATGTCA	TTATTGTAAAC	CTAGAAAGTG	2040
	CTTTGAAAAA	TTGATGTGGG	GAGGTTTAT	GAGCACAAGA	TGTATTTCAG	CCCATGCCCC	2100
	CTCCCCAAAA	GAAATGTGATA	AGTAAAAGCT	TCGTATATACA	TTTGAATAAG	AAATCACCACA	2160
	GCTTTAAAGC	TGCTTTTAAAC	AATGAAAGAT	GAACAGAGTT	CAGCAATTTT	GATTAAATTA	2220
	AGACTTGGGG	GTGAAACTTT	CCAGTTTACT	GAATCCAGA	CCATGCATGT	AGTCCACTCC	2280
30	AGAAATCATG	CTCGCTTCCC	TTGGCACACC	AGTGTCTTCC	TGCCAAATGA	CCCTAGACCC	2340
	TCTGTCTCTG	AGAGTCAGGG	TGGCTTTTCC	CCTGACTGTG	TCGATGATCA	AGGAGTCCTG	2400
	GCCTCCGACG	ATGCTTCAAT	TTGACCCCTG	GCTGCAGTGG	AAGTCAGCAC	AGAGCAGTGC	2460
	CCTGGCTGTG	TCTGGACGG	GTGGACTTAG	CTAGGAGAGAA	AGTCGAGGCA	GCAGCCCTCG	2520
	AGGCCCTCAC	AGATGCTCAG	GCAGGCCCTCA	TTTCATCACG	CAGCATGTGC	AGGCCCTGGA	2580
35	GAGCAAAGCC	AAATCTCAGG	GAAGTCCTTG	GTTGATGTAT	CTGGGTCTCC	TCTGGAGCAC	2640
	TCTGCCCTCC	TGTCACCCAG	TAGAGTAAAT	AAACTTCTCT	GGCTCTTAAA	AAA	2693

Seq ID NO: C72 DNA Sequence

Nucleic Acid Accession #: NM_004938.1

Coding sequence: 337..4632

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45	GCAACTCGCA	GCGGACGGGT	CTGGGGCCCG	CGCCTGGGAG	GGATCTGCGC	CCCCCACTCA	120
	CTCCCTAGCT	GTGTTCCCGC	CGCCGCCCCG	GCTAGTCTCC	GGCGCTGGCG	CCTATGGTCG	180
	GCCTCCGACA	GCGCTCCGGA	GGGACCGGGG	GAGCTCCAG	GCGCCCGGGA	CTGGAGACTG	240
	ATGCATGAGG	GGCCTACGGA	GCGCAGGAG	CGGTGGTGAT	GGTCTGGGAA	GCGGAGCTGA	300
	AGTCCCTCG	GCTTTGGTGA	GGCGTGACAG	TTTATCATGA	CGGTGTTTCA	GCAGGAAATC	360
50	GTGGATGATT	ACTACGACAC	CGCGGAGGAA	CTTGGCAGTG	GACAGTTTGC	GGTGTGTAAG	420
	AAATGCGCTG	AGAAAAGTAC	CGGCCCTCCG	TATGCCGCCA	AATTCATCAA	GAAGAGGAGG	480
	ACTAAGTCCA	GCGCGCGGGG	TGTGAGCCGC	GAGGACATCG	AGCGGGAGGT	CAGCATCTCT	540
	AAGGAGATCC	AGCACCACAA	TGTATATCAC	CTGCACGAGG	TCTATGAGAA	CAAGAAGGAC	600
	GTATCTCTGA	CTTTGGGAAT	GTTTGCAGGT	GGCGAGCTGT	TTGACTTCTT	AGCTGAAATG	660
55	GAATCTTTAA	CTGAAGAGGA	AGCAACTGAA	TTTCTCAAAC	AAATTTCTTAA	TGGTGTTTAC	720
	TACCTGCACT	CCCTTCAAA	CGCCCACTTT	GATCTTAAGC	CTGAGAACAT	AATGCTTTTG	780
	GATAGAAATG	TCCCAAAACC	TGGATCAAG	ATCATTGACT	TTGGGTTGGC	CCATAAAAT	840
	GACTTTGGAA	ATGAATTTAA	AAACATATTT	GGGACTCCAG	AGTTTGTGCG	TCTGAGATA	900
	GTCAACTATG	AACCTCTTGG	TCTTGAGGCA	GATATGTGGA	GTATCGGGGT	AATAACCTAT	960
60	ATCCTCTCAA	GTGGGGCCTC	CCCATTTCTT	GGAGACACTA	AGCAAGAAAC	GTTAGCAAA	1020
	GTATCCGCTG	TCAACTACGA	ATTGAGGAT	GAATACITCA	GTAATACCA	TGCCCTAGCC	1080
	AAAGATTTC	TAAGAAGACT	TCTGTTCAAG	GATCCAAAGA	AGAGAATGAC	AATTCAAGAT	1140
	AGTTTGCAGC	ATCCCTGGAT	CAAGCCTAAA	GATACACAAC	AGGCACCTAG	TAGAAAAGCA	1200
	TCAGCAGTAA	ACATGGAGAA	ATTCAAGAA	TTTGACGCCC	GGAAAAAATG	GAACAATCC	1260
65	GTTGCTTGA	TATCACTGTG	CCAAAGATTA	TCCAGGTCAT	TCCGTCCAG	AAGTAACATG	1320
	AGTGTGCGCA	GAAGCGATGA	TACTCTGGAT	GAGGAAGACT	CCTTTGTGAT	GAAGCCATC	1380
	ATCCATGCCA	TCAACGATGA	CAATGTCCCA	GGCCTGCAGC	ACCTTCTGGG	CTCATTATCC	1440
	AACTATGATG	TTAACCAACC	CAACAAGCAC	GGGACACCTC	CATTACTCAT	TGCTGCTGGC	1500
	TGTGGGAATA	TTCAAATACT	ACAGTTGCTC	ATTAAAAGAG	GCTCGAGAA	OGATGTCCAG	1560
70	GATAAGGGOG	GGTCCAATGC	CGTCTACTGG	GCTGCTCGGC	ATGGCCACGT	CGATACCTTG	1620
	AAATTTCTCA	GTGAGAACAA	ATGCCCTTTG	GATGTGAAG	ACAACTCTGG	AGAGATGGCC	1680
	CTCCACGTGG	CAGCTCGCTA	TGGCCATGCT	GACGTGGCTC	AAGTTACTTG	TGCAGCTTGG	1740
	GCTCAAAATC	CAATATCCAG	GACAAAGGAA	GAAGAAACCC	CCCTGCACCTG	TGCTGCTTGG	1800
	CACGGCTATT	ACTCTGTGGC	CAAGGCCCTT	TGTGAAGCCG	GCTGTAAAGT	GAACATCAAG	1860
75	AAACGAGAG	GAGAGAGGCC	CCTCCTGACA	GCCTCTGCCA	GGGGCTACCA	CGACATCGTG	1920
	GAGTGTCTGG	CCGAACATGG	AGCCGACCTT	AATGCTTGGC	ACAAAGGAGG	ACACATTGCC	1980
	CTTCATCTGG	GTGTGAGACG	GTGTGAGATG	GAGGTAATCA	AGACTCTCCT	CAGCCAAAGG	2040
	TGTTTCTGTG	ATTATCAAGA	CAGGCACGGC	AATACTCCCC	TCCATGTGGC	ATGTAAAGAT	2100
	GGCAACATGG	TATCATGGGT	GGCCCTCTGT	GAAGCAAACT	GCAATTTGGA	CATCTCCAA	2160
80	AAGTATGGGC	GAAAGCCTCT	GCACCTTGGC	GCCAAACACG	GAATCTTAGA	CGTGGTCCGG	2220
	TATCTCTGTC	TGATGGGAGC	CAGCGTTGAG	GCGCTGACCA	CGGACGAGAA	GAOCCGAGAA	2280
	GATCTTGCTA	GATCGGAACA	GCACGAGCAC	GTAGCAGGTC	TCCTTGCAAG	ACTTCGAAAG	2340
	GATACGCAAC	GAGGACTCTT	CATCCAGCAG	CTCCGACCCA	CACAGAACTT	GCAGCCAAAG	2400
	ATTAAGCTCA	AGCTGTTTGG	CCACTGCGGA	TCCGGGAAAA	CCACCTTGTG	AGAATCTCTC	2460
	AAGTGTGGGC	TGCTGAGGAG	CTTTTTCAGA	AGGCGTGGCC	CCAGACTGTC	TTCCACCAAC	2520

5	TCCAGCAGGT	TCCCACCTTC	ACCCCTGGCT	TCTAAGCCCA	CAGTCTCAGT	GAGCATCAAC	2580
	AACCTGTACC	CAGGCTGCGA	GAACGTGAGT	GTGAGGAGCC	GCAGCATGAT	GTTGAGCCCG	2640
	GGTCTTACCA	AAGGGATGCT	GGAGGTGTTT	GTGGCCCCGA	CCCACCAACC	GCATCTGCTCG	2700
	GCCGATGACC	AGTCCACCAA	GGCCATCGAC	ATCCAGAACG	CTTATTTGAA	TGGAGTTGGC	2760
	GATTTACAGC	TGTGGGAGTT	CTCTGGAAAT	CCTGTGTAAT	TCTGCTGTTA	TGACATATTT	2820
	GCTGCAATG	ATCCACGTC	AATCCATGTT	GTGTCTTTA	GTCTAGAAGA	GCCCTATGAG	2880
	ATCCAGCTGA	ACCCAGTGAT	TTTCTGGCTC	AGTTTCTGTA	AGTCCCTTGT	CCCAGTTGAA	2940
	GAACCCATAG	CCTTGGGTGG	CAAGCTGAAG	AACCCACTCC	AAGTTGTCTT	GGTGGCCACC	3000
10	CACGCTGACA	TCATGAATGT	TCCTGACCG	GCTGAGGCG	AGTTTGGATA	TGACAAAGAC	3060
	ACATGTTGTC	TGAAAGAGAT	TAGGAACAGG	TTTGGAAATG	ATCTTCACAT	TTCAAAATAG	3120
	CTGTTTGTTC	TGGATGCTGG	GGCTTCTGGG	TCAAAGGACA	TGAAGGTACT	TGAAATTCAT	3180
	CTGCAAGAAA	TACGAAGCCA	GATTGTTTCG	GTCTGTCTTC	CCATGACTCA	CCTGTGTGAG	3240
	AAAATCATCT	CCACGCTGCC	TTCTGTGAGG	AAGCTCAATG	GAOCCAAACA	GCTGATGTGG	3300
15	CTGCAGCAGT	TTGTGTACGA	CGTGACGAC	CAGCTGAACC	CCCTGGCCAG	CGAGGAGGAC	3360
	CTCAGGCGCA	TTGCTCAGCA	GCTCCACAGC	ACAGGCGAGA	TCAACATCAT	GCAAAGTGAA	3420
	ACAGTTTCAGG	ACGTGCTGCT	CCTGGACCCC	CGCTGGCTCT	GCACAAACGT	CCTGGGGAGG	3480
	TTGCTGTCCG	TGGAGACCCC	ACGGGCGCTG	CACCACTACC	GGGGCCGCTA	CACCGTGGAG	3540
	GACATCCAGC	GCCTGGTGCC	CGACAGCGAC	GTGGAGGAGC	TGCTGCAGAT	CCTCGATGCC	3600
20	ATGGACATCT	TGGCCCGGGA	CCTGACGAGC	GGGACCATGG	TGGACGTCCC	AGCCCTGATC	3660
	AAGACAGACA	ACCTGCACCG	CTCCTGGGCT	GATGAGGAGG	ACGAGGTGAT	GGTGTATGGT	3720
	GGCGTGCAGC	TGCTGCCCGT	GGAACACCTC	ACCCCTTCC	CATGTGGCAT	CTTTCACAA	3780
	GTCCAGGTGA	ACCTGTGCCG	GTGGATCCAC	CAGCAAGACA	CAGAGGGCGA	CGCGGACATC	3840
	CGCTGTGGG	TGAATGGCTG	CAAGCTGGCC	AACCGTGGG	CCGAGCTGCT	GGTGTCTCTG	3900
25	GTCAACCAAG	GCCAGGGCAT	TGAGGTCCAG	GTCCGTGGCC	TGGAGACGGA	GAAGATCAAG	3960
	TGCTGCCTGC	TGCTGGACTC	GGTGTGAGC	ACCATTGAGA	ACGTCAATGGC	CACCAAGCTG	4020
	CCAGGGCTCC	TGACCGTGAA	GCATTACCTG	AGCCCCCAGC	AGCTGCGGGA	GCACCATGAG	4080
	CCCGTCATGA	CTTACCAAGC	ACGGGACTTC	TTCCGGGCAC	AGACTCTGAA	GGAAACCTCA	4140
	CTGACCAACA	CCATGGGGGG	GTACAAGGAA	AGCTTCAGCA	GCATCATGTG	CTTCCGGTGT	4200
30	CACGACGCT	ACTCACAGGC	CAGCCTCGGC	ATGGACATCC	ATGCATCAGA	CCTGAACCTC	4260
	CTCATCGGAA	GGAACCTGAG	TGCGCTGCTG	GACCCGCCCC	ACCCCTTGGG	GAAGGACTGG	4320
	TGCGCTCTCG	CCATGAACCT	AGGCCCTCCCT	GACCTCGTGG	CAAAAGTACAA	CACCAATTAAC	4380
	GGGGCTCCGA	AGGATTTCTT	CCCCAGCCCC	CTCCAGCCCC	TGCTGCGGGA	ATGGACCAAC	4440
	TACCTTGAGA	GCACAGTGGG	CACCTCATG	TCCAAACTGA	GGGAGCTGGG	TGCGCGGGAT	4500
35	GCGCGAGACC	TTTTGCTGAA	GGCATCCTCT	GTGTTCAAAA	TCAACCTGGA	TGGCAATGGC	4560
	CAGGAGGCGT	ATGCCCTGAG	CTGCAACAGC	GGCACCTCTT	ACAATTCCAT	TAGCTCTGTT	4620
	GTATCCCGGT	GAGGGCAGCC	TCTGGCTTGG	ACAGGGTCTG	TTTGGACTGC	AGAACCAAGG	4680
	GGGTGATGTA	GCCCATCCTT	CCCTTTGGAG	ATGCTGAGGG	TGTTTCTTCC	TGCACCCACA	4740
	GCCAGGGGGA	TGCCACTCCT	CCCTCGGCT	TGACCTGTTT	CTCTGCGGCT	ACCTCCCTCC	4800
40	CGGTCTCATT	CGGTGTCTG	TGGATGGTCA	TTGCAGTTTA	AGAGCAGAAC	AGATCTTTTA	4860
	CTTTGGCGCG	TGAAAAGCT	AGTGTACCTC	CTCTCAGTGT	TTTGGACTCC	ATCTCTCATC	4920
	CTCCAGTACC	TTGCTCTTTA	CTGATAATTT	TGCTGGAATT	CCTAACTTTT	CAATGACATT	4980
	TTTTTTAACT	ATCATATTGA	TTGTCTTTTA	AAAAAGAAAA	GTGCATATTT	ATCCAAAATG	5040
	TGTATTTCTT	ATACGCTTTT	CTGTGTTATA	CCATTTCTTC	AGCTTATCTC	TTTTATATTT	5100
45	GTAGAGGAAA	CTCCCATGTA	TGGAATCCCA	CTGTATGATT	TATAAACAGA	CAATATGTGA	5160
	GTGCTTTTGG	CAGAAGAGGG	TGTGTTTGAA	ATCATCGGAG	TCAGCCAGGA	GCTGTCAACA	5220
	AGGAAAGCCT	ACCTCTCTGT	CCCTTGCTGT	ATGCTGATCA	TCGCCAGAGG	TGCTTCACCC	5280
	TGAGTTTGTG	TTTGTATTGT	TTTCTGACAG	TTTTTCTGTT	TTGTTTGGCA	AGGAAAGGGG	5340
	AGAAGGGGAA	CCTCTCCAG	GGTGATTTTA	TGATCAGTGT	TGTTGCTCTA	GGAAGACATT	5400
50	TTTCCGTTTG	CTTTTGTCC	AATGTCAATG	TGAACGTCCA	CATGAAACCT	ACACACTGTC	5460
	ATGCTTTCAT	ATTCCCTCTC	ATCTCAGSTA	GAAGGTTGAC	ACAGTTGTAG	GOTTACAGAG	5520
	ACCTATGTAA	GAATTACGAA	GACCCCTGAC	TCATCATTTG	TGGCAGTCCC	TTATAATTGG	5580
	TGCATAGCAG	ATGGTTTCCA	CATTTAGATC	CTGGTTTCAT	AACTTCTCTG	ACTTGAAGTC	5640
	TAAAGCTGCA	AAATAAAGGA	AGCAAGTTTT	CTTCCATGAT	TTTAAATTGT	GATCGAGTTT	5700
55	TAAATGTATA	GGAGGGAACA	TGTCTTAATT	CTTCTGCTCT	GAGAAGCATG	TAATGTTAAT	5760
	GTATATATAT	ATATATATAT	ATATATGCAC	TATGTATATA	CATATATATT	AATACTGGTA	5820
	TTTTTACTTA	ATCTATAAAA	TGCTGTAAAA	AAGTTGTTTG	TTTTTTTCTT	TTTTTATAAA	5880
	TAAACTGTGT	CTGTTAAAAA	AAAAAATAAA				5910

Seq ID NO: C73 DNA Sequence
Nucleic Acid Accession #: NM_002081.1
Coding sequence: 222..1898

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	CGGACCTTGG	GCTCTGCCCT	TGCGGGGCGG	GAACCTGCGA	GGACCGGCGC	AGGATCCGAG	180
	AGAGGGGCGG	GCGGGTGGCC	GGGGGCGCGG	CGGGCGCGCG	CATGGAGCTC	CGGGCGCGAG	240
70	GCTGGTGGCT	GCTATGTGCG	GCCGACGCGC	TGGTCGCGCT	CGCGCGCGGG	GACCGCGCCA	300
	GCAAGAGCCG	GAGCTGCGGC	GAGGTTCGCG	AGATCTAAGG	AGCCAAGGGC	TTGAGCTTGA	360
	GCGACGTGCC	CCAGGGGCGG	ATCTCGGGTG	AGCACCTGCG	GATCTGTCCC	CAGGGCTACA	420
	CCTGCTGAC	CAGCGAGATG	GAGGAGAAAC	TGGCCAAACG	CAGCCATGCC	GAGCTGGAGA	480
	CGCGGCTCCG	GCGACGACGC	CGGTCTCTGC	AGGCCATGCT	TGCCAACCGA	CTGCGCAGCT	540
75	TGATGACCA	CTTCCAGCAC	CTGCTGAACG	ACTCGGAGCG	GACGCTGCAG	GCCACCTTCC	600
	CCGGCGGCTT	CGGAGAGCTG	TACACGCGAG	ACGCGAGGGC	CTTCCGGGAC	CTGTACTCAG	660
	AGCTGCGCCT	GTACTACCGC	GGTGCCCAAC	TGCACCTGGA	GGAGACGCTG	GCGGAGTTCT	720
	GGGCGGCGCT	GCTCGAGCGC	CTCTTCAAGC	AGCTGACACC	CCAGCTGCTG	CTGCTGATG	780
	ACTACCTGGA	CTGCTGGGCG	AAGCAGGCGG	AGGCGCTGCG	GCCCTTCCGG	GAGGCCCCGA	840
80	GAGAGCTGCG	CCTGCGGGCC	ACCGTGCCT	TGCTGGCTGC	TGCTCTCTTT	GTGACGGGCC	900
	TGGGCGTGCG	CAGCGACGTG	GTCCGGAAG	TGGCTCAGGT	CCCCCTGGGC	CGGAGTGCT	960
	CGAGAGCTGT	CTGAAGCTG	GTCTACTGTG	CTCACTGCCT	GGGAGTCCCC	GGGCGCAGGC	1020
	CCTGCCCTGA	CTATTGCGGA	AATGTGCTCA	AGGGCTGCCT	TGCCAACCGA	GCCGACCTGG	1080
	ACGCGGAGTG	GAGGAACCTC	CTGGACTCCA	TGGTGCTCAT	CACCGACAAG	TTCTGGGGTA	1140
	CATCGGCTGT	GGAGAGTGTC	ATCGGCAGCG	TGCACAGTGT	GCTGGCGGAG	GCCATCAACG	1200

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45 Seq ID NO: C74 DNA Sequence
Nucleic Acid Accession #: BC030205.1
Coding sequence: 45..878

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80 Seq ID NO: C75 DNA Sequence
Nucleic Acid Accession #: NM_001982.1
Coding sequence: 199..4227

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	AGCCTGGCCC	GGGGCTCCGA	GGTGGGCAAC	TCTCAGGCAG	TGTGCTCTGG	GACTCTGAAT	300
5	GGCCTGAGTG	TGACCGGCGA	TGCTGAGAAC	CAATACCGA	CACGTGTACAA	GCTCTACGAG	360
	AGGTGTGAGG	TGGTGATGGG	GAACTTGGAG	ATTGTGCTCA	CGGACACAA	TGCGACCTC	420
	TCCTTCCTGC	AGTGGATTCG	AGAAGTGACA	GGCTATGTCC	TCGTGGCCAT	GAATGAATTC	480
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	CGCTTGACT	AGCTCACCGA	GATTCTGTCA	GGGGGTGTTT	ATATTGAGAA	GAACGATAAG	660
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15	TGTGTACCTC	GCTGTCCACA	GCCTCTTGTC	TACAACAAGC	TAACTTTCCA	GCTGGAAACC	1020
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	GGTTACCTGA	ACATCAGCTG	CTGGCCGCC	CACATGCACA	ACTTCAGTGT	TTTTTCCAAT	1440
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	GGTGCCAAAG	CGCCCAATCTA	CAAGTACCCA	GATGTTGAGA	ATGAATGTGC	CGCCTGCCAT	2040
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	AAGGCTAACA	AAGTCTTGGC	CAGAATCTTC	AAAGAGACAG	AGCTAAGGAA	GCTTAAAGTG	2340
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	CTGGACATAT	GCCAGGGGTC	ATCTCTGCAG	CTTGTCACTC	AATATTGCCC	TCTGGGTTCT	2580
	CTGCTGGATC	ATGTGAGACA	ACACCGGGGG	GCACTGGGGC	CACAGCTGCT	GCTCAACTGG	2640
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	ATTAAGTGGA	TGGCCCTTGA	GAGTATCCAC	TTTGGGAAAT	ACACACACCA	GAGTGTATGTC	2880
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	TAICTGTGTA	TAAAGAGAGA	GAGTGGGCCT	GGAAAGCCCC	CTGGGCCAGA	GCCCATAGGT	3180
	CTGACAAACA	AGAAGCTAGA	GGAAAGTAGAG	CTGGAGCCAG	AACTAGACCT	AGACCTAGAC	3240
	TTGGAAGCAG	AGGAGACAAA	CCTGGCAACC	ACCACTGAGG	GCTCCGCCCT	CAGCCTACCA	3300
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	ATGCCCATGA	ACCAAGGTAA	TCTTGGGGGG	TCTTGCCAGG	AGTCTGCAGT	TTCTGGGAGC	3420
	AGTGAACGGT	GGCCCGGTCC	AGTCTCTCTA	CACCCAATGC	CAOGGGGATG	CCTGGCATCA	3480
	GAGTCAATCAG	AGGGGATGTT	AACAGGCTCT	GAGGCTGAGC	TCCAGGAGAA	AGTGTCAATG	3540
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	CAGCGCCACA	GTCTGTGAC	TCCTGTATCC	CCACTCTCCC	CACCCGGGTT	AGAGGAAGAG	3660
	GATGTCAACG	GTTATGTCTAT	GCCAGATACA	CACCTCAAAG	GTACTCCCTC	CTCCCGGAA	3720
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	TTGACACAAA	ATTCCTTAGG	TATGTAGCCA	GCTGTGCACT	TTCTTCTCTT	TOCCAACCCC	4440
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Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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TCCCTCTGGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCCC 240
10 AGTGAAGAGG ATTACCCAG AGAGGAGGAT CACCCCGGAG AGGAGGATCT ACCTGGAGAG 300
GAGGATCTAC CTGGAGAGGA GATCTTACCT GAAGTTAAGC CTAAATCAGA AGAAGAGGGC 360
TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCGAG 420
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CCTCCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT 720
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25 CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCTCTC CTGACACCTT GTGGGGACCT 1140
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GAGGCTCCTT TCCTGCTGCG AGTGGACAGC AGTCTCTGGC CTGCTGAGCC AGTCCAGCTG 1260
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Seq ID NO: C77 DNA Sequence

Nucleic Acid Accession #: NM_004207.1

Coding sequence: 63..1460

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Seq ID NO: C78 DNA Sequence

Nucleic Acid Accession #: NM_000358.1

Coding sequence: 48..2099

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CGCCCAAGCT GCGTCTACCG CTGGTGTCTG AGCAGAGCAG GCTCGGGGCG CGCCAGCAAG 180
GCCCCAAGCT GTGTGCTGTG CAGAAGGTTA TTGGCACTAA TAGGAAGTAC TTCACCAACT 240
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5	GCAAGCAGTG	GTACCAAAAGG	AAAATCTGTG	GCAAATCAAC	AGTCATCAGC	TACGAGTGCT	300
	GTCTCTGGATA	TGAAAAGGTC	CCTGGGGAGA	AGGGCTGTCC	AGCAGCCCTA	CCACTCTCAA	360
	ACCTTTAGGA	GACCCCTGGGA	GTGTTGGAT	CCACCACCAC	TCAGCTGTAC	ACGGACCGCA	420
	CGGAGAACT	GAGGCTCTGAG	ATGGAGGGGC	CCGGCAGCTT	CACCATCTTC	GCCCCTAGCA	480
	ACGAGGCTCTG	GGCCTCCTTG	CCAGCTGAAG	TGCTGGACTC	CCTGGTCAGC	AATGTCAACA	540
	TTGAGCTGCT	CAATGCCCTC	CGCTACCATA	TGGTGGGCAG	GCGAGTCTTG	ACTGATGAGC	600
	TGAAACAAGG	CATGACCCCTC	ACCTCTATGT	ACCAAGATTC	CAACATCCAG	ATCCACCACT	660
	ATCCTAATGG	GATTGTAAC	GTGAACCTGTG	CCCGGCTCCT	GAAAGCCGAC	CACCATGCAG	720
10	CCAAACGGGT	GGTGCACCTC	ATCGATAAGG	TCATCTCCAC	CATCACCAAC	AACATCCAGC	780
	AGATCATTGA	GATCGAGGAC	ACCTTTGAGA	CCCTTCGGGC	TGCTGTGGCT	GCATCAGGGC	840
	TCAACACGAT	GCTTGAAGGT	AAOCCGACGT	ACAOGCTTTT	GGCCCCGACC	AATGAGGCT	900
	TGAGAGAAGAT	CCCTAGTGAG	ACTTTGAACC	GTATCCTGGG	CGACCCAGAA	GCCCTGAGAG	960
	ACCTGCTGAA	CAACCAATC	TTGAAGTCAG	CTATGTGTGC	TGAAGCCATC	GTTCGGGGGC	1020
15	TGCTGTGAGA	GACCCCTGGAG	GGCAGGACAC	TGGAGGTGGG	CTGCAGCGGG	GACATGCTCA	1080
	CTATCAACGG	GAAGGCGATC	ATCTCCAATA	AAGACATCTC	AGCCACCAAC	GGGGTGATCC	1140
	ACTACATTGA	TGAGCTACTC	ATCCAGACT	CAGCCAGAC	ACTATTGAA	TGGCTGCAG	1200
	AGTCTGATGT	GTCCACAGCC	ATTGACCTTT	TCAGACAAGC	CGGCTCGGC	AATCATCTCT	1260
	CTGGAAGTGA	GCGGTGACC	CTCCTGGCTC	CCCTGAATTC	TGTATTCAA	GATGGAACCC	1320
20	CTCCAATTGA	TGCCCATACA	AGGAATTGTC	TTCGGAACCA	CATAATTAA	GACCAAGCTGG	1380
	CCTCTAAGTA	TCTGTACCAT	GGACAGACC	TGGAACTCT	GGGCGGCAAA	AAACTGAGAG	1440
	TTTTTGTGTTA	TGTAATAGC	CTCTGATTG	AGAACAGCTG	CATCGCGGCC	CACGACAAGA	1500
	GGGGGAGGTA	CGGGACCTG	TTCAAGATGG	ACCGGGTGCT	GACCCCCCA	ATGGGGACTG	1560
	TCATGGATGT	CCTGAAGGGA	GACAATCGCT	TTAGCATGCT	GCTAGCTGCC	ATCCAGTCTG	1620
25	CAGGACTGAC	GAGAGCCCTC	AACCGGGAAG	GAGTCTACAC	AGTCTTTGCT	CCCAAAATG	1680
	AAGCCCTCCG	AGCCCTGCCA	CCAAGAGAAC	GGAGCAGACT	CTTGGGAGAT	GCCAAGGAAC	1740
	TTGCCAACAT	CCTGAAATAC	CACATTGGTG	ATGAAATCCT	GGTTAGCGGA	GGCATCGGGG	1800
	CCCTGGTGCG	GCTAAAGTCT	CTCCAAGGTG	ACAAGCTGGA	AGTCAGCTTG	AAAAACAATG	1860
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30	TCCATGTGAT	CACCAATGTT	CTGCAGCCTC	CAGCCACAG	ACCTCAGGAA	AGAGGGGATG	1980
	AACTTGACAG	CTCTGCGCTT	GAGATCTTCA	AACAAGCATC	AGCGTTTTCC	AGGGCTTCCC	2040
	AGAGGTCTGT	GCGACTAGCC	CCTGTCTATC	AAAAGTTATT	AGAGAGGATG	AAGCATTAGC	2100
	TTGAAGCACT	ACAGGAGGAA	TGCACCAACG	CAGCTCTCCG	CCAATTCTC	TCAGATTTC	2160
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35	CCATAATGAT	ATGTGAGCCT	TGTGCATGTG	GGGGAGGAGG	GAGAGAGATG	TACTTTTTAA	2280
	ATCATGTTCC	CCCTAAACAT	GGCTGTTAAC	CCACTGCATG	CAGAACTTG	GATGTCACTG	2340
	CCTGACATTC	ACTTCCAGAG	AGGACCTATC	CCAAATGTGG	AATTGACTGC	CTATGCCAAG	2400
	TCCCTGGAAA	AGGAGCTTCA	GTATTGTGGG	GCTCATAAAA	CATGAATCAA	GCAATCCAGC	2460
	CTCATGGGAA	GTCTGGGCAC	AGTTTTTGTA	AAGCCCTTGC	ACAGCTGGAG	AAATGGCATC	2520
40	ATTATTAAGT	ATGAGTTGAA	ATGTTCTGTC	AAATGTGTCT	CACATCTACA	CGTGGCTTGG	2580
	AGGCTTTTAT	GGGGCCCTGT	CCAGGTAGAA	AAGAAATGGT	ATGTAGAGCT	TAGATTTCCC	2640
	TATTGTGACA	GAGCCATGGT	GTGTTGTGTA	TAATAAAACC	AAAGAAACAT	A	2691

Seq ID NO: C79 DNA Sequence
Nucleic Acid Accession #: NM_006536.2
Coding sequence: 109..2940

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	AGCATTCGAC	GTCCCTATTG	CAACCTGAAG	TTTGTGACTC	TCTGTGGTGC	CTTAAGTTCA	180
	GAACCTCCAT	TCTTGGGAGC	TGGAGTACAG	CTTCAAGACA	ATGGGTATAA	TGGATTGCTC	240
55	ATTGCAATTA	ATCCTCAGGT	ACCTGAGAAT	CAGAACCTCA	TCTCAACAT	TAAGGAAATG	300
	ATAACTGAAG	CTTCACTTTA	CCTATTTAAT	GCTACCAAGA	GAAGAGTATT	TTTCAGAAAT	360
	ATAAAGATTT	TAATACCTGC	CACATGGAAG	GCTAATAATA	ACAGCAAAAT	AAACAAAGAA	420
	TCATATGAAA	AGGCAAAATG	CATAGTGACT	GACTGGTATG	GGGCACATGG	AGATGATCCA	480
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	GGATGCACCT	TTATCTACAA	TAGCACCCAA	AATGCAACTG	CATCAATAAT	GTTCATGCAA	840
65	AGTTTATCTT	CTGTGGTTGA	ATTTTGTAA	GCAAGTACCC	ACACCAAGA	AGCACCAAAC	900
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	TTTACACACA	GCTTTCCCAT	GAATGGGACT	GAGCTTCCAC	CTCCTCCAC	ATTCCTGCTT	1020
	GTACAGGCTG	GTGACAAAGT	GGTCTGTTA	GTGCTGGATG	TGTCCAGCAA	GATGGCAGAG	1080
	GCTGACAGAC	TCCTTCAACT	ACAAACAAGCC	GCAGAAATTT	ATTGTATGCA	GATTGTTGAA	1140
70	ATTCAATCTT	TGTTGGGCAT	TGCCAGTTTC	GACAGCAAAG	GAGAGATCAG	AGCCAGGCTA	1200
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	TCTCTGCAAG	CCCTGAAAGT	GACAGTGACC	TCTCGCGCCT	CCAATCAGC	TGTGCCCCCA	1920
	GCCACTGTGG	AAGCCTTTGT	GGAAAGAGAG	AGCCTCCATT	TTCCTCATCC	TGTGATGATT	1980
	TATGCCAATG	TGAACACGGG	ATTTTATCCC	ATTCTTAATG	CCACTGTGAC	TGCCACAGTT	2040
	GAGCCAGAGA	CTGGAGATCC	TGTTACGCTG	AGACTCCTTG	ATGATGAGAC	AGGTGCTGAT	2100

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30 Seq ID NO: C80 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1413

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 40 ACATCTACCC TGGAGATGAT GCAAGCACCT CGATGTGGAG TCCCGATGT CCATCAITTC 300
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 GAGCCAAATT ATCCCAAGAG CATACATCTT TTTGGTTTTC CTAACCTTGT GAAAAAATTT 1140
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 60 ACACGAAAA GCAATAGCTG GTTTGGTTGT TGA 1413

Seq ID NO: C81 DNA Sequence
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 Coding sequence: 1..1413

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 70 AAGGAAAAAA TCCAAGAAAT GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC 240
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 75 GTGTTTITG CCGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC 540
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Seq ID NO: C82 DNA Sequence
 Nucleic Acid Accession #: NM_006952.1
 Coding sequence: 11..793

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Seq ID NO: C83 DNA Sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71..2560

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CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
TGGCGAGACA GTCCAGGAAA GAAGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCAA TATCTTCCC 420
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Seq ID NO: C84 DNA Sequence
 Nucleic Acid Accession #: NM_005629.1
 Coding sequence: 639..2546

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 CCGCCGCGCAC CACCGCCACC GAGTTCGCGG CCGAGCGCGG CAGCTTCGCG GGGCCCGCGC 180
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 15 CCGATGTGCG CCGCGCGCGG TTAGGATGAG TCTCGGGTGC GCGGAGGAGC GCGCGCAGCC 300
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 25 TCGCGCGCGG CCGCGCGCGG GCGCGCGCGG GCGCGCGCGG GCGCGCGCGG GCGCGCGCGG 900
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 ACATCATGGT GCTGGCTTGG GCGCTTCTAT ACCTGGTCAA GTCTTACTAC ACCACGCTGC 1140
 30 CCGCGCGCGG ATGTGGCCAC ACCTGGAAAC CTCCGACTG GCGCGCGCGG GCGCGCGCGG 1200
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 35 TCTGTGTCTG GAGGGGGTGC AAATCCACGG GAAAGATCGT GTACTTCACT GCTACATTCC 1440
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 40 ACAGTGGGAC CAGCTTCTTT GCTGGCTTGC TGGTCTTCTC CATCTGCGG TTCTATGGCTG 1740
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 45 GCGCTCTGGA CCGCGCGCGG GCGCTCTACT ACTTCCGTTT CCGCGCGCGG ATCTCTGTGG 1980
 CCGCTCTGTT TCGCGCGCGG TTTGTCTATG ATCTCTCCAT GGTGACTGAT GCGCGCGCGG 2040
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 65 TATAGATCTC TATCTCTTAG CAAAGGTGAA TGCCAGATGT AAATGGCGCC TCTGGGCAAA 3240
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80

Seq ID NO: C85 DNA Sequence
 Nucleic Acid Accession #: NM_006516.1
 Coding sequence: 180..1658

1 11 21 31 41 51
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5	GTCAAGATCG	CAGTGGGAGT	CCCCGGACCG	GAGCAAGAGC	CTGAGCGGGA	GAGCGCGGCT	120
	CGCAGCCCG	TGCCACCCG	CGTACCCGCG	GCAGCCAGAG	CCACCAGCGC	AGCGCTGCCA	180
	TGGAGCCCG	CAGCAAGAAG	CTGACGGGTC	GCCTCATGCT	GGCTGTGGGA	GGAGCAGTGC	240
	TTGGCTCCCT	GCAGTTTGGC	TACAACTG	GAGTCATCAA	TGCCCCCAG	AAGGTGATGC	300
	AGGAGTTCTA	CAACCAAGACA	TGGGTCCACC	GCTATGGGGA	GAGCATCTCG	CCCAACACGC	360
	TCACCACGCT	CTGGTCCCTC	TCAGTGGCCA	TCTTTTCTGT	TGGGGGCATG	ATTGGCTCCT	420
	TCTCTGTGGG	CCTTTTGGTT	AACCGCTTGG	GCGGGCGGAA	TTCAATGCTG	ATGATGAACC	480
	TGCTGGCCCT	CGTGTCCGCC	GTGCTCATGG	GCTTCTCGAA	ACTGGGCAAG	TCCTTTGAGA	540
10	TCGTGATCCT	GGGCCGCTTC	ATCATCGGTG	TGTACTGGCG	CCTGACCACA	GGCTCGTGCC	600
	CCATGTATGT	GGGTGAAGTG	TCACCCACAG	CCTTTCGTGG	GGCCCTGGGC	ACCCATGACC	660
	AGCTGGGCAT	CGTCGTGGGC	ATCCCTCATG	CCAGGTGTTT	CGGCTTGGAC	TCCATCATGG	720
	GCAACAAGGA	CCTGTGGCCC	CTGCTGCTGA	GCATCATCTT	CATCCGCGCC	CTGCTGCAGT	780
	GCATCGTGCT	GGCCTTCTGC	CCCGAGAGTC	CCCGCTTCTT	GCTCATCAAC	CGCAACGAGG	840
15	AGAACCGGGC	CAAGATGTGT	CTAAAGAAGC	TGCGCGGGAC	AGCTGACGTG	ACCCATGACC	900
	TGCAGGAGAT	GAAGGAAGAG	AGTCGGCAGA	TGATGCGGGA	GAAGAAGGTC	ACCATCTCTG	960
	AGCTGTTCGG	CTCCCGCGCC	TACCGCCAGC	CCATCTCAT	CGCTGTGGTG	CTGCAGCTGT	1020
	CCCAGCAGCT	GTCCTGGCATC	AAOGCTGTCT	TCTATTACTC	CACGAGCATC	TTGAGAAGG	1080
	CGGGGGTGCA	CGAGCCTGTG	TATGCCACCA	TTGGCTCGCG	TATCGTCAAC	ACGGCTTCA	1140
20	CTGTCTGTGT	CGTGTGTGTG	GTGGAGCGAG	CAGGCCGGCG	GACCTGACAC	CTCATAGGCC	1200
	TCGCTGGCAT	GGCGGGTGTG	GCCATACTCA	TGACCATCGC	GCTAGCACTG	CTGGAGCAGC	1260
	TACCTCGGAT	GTCTTATCTG	AGCATCGTGG	CCATCTTTGG	CTTTGTGGCC	TTCTTTGAAG	1320
	TGGGTCTCGG	CCCCAGCCCC	TGGTTTCATG	TGGCTGAAC	CTTCAGCCAG	GGTCCACGTC	1380
	CAGCTGCCAT	TGCGGTGCA	GGCTTCTCCA	ACTGGACCTC	AAATTTCAAT	GTGGGCATGT	1440
25	GCTTCCAGTA	TGTGGAGCAA	CTGTGTGTGT	CCTACGTCTT	CATCATCTTC	ACTGTGCTCC	1500
	TGGTTCTGTT	CTTCACTCTC	ACCTACTTCA	AAGTTCTTGA	GACTAAAGGC	CGGACCTTGG	1560
	ATGAGATCGC	TTCCGGCTTC	CGGCAGGGGG	GAGCCAGCCA	AAGTGAATAAG	ACACCGGAGG	1620
	AGCTGTTCCT	TCCCGTGGGG	GCTGATTCCC	AAGTGTGAGT	CGCCCCAGAT	CACGAGCCCG	1680
	GCCTGTCTCC	AGCAGCCCTA	AGGATCTCTC	AGGAGCACAG	GCAGCTGGAT	GAGACTTCCA	1740
30	AACCTGACAG	ATGTCAGCCG	AGCCGGGCGT	GGGGCTCCTT	TCTCCAGCCA	GCAATGATGT	1800
	CCAGAAGAT	ATTCAGGACT	TAACGGCTCC	AGGATTTTAA	CAAAAGCAAG	ACTGTTGCTC	1860
	AAATCTATTC	AGACAGCAAA	CAGGTTTAT	AAATTTTATA	TACTGATTT	TGTTATTTT	1920
	ATATCAGCCT	GAGTCTCTGT	TGCCACATC	CCAGGCTTCA	CCCTGAATGG	TTCCATGCGT	1980
	GAGGGTGAG	ACTAAGCCCT	GTCGAGACAC	TTGCCTTCTT	CACCCAGCTA	ATCTGTAGGG	2040
35	CTGGACCTAT	GTCTTAAGGA	CACACTAATC	GAATATGAA	CTACAAAGCT	TCTATCCCAG	2100
	GAGGTGGCTA	TGGCCACCGG	TTCTGCTGGC	CTGGATCTCC	CCACTCTAGG	GGTCAGGCTC	2160
	CATTAGAGTT	TGCCCTTCCC	CATCTCTTCC	TACCCAAACCA	CTCAAATTA	TCTTTCTTTA	2220
	CCTGAGACCA	TTGGGAGGCA	CTGGAGTGCA	GGGAGGAGAG	GGGAAGGGCC	AGTCTGGGCT	2280
	GGCGGGTCT	AGTCTCTCTT	GCACTGAGGG	CCACACTATT	ACCATGAGAA	GAGGGCTGT	2340
40	GGGAGCCTGC	AAACTCACTG	CTCAAGAAGA	CATGGAGACT	CCTGCCCTGT	TGTGTATAGA	2400
	TGCAAGATAT	TTATATATAT	TTTGGTTGT	CAATATTAA	TACAGACACT	AAGTTATAGT	2460
	ATATCTGGAG	AAGCCAACTT	GTAATATAC	CACCTCACTC	CTGTTACTTA	CCTAAACAGA	2520
	TATAAATGGT	TGGTTTATAG	AAACATGGTT	TTGAATGCT	TGTGGATTGA	GGGTAGGAGG	2580
	TTTGGATGGG	AGTGAGACAG	AAGTAAGTGG	GGTTGCAACC	ACTGCAACGG	CTTAGACTTC	2640
45	GACTCAGGAT	CCAGTCCCTT	ACACGTACCT	CTCATCAGTG	TCCTCTTGCT	CAAAAATCTG	2700
	TTGATCCCT	GTTATCCAGA	GAATATATAC	ATTCTTTATC	TTGACATTCA	AGGCATTCTC	2760
	ATCACAATAT	TGATAGTTGG	TGTTCAAAAA	AACACTAGTT	TTGTGCCAGC	CGTGATGCTC	2820
	AGGCTTGAAA	TCGCATTATT	TTGAATGTGA	AGGGAA			2856

Seq ID NO: C86 DNA Sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53..1576

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	TGCGGGCCCG	AAGCGCGCGG	CGCTAGCGGC	GCOCGCGGCC	GAGGAGAAGG	AAGAGGCGCG	120
	GGAGAAGATG	CTGGCCGCCA	AGAGCGCGGA	CGGCTCGGCG	CCGGCAGGCG	AGGGCGAGGG	180
	CGTGACCCCTG	CAGCGGAACA	TCACGCTGCT	CAACGGCGTG	GCCATCATCG	TGGGGACCAT	240
60	TATCGGCTCG	GGCATCTTCG	TGACGCCAC	GGCGTGCTC	AAGGAGGCAG	GCTCGCGGG	300
	GCTGGCGCTG	GTGGTGTGGG	CGCGTGGCG	CGTCTTCTCC	ATCGTGGGCG	CGCTCTGCTA	360
	CGCGGAGCTC	GGCACCACCA	TCTCCAAATC	GGCGCGGAC	TACGCTTACA	TGCTGGAGGT	420
	CTACGGCTCG	CTGCCCGCCT	TCTCAAGCT	CTGGATCGAG	CTGCTCATCA	TCGGGCTTTC	480
	ATCGCAGTAC	ATCGTGGCCC	TGGTCTTCGC	CACCTACCTG	CTCAAGCGCG	TCTTCCOCAC	540
65	CTGCCCGGTG	CCCGAGGAGG	CAGCCAAGCT	CGTGGCTGCG	CTCTGCGTGC	TGCTGTCTAC	600
	GGCCGTGAAC	TGCTACAGCG	TGAAGGCGCG	CACCCGGGTC	CAGGATGCTC	TTGCCGCGCG	660
	CAAGCTCCTG	GGCCTGGCCC	TGATCATCCT	GCTGGGCTTC	GTCCAGATCG	GAAAGGGTGA	720
	TGTGTCCAAAT	CTAGATCCCA	ACTTCTCAT	TGAAGGCACC	AAACTGGATG	TGGGGAACAT	780
	TGTGTGGCA	TTATACAGCG	GCTCTTTGCG	CTATGGAGGA	TGGAATTACT	TGAATTTGCT	840
70	CACAGAGGAA	ATGATCAACC	CCTACAGAAA	CCTGCCCTCG	GCCATCATCA	TCTCCCTGCC	900
	CATCGTGACG	CTGGTGTACG	TGCTGACCAA	CCTGGCCTAC	TTACCAACCC	TGTCCACCGA	960
	GCAGATGCTG	TCGTCCGAGG	CGTGGCCGT	GGACTTGGGG	AACTATCACC	TGGGCGTCAT	1020
	GTCTGGATTC	ATCCCGCTCT	TCGTGGGCTT	GTCTCTGCTC	GGCTCCGCTG	ATGGGTCCCT	1080
	GTTCACTCCC	TCAGGCTCT	TCTTGTGGG	GTCCCGGGA	GGCCACCTGC	CCTCCATCCT	1140
75	CTCCATGATC	CACCCACAGC	TCCTCACCCC	CGTGCCTGCC	CTCGTGTTC	CGTGTGTGAT	1200
	GAGCTGTCTC	TACGCTTCT	CCAAGGACAT	CTTCTCGTTC	ATCACTTCTT	TCAGCTTCTT	1260
	CAACTGTCTG	TGCGTGGCCC	TGGCCATCAT	CGGCATGATC	TGGCTGCGCC	ACAGAAAGCC	1320
	TGAGCTTGAG	CGGCCCATCA	AGGTGAACCT	GGCCCTGCCT	GTGTTCTTCA	TCTTGGCCTG	1380
	CCTCTTCCCTG	ATCGCGTCT	CCTTCTGGAA	GACACCGGTG	GAGTGTGGCA	TCGGCTTCTC	1440
80	CATCATCTCT	AGCGGCTGCG	CCGTCTACTT	CTTCGGGGTC	TGGTGGAAAA	ACAAGCCCAA	1500
	GTGGCTCTCT	CAGGGCATCT	TCTCCAGGAC	CGTCTGTGTT	CAGAAGCTCA	TGCAGGTGGT	1560
	CCCCAGGAG	ACATAGCCAG	GAGGCGGAGT	GGCTGCCGGA	GGAGCATGC		1609

Seq ID NO: C87 DNA Sequence
Nucleic Acid Accession #: NM_005268.1

Coding sequence: 168..989

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AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGGGTGG GTCCACCATG AACTGGAGTA 180
TCTTTGAGGG ACTCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
TGCTCTGGGT CTTCATCTTC CGGTGCTGG TGTACCTGGT GACGGCGAG CGTGTGTGGA 300
10     GTGATGACCA CAAGGACTTC GACTGCAATA CTGCCAGCC CGGCTGCTCC AACGCTGTCT 360
TTGATGAGTT CTTCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA 420
CATGCCCTC ACTGTCTGTG GTCATGCACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
ACCGAGAAGC CCATGGGAGG AACAGTGGGC GCCTCTACCT GAACCCCGG GAGAAGCGGG 540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GCGAGGGTG GACATCGCCT 600
15     TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCCTCCTGTG GTCAAGTGCC 660
ACGCAGATCC ATGTCCCAAT ATAGTGACTT GCTTCATCTC CAAGCCCTCA GAGAAGAAC 720
TTTTCACTCT TTTCATGTGTG GCCACAGCTG CCATCTGCACT CTGCTCAAC CTGCTGGAGC 780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCTGGC AGCAAGGAAA GCTCAAGCCA 840
20     TGTGCACAGG TCATCACCCC CAGGTACCA CCTCTTCTCG CAAACAAGAC GACCTCCTTT 900
CGGGTGACCT CATCTTCTTG GGCTCAGACA GTCATCTCTC TCTCTTACCA GACGCGCCCC 960
GAGACCATGT GAAGAAAACC ATCTTGAGAG GGGCTGCCTG GACTGTGCTG GCAGGTTGGG 1020
CTGAGGAGAG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCTAGTCC 1140
25     TCAACTCCAG CCACCTGCCC CAGCTGACG GCACTGGGCC AGTTCCCCCT CTGCTCTGCA 1200
GCTCGGTTTC CTTTCTAGA ATGGAATAG TGAGGGCCAA TGC 1243
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Seq ID NO: C88 DNA Sequence

Nucleic Acid Accession #: NM_005130

Coding sequence: 98..802

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CGTGTGCTCA GAACAAGGTG AACGCCACGC TGACGCCATG AAGATCTGTA GCCTCACCTT 120
GCTCTCCTTC CTCCTACTGG CTGCTCAGGT GCTCCTGGTG GAGGGGAAAA AAAAAAGTGA 180
GAATGGACTT CACAGCAAGG TGGTCTCAGA ACAAAGGAC ACTCTGGGCA ACACCCAGAT 240
TAAGCAGAAA AGCAGGCCCG GGAACAAAGG CAAGTTTGTC ACCAAGACC AAGCCAACTG 300
CAGATGGGCT GCTACTGAGC AGGAGGAGGG CATCTCTCTC AAGGTTGAGT GCACTCAATT 360
GGACCATGAA TTTTCTGTG TCTTTGCTGG CAATCCAAAC TCATGCTTAA AGCTCAAGGA 420
TGAGAGATCT TATTGGAAAC AAGTTGCCCG GAATCTGCGC TCACAGAAAG ACATCTGTAG 480
ATATTCCAAG ACAGCTGTGA AAACCAAGAT GTGCAGAAAG GATTTTCCAG AATCCAGTCT 540
TAAGCTAGTC AGCTCCACTC TATTGGGAAA CACAAGCCC AGGAAGGAGA AAACAGAGAT 600
GTCCCCCAGG GAGCAGATCA AGGGCAAAGA GACCACCCCT TCTAGCTTAG CAGTGACCCA 660
GACCATGGCC ACCAAAGCTC CCGAGTGTGT GGAGGACCCA GATATGGCAA ACCAGAGGAA 720
45     GACTGCCCTG GAGTTCTGTG GAGAGACTTG GAGCTCTCTC TGCACTTCT TCTCAGCAT 780
AGTGCAGCAG ACCTCATGCT AATGAGGTCA AAAGAGAACG GGTTCCTTTA AGAGATGTCA 840
TGTCGTAAGT CCCTCTGTAT ACTTTAAAGC TCTCTACAGT CCCCCCAAAA TATGAACCTT 900
TGTCGTAGT GAGTGCACAG AATATTTTAA ACAAGTTTTC TATTTTTCG TTTTGTGTTT 960
50     TGGAATTTGC CTATTTTTC TTGGATGCGA TGTTTCAGAG CTGTTTCTCG CAGCATGTAT 1020
TTCCATGGCC CACACAGCTA TGTGTTTGG CAGCGAAGAG TCTTTGAGCT GAATGAGCCA 1080
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Seq ID NO: C89 DNA Sequence

Nucleic Acid Accession #: BC022542

Coding sequence: 274..927

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TGGCGGCTCG GTTGGCGGGG GTTGGGCGGG CCGCTCTGGT GCTCCTGGG GCGCGCACGG 180
GGCTCACGCG CGGCGCCCGC ACGGCCTTCA CCGCGCGCGC CTCTGAAGCC GGCATAAGGG 240
65     CCATGTGTTC TGAATTTATT TTGAGGCAAG AAGTTTGTAA AGATGGTTTC CACAGAGACC 300
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TTAAACAGGA CATTCCTGCA GGACTTTATG TGGATCOGTA TGAGTTGGCT TCATTAGGAG 420
AGAGAAACAT AACAGAGGCA GTGATGTTT CAGAAAAATT TGATATAGAG GCCCTAACT 480
ATTGTGCCAA GGAGTCTGAA GTTCTCATT ATGCCAGACG AGATTTCAG TGCAATTGACT 540
70     GTTTTCAAGC CTTTTTCCT GTGCACTGCC GCTATCATCG GCGGCACAGT GAAGATGGAG 600
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TTTGTGAATG CTGGGCTTAC TCAGAAGTGG CAGCCCTTGG TGCTTTGGAT AATGAGGATA 720
TATGCCAATG GAACAAGATG AAGTATAAAT CAGTATATAA GAATGTGATT CTACAAGTTC 780
CAGTGGGACT GACTGTACAT ACCTCTCTAG TATGTTCTGT GACTCTGCTC ATTACAATCC 840
75     TGTGCTCTAC ATTGATCCTT GTAGCAGTTT TCAAAATAGG CCATTTTTC CTATAAGTTT 900
TATGTAGTTA AATGCTTCTT AGAAACCTAA ATAAGATCTA TTAATTTCTG ACGAGAGGTG 960
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TAGAGGAAAT TTGGGATCAT TCTCAGCTAA TTCCAAAATG TAGTGTCTTA TTGCATGGAT 1080
80     CCTTGGTAAT CCAAGCAT CAGATGCCAT AAGGGGAAAC TTAATTCCTG TAAATTAATG 1140
TTTATTTTGT GAGAAGTGAC TTTATCTTCA TTTGGGCTAG AAAAATTAT TCTTTATGTA 1200
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TTTGGGAGGC CGAGGTGGGC GGATCACCAG AGGTCAAGAG TTTGAGACCA GCTTGGTGAA 1380
ACCTGTCTCT TACTAAAAAT ACAAAAGTTA GCTGGGCTG GTGGTGGCA TCTGTAGTCC 1440
CAGCTAATTG GAAGGGTGGG GCGGAGGAT CGCTTGAACC TGGGAGGCG AGGTTCCAGA 1500
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GAGCCAAGAT CGCACCACCTG CACTACAGCC TGGGCGACAG AAGAGACCC TGTCTCCAAA 1560
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ATGTCATGAG ACTATTAAAG ATGTGCCAGA GTTTCATAGA AAATCATTAA AGTAGGACAG 1680
CTAAGAAATT AATATTAAATA TAAAAATTAT TGATAATCTT AAATTATTGA TTATTCCTTA 1740
AGCACTCCA TTCTCCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA 1800
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Seq ID NO: C90 DNA Sequence
Nucleic Acid Accession #: NM_004994
Coding sequence: 20..2143

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CCTGAGAAC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA 180
CACTCGGGTG GCAGAGATGC GTGGAGAGTC GAAATCTCTG GGGCTGCGC TGCTGCTTCT 240
CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT 300
GGGAACCCCA CGGTGCGGGG TCCAGACCTT GGGCAGATT CAAACCTTTG AGGGCGACCT 360
CAAGTGGCAC CACCAACAAC TCACCTATTG GATCCAAAC TACTCGGAAG ACTTCCCGCG 420
GGCGTGATT GACGACGCTT TTGCCCGCGC CTTCGCACTG TGGAGCGGGG TGACGCGGCT 480
CACTTCACT CGGTGTGACA GCGGGGACGC AGACATCGTC ATCCAGTTTG GTGTGCGGGA 540
GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACAGC CCTTTCCTCC 600
TGGCCCCGGC ATTACGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA 660
GGGCGTCTGT GTTCCAACTC GGTTTGGAAG CGCAGATGGC GCGGCTGCGC ACTTCCCTCT 720
CATCTTCGAG GCGCTCTCT ACTCTGCTGT CACCACGAC GGTGCTTCCG ACGCTTGGC 780
CTGTGTCAGT ACCACGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCCAGCGA 840
GAGACTCTAC ACCCGGGACG GCAATGCTGA TGGGAAACCC TGCCAGTTTC CATTCATCTT 900
CCAAGGCCAA TCTACTCCG CCTGCACCC GGAAGGTGCG TCCGACGGCT ACGCTGGTG 960
CGCCACACCC GCGCACTACG ACCGGGACAA GCTCTTCCGC TTCTGCGCGA CCGAGCTGA 1020
CTGACGGTG ATGGGGGCA ACTCGGCGG GAGCTGTGCT GTCTTCCCT TCACTTTCCT 1080
GGTAAGGAG TACTCGACCT GTACGACGCA GGGCGCGGGA GATGGGCGCC TCTGGTGGC 1140
TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG 1200
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Coding sequence: 188.5656

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Seq ID NO: C96 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1_4247

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Nucleic Acid Accession #: XM_031379
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Nucleic Acid Accession #: NM_002851
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 TGGGAGATTT TCACCTATGG CAACAGCCCG TGGTACCAGC TGTCAACAA TGAGGTGATA 2640
 GAGTGTATCA CTCAGGGCCG AGTCTGCGAG CGACCCCGCA CGTGCCCGCA GGAGGTGTAT 2700
 GAGCTGATGC TGGGGTCTGT GCAGCGAGAG CCCCACATGA GGAAGAACAT CAAGGGCATC 2760
 CATACCTCC TTCAGAACTT GGCCAAGSCA TCTCGGTCT ACCTGGACAT TCTAGGCTAG 2820
 GGCCCTTTTC CCCAGACGGA TCCCTCCCAA CGTACTCTCT AGACGGGCTG AGAGGATGAA 2880
 CATCTTTTAA CTGCGCGCTG AGGCCACCAA GCTGCTCTCC TTCACTCTGA CAGTATTAA 2940
 ATCAAAGACT CCGAGAAGCT CTGAGGGGAA GCACTGTGTA CTCTTCTATC CATAGACACA 3000
 GTATTGACTT CTTTGTGGCA TTATCTCTTT CTCTCTTTCC ATCTCCCTTG GTTGTCTCTT 3060
 TTTCTTTTTT TAAATTTTCT TTTTCTTCTT TTTTCTGCTC TTCCCTGCTT CACGATTCTT 3120
 ACCCTTCTCT TTGAATCAAT CTGGCTTCTG CATTACTATT AACTCTGCAT AGACAAAGGC 3180
 CTTAACAAC GTAATTTGTT ATATCAGCAG ACACCTCAGT TTGCCACCA CAACTAACAA 3240
 TGCCCTGTGT TATTCCTGCC TTTGATGTGG ATGAAAAA GGGAAAAA ATATTTCAT 3300
 TAAACTTGT CACTTCTGCT GTACAGATAT CGAGAGTTTC TATGATTCA CTCTATTATA 3360
 TTTATTATTA TTACTGTTCT TATTGTTTTT GGATGGCTTA AGCCTGTGTA TAAAAAGAA 3420
 AACTTGTGTT CAATCTGTGA AGCCTTTATC TATGGGAGAT TAAACCAGA GAGAAAGAA 3480
 ATTTATTATG AACGCAATA TGGGAGGAAC AAAGACAACC ACTGGGATCA GCTGGTGTCA 3540
 GTCCCTACTT AGGAAATACT CAGCAACTGT TAGCTGGGAA GAATGTATTG GGCACCTTCC 3600
 CCTGAGGACC TTTCTAGGGA GTAAAAAGAC TACTGGCCTC TGTGCCATGG ATGATTCTTT 3660
 TCCATCACC AGAATGATA GCGTGCAGTA GAGAGCAAG ATGGCTT 3707

Seq ID NO: C110 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 939..2372

1 11 21 31 41 51

	AAGACGGATT	CTCAGACAAG	GCTTGCAAAT	GCCCCGCAGC	CATCATTTAA	CTGCACCCGC	60
	AGAATAGTTA	CGGTTTGTCA	CCCGACCCCT	CCGGATCGCC	TAATTGTGCC	CTAGTGAGAC	120
5	CCCGAGGCTC	TGCCCGCGCC	TGGCTTCTTC	GTAGCTGGAT	GCATATCGTG	CTCCGGGCAG	180
	CGCGGGCGCA	GGGCAOCCGT	TGCGCACAC	CCTAGCACAC	ATGAACACGC	GCAAGAGCTG	240
	AACCAAGCAC	GGTTTCCATT	TCAAAAAGGG	AGACAGCCTC	TACCGCGATT	GTAGAAGAGA	300
	CTGTGGTGTG	AATTAGGGAC	CGGGAGGGGT	OGAACGGAGG	AAOGGTTTAT	CTTAGAGACT	360
	AATTTCTCGG	AGTTTCTGCC	CCTGCTCTGC	GTACAGCCCTC	ACGTCACTTC	GCCAGCAGTA	420
10	GCAGAGGCGG	CGGCGGCGGC	TCCCGGAAAT	GGTTTGGAGC	AGGAGCCTCG	CTGGCTGCTT	480
	CGCTCGCGCT	CTACGCGCTC	AGTCCCGGCG	GGTAGCAGGA	GCCTGGACCC	AGGCGCCGCC	540
	GGCGGGCGTG	AGGGCGCGGA	GCCCGGCCCT	GAGGTGCATA	CCGGACCCCC	ATTOGCATCT	600
	AACAAGGAAT	CTGCGCCCCA	GAGAGTCCCG	GGAGCGCCGC	CGTCCGGTGC	CCGGCGCGCC	660
	GGGCCATGCA	GCGACGCGCG	CCGCGGAGCT	CCGAGCAGCG	GTAGCGCCCC	CCTGTAAAGC	720
	GGTTGCGTAT	GCGGGGCCCA	CTGTGAACCC	TGCGCCTGCG	CGGAACACTC	TTGCTCCGGG	780
15	ACCAGCTCAG	CCTCTGATAA	GCTGGACTCG	GCACGCCCGC	AACAAGCACC	GAGGAGTTAA	840
	GAGAGCCGCA	AGCGCAGGGA	AGGCCCTCCC	GCACGGGTGG	GGGAAAGCGG	CCGGTGCAGC	900
	GCGGGGATAC	GCAGCTGGGC	TGGCACTGGC	TGCTAGGGAT	GTGCTCTTGG	ATAAGGTGGC	960
	ATGGACCCCG	CATGGCGCGG	CTCTGGGGCT	TCTGCTGGCT	GGTTGTGGGC	TTCTGGAGGG	1020
	CCGCTTTTGC	CTGTCCCAAG	TCCTGCAAAAT	GCAGTGCCTC	TCGGATCTGG	TGCAGCGACC	1080
20	CTTCTCTCGG	CATCGTGGCA	TTTCCGAGAT	TGGAGCCTAA	CAGTGTAGAT	CCTGAGAACA	1140
	TCACCGAAAT	TTTCACTGCA	AACCCAGAAA	GGTTAGAAAT	CATCAACGAA	GATGATGTTG	1200
	AAGCTTATGT	GCGACTGAGA	AATCTGACAA	TTGTGGATTG	TGGATTAAAA	TTTGTGGCTC	1260
	ATAAAGCATT	TCTGAAAAAC	AGCAACCTGC	AGCACATCAA	TTTACCCGA	AACAACTGA	1320
25	CGAGTTTGTC	TAGGAAACAT	TTCCGTCAAC	TTGACTTGTC	TGAACCTGATC	CTGGTGGGCA	1380
	ATCCATTAC	ATGCTCTCTG	GACATTATGT	GGATCAAGAC	TCTCCAAGAG	GCTAAATCCA	1440
	GTCCAGACAC	TCAGGATTGG	TACTGCCTGA	ATGAAAGCAG	CAAGAAATAT	CCCTTGGCAA	1500
	ACCTGCAATG	ACCCAAATGT	GGTTTGGCAT	CTGCAAACTC	GGCCGCACTC	AACCTCACTG	1560
	TGGAGGAAGG	AAAGTCTATC	ACATTATCTC	GTAGTGTGGC	AGGTGATCCG	GTTCCTAATA	1620
30	TGTATTGGGA	TGTTGGTAAC	CTGGTTTCCA	AACATATGAA	TGAAACAAGC	CACACACAGG	1680
	GCTCCTTAAG	GATAACTAAC	ATTTCACTCG	ATGACAGTGG	GAGCAGATC	TCTTGTGTGG	1740
	CGGAAATCT	TGTAGGAGAA	GATCAAGATT	CTGTCAACCT	CACGTGTGAT	TTTGCAACCA	1800
	CTATCACTAT	TCTCGAATCT	CCAACTCAG	ACCACTCAG	GTGCATTCCA	TTCACTGTGA	1860
	AAGGCAACCC	CAAACCCAGC	CTTCAGTGGT	TCTATAACGG	GGCAATATTG	AATGAGTCCA	1920
35	AATACATCTG	TACTAAAATA	CATGTTACCA	ATCACAAGGA	GTACCAAGCG	TGCCTCCAGC	1980
	TGGATAATCC	GACTCACATG	AACAATGGGG	ACTCACTCT	AATAGCCAA	AATGAGTATG	2040
	GGAAAGGATG	GAAACAGATT	TCTGCTCACT	TCACTGGGCTG	GCCTGGAATT	GACGATGGTG	2100
	CAAAACCCAA	TATCTCTGAT	GTAATTATG	AAGATTATGG	AACCTGCAGCG	AATGACATCG	2160
	GGGACACCAC	GAACAGAAGT	AATGAAATCC	CTTCCACAGA	CGTCACTGAT	AAAAACGGTC	2220
40	GGGAACATCT	CTCGTCTCTG	GCTGTGGTGG	TGATTGGGTC	TGTGGTGGGA	TTTGTGCTTT	2280
	TGGTAATGCT	TTTCTGCTTT	AAGTTGGCAA	GACACTCCAA	GTTTGGCATG	AAAGGTTTTG	2340
	TTTTGTTC	TAAATCCCA	CTGGATGGGT	AGCTGAAATA	AAGGAAAGA	CAGAGAAAGG	2400
	GGCTGTGGTG	CTGTGTGGTT	GATGCTGCCA	TGTAAGCTGG	ACTCCTGGGA	CTGCTGTTGG	2460
	CTTATCCCGG	GAAATGGCTG	TTTCTGGGG	TTTCTGGTA	GATGTGGGCG	GTGTTTGGAG	2520
45	GCTGTACTAT	ATGAAGCCTG	CATATACTGT	GAGCTGTGAT	TGGGAACAC	CAATGCAGAG	2580
	GTAACCTCCA	GGCAGCTAAG	CAGCACTCA	AGAAACATG	TAAATTAAT	GCTTCTCTTC	2640
	TTACAGTAGT	TCAAATACAA	AACTGAAATG	AAATCCCAIT	GGATTGTACT	TCTCTCTGTA	2700
	AAAGTGTGCT	TTTTGACCOCT	ACTGGACATT	TATTGACTTA	ATTGCTTCTG	TTTATTAATA	2760
	TTGACCTGCA	AAGTTAAAAA	AAAATTAAAG	TTGAGAACAG	GTATAAGTGC	ACACTGAATA	2820
50	GTCTAATCTA	CATGTAAAC	ATATTTTAGT	GTGATTTTCT	ATACTCTAAT	CAGCACTGAA	2880
	TTCAAGGGGT	GTTTCTGAT	CATCTATAAC	ACAGTGACTA	AAAGAGTTAA	GGGTATATAT	2940
	ACCATCACTT	TGGGACTTGG	TAGTATTATT	AAAAGGTTAT	TTCTTCACT	GTCAATAAAA	3000
	GTCCAAATGT	TTAGCTTAGG	TCTGAGAGTC	AAACAATGTT	AAGGATTGTC	TTAAAGTTCC	3060
	TTAGCCAGCA	AAACAAAACA	AAACAAATGAA	AAAGCTTTAA	AAAGAGAAAG		3120
	AAAGAAAAAA	ACAGAAACAA	GCAGCAACAG	CTGTTTGTGT	GGGGCTATAG	ATTAAAGTTA	3180
55	GGCATAGTCA	ATTTCAAGAT	AACTAAGAGT	GGAATATATG	CATATGGTGA	AATTATAACC	3240
	TTGCCCTTTT	TTATTGCCCC	TCTGGGATCC	ACCTGCTTTT	TAGAAGTCTG	CCGAGTGAGA	3300
	AGGCACAGT	ATCTCATGCT	GTTTGCATTA	CAGAACTGCA	GCTTTTCTAC	TCTGAAAAGG	3360
	CCTGGGAGCA	GAAATGGCTG	CCTGCTGTGA	GCAGGAGAGG	AGATTCTAAG	AAGGATAGTC	3420
60	CCCCCTACAA	CATACTGTCA	TACTGCTGGG	TTTTCATGGG	TAGGAAAGCT	TGTOCTGACC	3480
	CCAGCAGCAA	AGAGGTGGCA	GGTGGCTAAT	GAATATATGC	TTTATAATGT	CCTTCTTCAT	3540
	TGCTGAGAGG	GCAGCCTTAG	AGCTGTGGAT	TTCTGCATCC	CCCTGAGTC	TGACCCATGG	3600
	ACACCTGTGT	CATTCACTTT	AGCATCACAG	TGACCTTTGT	ATGCTCTGTT	CAGTCTGTGT	3660
	CAGGCAGTAT	GCTTGTCTGT	AAGAGAGGTT	TGGCTATCCC	CACCCACACC	CACCCACACC	3720
	TGTTCCCTTT	TTATCAGGAG	GACTTCAGAG	CCAGGCCTGC	AGCATTTTGT	TTGAAAACAC	3780
65	AATCAGCTCT	GACAGTTAGA	CATGCACACA	GACGCCATAG	CTGGATTGGA	AACATTGATG	3840
	TTTTAAAAAT	TTATTTTTTT	TGGAAATAGT	TGCACAAATG	CTGCAATTTA	GCTTTAAGGT	3900
	TCTATAGATT	TTTAAGTAGT	CCAACACAGT	CAGAAACATT	GTTTGAATC	CTCTGTAATC	3960
	CAAGGCATTA	ATCTTAATAA	ACCAGGATCC	ATTTAGGTAC	CACCTGATAT	AAAAAGGATA	4020
70	TCCATAATGA	ATATTTTATA	CTGCATCCTT	TACATTAGCC	ACTAAATAG	TTATTGCTTG	4080
	ATGAAGACCT	TTACAGAAAT	CCTATGGATT	GCAGCAATTC	ACTTGGCTAC	TTTATACCCA	4140
	TGCCCTTAAG	AGGGGCGAGT	TCTCAAAAGC	AGAAACATGC	CGCCAGTTCT	CAAGTTTTTC	4200
	TCTCAACTCC	ATTGTAATGT	AAGGGCAGCT	GGCCCCCAAT	GTGGGGAGGT	CCGAACATTT	4260
	TCTGAATCCC	CATTCTCTGT	TTCGGGGCTA	AATGACAGTT	TCTGTCTATA	CTTAGATTCC	4320
75	GATCTTTCCC	AAAGGTGTGT	ATTTACAAAG	AGGCCAGCTA	ATAGCAGAAA	TCATGACCCCT	4380
	GAAAGAGAGA	TGAAATTCRA	GCTGTGAGCC	AGGCAGGAGC	TCAGTATGGC	AAAGGTTCTT	4440
	GAGAATCAGC	CATTGTGTAC	AAAAAAGATT	TTTAAAGCTT	TTATGTTATA	CCATGGAGCC	4500
	ATAGAAAGGC	TATGGATTGT	TTAAGAACTA	TTTAAAGTGT	TTCCAGACCC	AAAAAGGAAA	4560
	AATAAAAAAA	AAGGAATATT	TGTACCCAAC	AGCTAGAAGG	ATTGCAAGGT	AGATTTTGTG	4620
80	TTTAAATGGA	AGAGAAGTGG	ACAGATAAGG	CCATTTAATA	TATCAAGAT	CAGTTGACAT	4680
	CTCCTAGGGA	ATGATGAAAA	CAGCAGGCTA	T			4711

Seq ID NO: C11 DNA Sequence
Nucleic Acid Accession #: NM_130830.1
Coding sequence: 1..1746

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	GCCTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCCAGGT	GGAGTGCACC	120
	GGGGCACGCA	TTGTGGGGT	GCCCAACCCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
	CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCCCGGTTCC	TCAATATCTC	AGCCCTCATC	240
	GCCCTGAGGA	TTGAGAAGAA	TGAGCTGTGC	GGCATCACGC	CTGGGGCCCT	CCGAAACCTG	300
10	GGCTCGCTGC	GCTATCTCAG	CCTGGCCAAC	AACAAGCTGC	AGGTTCTGCC	CATCGGCCTC	360
	TTCCAGGGCC	TGACAGAGCT	TGAGTCTCTC	CTTCTGTCCA	GTAACAGCT	GTTCGAGATC	420
	CAGCCGGCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCA	480
	CTGGAATACA	TCCTGACCG	AGCCTTCGAC	CACCTGGTAG	GACTCACGAA	GCTCAATCTG	540
	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
15	GTCTCTCGGC	TGTATGAGAA	CAGGCTCAGC	GATATCCCCA	TGGGCACTTT	TGATGGGCTT	660
	GTTAACCTGC	AGGAACCTGC	TCTACAGCAG	AACCAGATTG	GACTGCTCTC	CCCTGGTCTC	720
	TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCAAT	CTCCACAGCT	780
	CCACCCAGCA	TCCTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTCGGG	CCCATGCCCC	ACCTGCGGGA	GCTTTGGCTC	900
20	TATGACAACC	ACATCTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTGTATTC	TTAGCCGCAA	TCAGATCAGC	TTTACTCTCC	CGGGTGCCCT	CAACGGGCTA	1020
	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AAAGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
	TTCCGCTATG	TGGCCAACTT	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCCTGCCCAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAACCA	1200
25	CTGGAGAATC	TGCCCTCGGG	CATCTTCGAT	CACCTGGGGA	AATGTGTGTA	GCTGGGCTG	1260
	TATGACAATC	CCTGGAGGTG	TGACTCAGAC	ATCCTTCCCG	TCCGCAACTG	GCTCCTGCTC	1320
	AACCAGCCTA	GGTTAGGGAC	GSACACTGTA	CCTGTGTGTT	TCAGCCCGAC	CAATGTCCGA	1380
	GGCCAGTCCC	TCATTATCAT	CAATGTCAAC	GTTCGTGTTT	CAAGCGTCCA	TGTCCTGAG	1440
	GTGCTTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
30	TCCGTCTCTT	CTCAACTGTA	GCTAACCAGC	CCTGTGGAAG	ACTACACTGA	TCTGACTACC	1560
	ATTGAGGTCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCAGAG	CGGGCTGGCC	1620
	ATTGCCGCCA	TTGTAATTGG	CATGTGCGCC	CTGGCCCTGT	CCCTGGCTGC	CTGCGTGGC	1680
	TGTTGCTGCT	GCAAGAAGAG	GAGCCAAAGT	GTCTGATGTC	AGATGAAGGC	ACCCAATGAG	1740
	TGTTAA						1746

Seq ID NO: C112 DNA Sequence
Nucleic Acid Accession #: NM_002658.1
Coding sequence: 77..1372

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40	GTCCCCGCG	CGCCGTCGGG	CCCTCTGCCC	GCAGGCCACC	GAGGCGCGCG	CCGTCTAGCG	60
	CCCGACCTTC	GCCACCATGA	GAGCCCTGCT	GGCGCGCCTG	CTTCTCTGCG	TCCTGGTCGT	120
	GAGGCGATCC	AAAGGCGAGCA	ATGAACCTCA	TCAAGTTCCA	TGCAACTGTG	ACTGCTTAAA	180
45	TGGAGGAACA	TGTGTGTCCA	ACAAAGTACT	CTCCAACATT	CACTGGTGCA	ACTGCCCAAA	240
	GAAATTCGGA	GGGCGAGCACT	GTGAAATAGA	TAAGTCAAAA	ACCTGCTATG	AGGGGAATGG	300
	TCATTTTATC	CGAGGAAAGG	CCAGCACTGA	CACCATGGGC	CGGCCCTGCC	TGCCCTGGAA	360
	CTCTGCCACT	GTCCCTTCAGC	AAAAGTACCA	TGCCCAACAG	TCTGATGCTC	TTCACTGGGG	420
	CCTGGGAAAA	CATAATTACT	GCAGGAACCC	AGACAACCGG	AGGCGACCCCT	GGTGCTATGT	480
50	GCAGGTGGGC	CTAAAGCCGC	TTGTCCAGAA	GTGCATGGTG	CATGACTGCG	CAGATGGAAA	540
	AAAGCCCTCC	TCTCTCCAG	AGGAATTAAG	ATTTCAGTGT	GGCCAAAGAA	CTCTGAGGCC	600
	CGGCTTTAAG	ATTATTGGGG	GAGAATTCAC	CACCATGGAG	AACAGCCCT	GGTTTGGGGC	660
	CATCTACAGC	AGGCACCGGG	GGGGCTCTGT	CACCTACGTG	TGTGGAGGCA	GCCTCATCAG	720
	CCCTGTCTGG	GTGATCAGCG	CCACACACTG	CTTCAATTGAT	TACCCAAAGA	AGGAGGACTA	780
55	CATCGTCTAC	CTGGGTCTGT	CAAGGCTTAA	CTCCAACACG	CAAGGGGAGA	TGAAGTTTGA	840
	GGTGGAAAGC	CTCATCTTAC	ACAAAGGACTA	CAGGCTGTAC	ACGCTTGCTC	ACCACAACGA	900
	CATTGCTTTG	CTGAAGATCC	GTTCGAAGGA	GGGCGAGTGT	GCGCAGCCAT	CCCGGACTAT	960
	ACAGACCATC	TGCCCTGCCCT	CGATGTATAA	CGATCCCCAG	TTTGGCACAA	GCTGTGAGAT	1020
	CATCGGCTTT	GGAAAGAGAG	ATTCTACCGA	CTATCTCTAT	CCGAGGACGC	TGAAAATGAC	1080
60	TGTTGTGAAG	CTGATTTCCC	ACCGGGAGTG	TCAGCAGCCC	CATCTACTAG	GCTCTGAAGT	1140
	CACCAACAAA	ATGCTATGTG	CTGCTGACCC	CCAATGGAAA	ACAGATTCTT	GCCAGGGAGA	1200
	CTCAGGGGGA	CCCTCTGTCT	GTTCCTTCCA	AGGCCGATG	ACTTTGACTG	GAATTGTGAG	1260
	CTGGGGCCGT	GGATGTGCC	TGAAGGACAA	GCCAGGGGTC	TACACGAGAG	TCTCACACTT	1320
	CTTACCCCTG	ATCCGCACTC	ACACCAAGGA	AGAGAATGGC	CTGGCCCTCT	GAGGGTCCCC	1380
65	AGGGAGGAAA	CGGGCACCAC	CCGCTTTCTT	GCTGGTTGTC	ATTTTTCGAG	TAGAGTCAATC	1440
	TCCATCAGCT	GTAAGAAGAG	ACTGGGAAGA	TAGGCTCTGC	ACAGATGGAT	TTGCCTGTGG	1500
	CACCAACAGG	GTGAACGACA	ATAGCTTTAC	CCTCACGGAT	AGGCCTGGGT	GCTGGCTGCC	1560
	CAGACCCCTT	GGCCAGGATG	GAGGGGTGGT	CCTGACTCAA	CATGTTACTG	ACCAGCAACT	1620
	TGCTTTTTTC	TGGACTGAAG	CCTGCAGGAG	TTAAAAAGGG	CAGGGCATCT	CCTGTGATG	1680
70	GGCTCGAAGG	GAGAGCCAGC	TCCCCCGACC	GGTGGGCATT	TGTGAGGCCC	ATGGTTGAGA	1740
	AATGAATAAT	TTCCCAATTA	GGAAGGTGTA	GCAGCTGAGG	TCTCTTGAGG	GAGCTTAGCC	1800
	AATGTGGGAG	CAGCGGTTTG	GGGAGCAGAG	ACACTAAAGA	CTTCAGGGCA	GGGCTCTGAT	1860
	ATTCCATGAA	TGTATCAGGA	AATATATATG	TGTGTGTATG	TTTGACACTT	TGTTGTGTTG	1920
	GCTGTGAGTG	TAGTGTGAG	TAGAGCTGG	TGCTGTATG	TTAAGTCTAA	ATATTCTCTT	1980
75	AAACTGTGTG	GACTGTGATG	CCACACAGAG	TGGTCTTTCT	GGAGAGGTTA	TAGGTCACCTC	2040
	CTGGGGCCTC	TGGGTCCCG	CACGTGACAG	TGCCCTGGAA	TGTACTTATT	CTGCAGCATG	2100
	ACCTGTGACC	AGCACTGTCT	CAGTTTCACT	TTACATAGA	TGTCCTTTTC	TTGGCCAGTT	2160
	ATCCCTTCTT	TTTAGCCTAG	TTTATCCAAT	CCTCACTGGG	TGGGTGAGG	ACCCTCTCTT	2220
	ACACTGAATA	TTTATATTTC	ACTATTTTAA	TTTATATTTC	TGTAATTTTA	AATAAAGTGG	2280
80	ATCAATAAAA	TGTGATTTTT	CTGA				2304

Seq ID NO: C113 DNA Sequence
Nucleic Acid Accession #: XM_087254.1
Coding sequence: 47..2332

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5	ATGTTCAATT	AATGGCATGA	AATACCAAGA	AATTAAATGT	AGACTTGTAC	CCGAAGGACC	120
	AACACCAGAC	TCTTCAGAA	GAAACTTATC	TTATCTTAGT	AGTTTATCCC	ATCTTAACAA	180
	CTTATCCCAT	CTTACAACCA	GTTCTCTTT	CAGAACCAGT	CCTGAAAATG	AAACTGAACT	240
	AATTAAGAA	CATGATCTCT	TCTTTAAAGC	AGTCAGTCTC	TGTCACTCTG	TACAGATTAG	300
	CAATGTTCAA	ACTGACTGCA	CTGGTGATGG	TCCCTGGCAA	TCCAACCTGG	CACCATCGCA	360
10	GTTGGAGTAC	TATGTCATCT	CACCAGATGA	AAAGGCTCTA	GTAGAAGCTG	CTGCAAGGAT	420
	TGGTATTGTG	TTTATTGGCA	ATTCTGAAGA	AACTATGGAG	GTTAAACTCT	TTGGAAGAACT	480
	GGAAACGGTAC	AAACTGCTTC	ATATTCTGGA	ATTGATTCA	GATCGTAGGA	GAATGAGTGT	540
	AATTGTTTCA	GCACCTTCAG	GTGAGAAGTT	ATTATTGTCT	AAAGGAGCTG	AGTCATCAAT	600
	TCTCCCTAAA	TGTATAGGTG	GAGAAATAGA	AAAAACCAGA	ATTCATGTAG	ATGAATTTGC	660
15	TTTGAAGGGG	CTAAGAACTC	TGTGTATAGC	ATATAGAAAA	TTTACATCAA	AAGAGTATGA	720
	GGAAATAGAT	AAACGCATAT	TTGAAGCCAG	GACTGCCTTG	CAGCAGCGGG	AAGAGAAAT	780
	GGCAGCTGTT	TTCCAGTTCA	TAGAGAAAGA	CCTGATATTA	CTTGGAGCCA	CAGCAGTAGA	840
	AGACAGACTA	CAAGATAAAG	TTCCGAGAAC	TATTGAAGCA	TTGAGAATGG	CTGGTATCAA	900
	AGTATGGGTA	CTTACTGGGG	ATAAACATGA	AACAGCTGTT	AGTGTGAGTT	TATCATGTGG	960
20	CCATTTTTCAT	AGAACCATGA	ACATCCTTGA	ACTTATAAAC	CAGAAATCAG	ACAGCGAGTG	1020
	TGCTGAACAA	TTGAGGCAGC	TTGCCAGAAG	AATTACAGAG	GATCATGTGA	TTGAGCATGG	1080
	GCTGTGAGTG	GATGGGACCA	GCCTATCTCT	TGCACTCAGG	GAGCATGAAA	AACTATTTCAT	1140
	GGAAAGTTGC	AGAAATTTGT	CAGCTGTATT	ATGCTGTCTG	ATGGCTCCAC	TGCAGAAAGC	1200
	AAAAGTAATA	AGACTAATAA	AAATATCACC	TGAGAAACCT	ATAACATTGG	CTGTGGGTGA	1260
25	TGGTGCTAAT	GACGTAAGCA	TGATACAAGA	AGCCCATGTT	GGCATAGGAA	TCATGGGTAA	1320
	AGAAGGAAGA	CAGGCTGCAA	GAAACAGTGA	CTATGCAATA	GCCAGATTTA	AGTTCTCTCTC	1380
	CAAATTTGCTT	TTTGTTCATG	GTCAITTTTA	TTATATTAGA	ATAGCTACCC	TTGTACAGTA	1440
	TTTTTTTTAT	AAGAAATGTT	GCTTTATCAC	ACCCAGTTT	TTATATCAGT	TCTACTGTTT	1500
	GTTTTCTCAG	CAACCATTTG	ATGACAGCGT	GTACCTGACT	TTATACAATA	TTTGTTTTAC	1560
30	TTCCCTACCT	ATTCTGATAT	ATAGTCTTTT	GGAAACAGCAT	GTAGACCCCTC	ATGTGTTACA	1620
	AAATAAGCCC	ACCCCTTATC	GAGACATTAG	TAAAAACCGC	CTCTTAAGTA	TTAAACATT	1680
	TCCTTTATTGG	ACCATCTGGG	GCCTCAGTCA	TGCTTTTATT	TTCTTTTGTG	GATCCTATTT	1740
	ACTAATAGGG	AAAGATACAT	CTCTGCTTGG	AAATGGCCAG	ATGTTTGGAA	ACTGGACATT	1800
	TGGCACTTTG	GTCTTCACAG	TCATGGTTAT	TACAGTCACA	GTAAAGATGG	CTCTGGAAAC	1860
35	TCATTTTGG	ACTTGGATCA	ACCATCTCGT	TACCTGGGGA	TCTATTATAT	TTTATTTTGT	1920
	ATTTTCTCTG	TTTATGGAG	GGATTCTCTG	GCCATTTTGT	GGCTCCAGGA	ATATGTATTT	1980
	TGTGTTTATT	CAGCTCTCTG	CAAGTGGTTC	TGCTTGGTIT	GCCATAATCC	TCATGGTTGT	2040
	TACATGTCTA	TTTCTTGATA	TCATAAAGAA	GGTCTTTGAC	CGACACCTCC	ACCCTACAA	2100
40	TACTGAAAG	GCACAGCTTA	CTGAACAA	TGCAGGTATC	AAGTGCTTGG	ACTCCATGTG	2160
	CTGTTTCCCG	GAAGGAGAAG	CAGCGTGTGC	ATCTGTGGA	AGAATGCTGG	AACGAGTTAT	2220
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Coding sequence: 127..1215

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Coding sequence: 82..6903

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	AAAACCTGACA	TCTTAAGGCT	ACATGAACCTA	ACCAAGATTT	ATCTGGGCAC	CTCCAGCCCA	5940
	GCAGTGGACA	GGCTGTGTGT	CGGAGTTCCG	CCTGGAGAGT	GCTTTGGCCT	CCTGGGAGTG	6000
35	AATGGTGGCG	GCAAAACAAC	CACATTTCAAG	ATGCTCACTG	GGGACACCACT	AGTGACCTCA	6060
	GGGGATGCCA	CCGTAGCAGG	CAAGAGTATT	TTAACCAATA	TTTCTGAAGT	CCATCAAAAT	6120
	ATGGGCTACT	GTCTCAGTT	TGATGCAATC	GATGAGCTGC	TCACAGGACG	AGAACATCTT	6180
	TACCTTTATG	CCCGGCTTCG	AGGTGTACCA	GCAGAAAGAA	TCGAAAAGGT	TGCAAACTGG	6240
	AGTATTAAGA	GCTTGGGCTC	GACTGTCTAC	GCCGACTGCC	TGGCTGGCAC	GTACAGTGGG	6300
40	GGCAACAAGC	GGAAACTCTC	CACAGCCATC	GCACTCAATT	GCTGCCACCC	GCTGTGCTG	6360
	CTGGATGAGC	CCACCAACAG	GATGACCCCC	CAGGCAAGCC	GCATGCTGTG	GAACGTCTATC	6420
	GTGAGCATCA	TCAGAAAGG	GAGGGCTGTG	GTCTTCACAT	CCCAAGCAT	GGAAAGATGT	6480
	GAGGCACTGT	GTACCCGGCT	GGCCATCATG	GTAAGGGGCG	CCTTTCGATG	TATGGGCACC	6540
	ATTACAGATC	TCAGTCCCAA	ATTGAGAGAT	GGCTATATCG	TCACAAATGA	GATCAAAATCC	6600
45	CCGAAGGAGC	ACCTGCTTCC	TGACCTGAAC	CCTGTGGAGC	AGTTCTTCCA	GGGGAACCTC	6660
	CCAGGCAAGT	TGCAGAGGGA	GAGGCACTAC	AACATGCTCC	AGTTCCAGGT	CTCCTCCTCC	6720
	TCCTTGGCGA	GGATCTTCCA	GCTCCTCTCT	TCCCACAGG	ACAGCCTGCT	CATCGAGGAG	6780
	TACTCAGTCA	CACAGACCAC	ACTGGAACAG	GTGTTTGTA	ATTTTGCTAA	ACAGCAGATG	6840
	GAAGATCATG	ACCTCCCTCT	GCACCTCGA	GCTGCTGGAG	CCAGTCGACA	AGCCCAAGGAC	6900
50	TGATCTTTCA	CACCGCTCGT	TCCTGCAGCC	AGAAAGGAAC	TCTGGGCAGC	TGGAGGGCGCA	6960
	GGAGCCTGTG	CCCATATGGT	CATCCAAATG	GACTGGCCCA	GGGTAAATGA	CCCCACTGCA	7020
	GCAGAAAACA	AACACACGAG	GAGCATGCAG	CGAATTGAGA	AAGAGGTCTT	TCAGAAAGGAA	7080
	ACOGAAACTG	ACTTGCTCAC	CTGGAACACC	TGATGGTGAA	ACCAAAACAA	TACAAAATCC	7140
	TTCTCCAGAC	CCCAAGAACTA	GAAACCCCGG	GCCATCCAC	TAGCAGCTTT	GGCCTCCATA	7200
55	TGCTCTCAT	TTCAAGCAGA	TCTGCTTTTC	TGCATGTTTG	TCTGTGTGTC	TGCGTTGTGT	7260
	GTGATTTTCA	TGGAATAATA	AAATGCAAAAT	GCATCATCA	CAAAAAAATA	AAAAAATA	7318

Seq ID NO: C117 DNA Sequence
Nucleic Acid Accession #: NM_006671.2
Coding sequence: 138..1820

60	1	11	21	31	41	51	
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65	GCCACAGACC	TGTGCCCCCG	GCCGGGCTCT	CATGCTGGGA	ATGGTGTCTGT	GCCCCCTGCC	120
	AGCAGGCCAG	GCTCACCATG	GTGCCGCATG	CCATCTTGGC	ACGGGGGAGG	GACGTGTGCA	180
	GGCGGAATGG	ACTCCTCATC	CTGTCTGTGC	TGTCTGTCTAT	CGTGGGCTGC	CTCCTCGGCT	240
	TCTTCTTGAG	GACCCGGCGC	CTCTCACCCAC	AGGAAATTAG	TACTTCCAG	TTCCCTGGAG	300
	AGCTCCTGAT	GAGGATGCTG	AAGATGATGA	TCTTGCCACT	GGTGGTCTCC	AGCTTGATGT	360
70	CGGACTTGC	TCTCCTGGAT	GCCAGACCTT	CTAGCCGCTT	GGGCGTCTCT	ACCGTGGGCT	420
	ACTACCTGTG	GACCACCTTC	ATGGCTGTCA	TGGTGGGCAT	CTTCATGGTC	TCCATCATCC	480
	ACCCAGGCAG	CGCGGCCAG	AAGGAGACCA	CGGAGCAGAG	TGGGAAGCCC	ATCATGAGCT	540
	CAGCCGATGC	CCTGTTGGAC	CTCATCCGGA	ACATGTTCCC	AGCCAACTTA	GTAGAAGCCA	600
	CATTCAAAAC	GTACCCGACC	AAGACCAACC	CAGTTGTCAA	GTCCCCCAAG	GTGGCACCAG	660
75	AGGAGGCCCT	TCTTCGGCGG	ATCCTCATCT	ACGGGGTCCA	GGAGGAGAAT	GGCTCCCATG	720
	TGCAGAACTT	CGCCCTGGAC	CTGACCCCGC	CGCCCGAGGT	CGTTTACAAG	TCAGAGCCGG	780
	GCACCAGCGA	TGGCATGAAT	GTGCTGGGCA	TGCTCTTCTT	CTCTGCCACC	ATGGGCATCA	840
	TGCTGGGCCG	CATGGGTGAC	AGCGGGGCC	CCCTGGTCTG	CTTCTGCCAG	TGCTTCAATG	900
	AGTCGGTCTAT	GAAGATCTGT	GCGGTGGCTG	TGTGGTATTT	CCCTTCCGCG	ATTGTGTTCC	960
80	CTATTGCGGG	TAAGATCTCT	GAGATGGAGG	ACCCACGGGC	CGTGGGCAAG	AAGCTGGGCT	1020
	TCTACTCAGT	CACCGTGGTG	TGCGGGCTGG	TGCTCCACGG	GCTCTTTATC	CTGCCCTGTC	1080
	TCTACTTCTT	CATCACCAAG	AAGAATCCCA	TGCTCTTCAT	CCGCGGCATC	CTGCAGGCTC	1140
	TGCTCATGCG	GCTGGCCACC	TCTCCAGCT	CAGCCACACT	GGCCATCACC	TTCAAGTGCC	1200
	TGCTGGAGAA	CAACCACTAC	GACCGGCGCA	TGCTCGCTT	CGTGTGCCCC	GTGGGTGCCA	1260
	CCATCAACAT	GGACGGCACT	GCGCTCTACG	AGGCTGTGGC	GGCCATCTTC	ATCGCCCAAG	1320

5 TCAACAACCTA CGAGCTGGAC TTTGGCCAGA TCATCACCAT CAGTATCACA GCCACTGCAG 1380
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 CCTCCGTGGG ACTGCCACC GATGACATCA CCTCATCAT TGCCTGTGAC TGGGCTCTGG 1500
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 TAGCCGAGGC TCCGAGCTC ACCCTGGGCC CCACTTGCCC CCACCACGTC CCGTTCAAG 1740
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 10 AGCTGGAGAC CAATGTCTGA GCCTGCGGAG CTGCAGGGGC AGGCGAGGCC TCCAGGGGCA 1860
 GGGTCCTGAG GCAGGAACCT GACTCTCCAA CCTCTCTGAG CAGCGGCGAG GGGCCAGGAT 1920
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 CAGAGAAGGG AAAGGCTGCA TGGGGGAGCC CCATCCAGGG AGTGATGGGC CCGGCATTGC 2040
 CTGAGGCCCC GCTGTGACAG TTTCCCGGCT GTGAGCCCGG TGAGGGCGGC AGGCAGGGGT 2100
 15 TATCCGCCCC CACTTTCTGG ATGACAGACT TGAGGCTCTG AGAGCTGAAA ACCTTTGTCC 2160
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 GGAGGACAGG GCAGCCTGCA GCTGTGTCCA GGGCCAGGCC CCACCCACATA ACAGGTGGCC 2280
 TCAGCCACAC AGTTCTCCCC AAGGGGAGCA GCCCAGGGCC AAGCCCCGCT GCCTTCCCCA 2340
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 20 GGAGACAGAT GTCTTTACTA GAGCTGAAAG GCCCCTTGA CACATCCAGG CCAACCTCCC 2460
 ATGGAATAGG TAGGCAAGCC AGGACTCCGG GAAGGAGGTG CAGCCAGGAT GCTCTGGTGG 2520
 AGCTGCCGAT GGGGCCCTGG TGTCAGAACT CCCCAGAGGC CTGTGCGTCC AAGTGGAGTC 2580
 AGGTTTCTA TTTCTTTCTG TGTTTGCAAA TTCAGTGTTA ACTAAATAAA GGTATTTTGT 2640
 TTTTCAAAA AAAAAAAAAA AAA 2663

25 Seq ID NO: C118 DNA Sequence
 Nucleic Acid Accession #: NM_005689
 Coding sequence: 278..2806

30 1 11 21 31 41 51
 GGGCCTGCAG TTGGCAGAAG GGTCCCGGGC CCAGAGCCAG CGGGGCGGTG CTGAGACGGC 60
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 CCTGTGCCAC GTGCGTCCCT TCCCGGGACC CCGCAGCTT GCGCGCCAGC GGCTACGTGA 180
 35 GCCAAGGCAC CCGGATGTCC GCGCCCTCT CCGAGTGACA AGTCCCGGCC TCGGCTCCGC 240
 CAGTGCCGCG AGCTTCGGCG GCGCTCCAGC CATTGCCATG GTGACTGTGG GCAACTACTG 300
 CGAGGCCGAA GGGCCCGTGG GTCCGCGCTG GATGACAGAT GGCCTGAGTC CCTGCTTCTT 360
 CTTACGCTC GTGCCCTCGA CGCGGATGGC TCTAGGAGCT CTGGCCTTGG TGCTGGCTCT 420
 TCCCTGCAGA CGCGGGGAGC GGCCTGCTGG TGCTGATTGG CTGTCTTGGG GGGCCGGCCC 480
 40 TGCCATCTCT CCTACGTGTC TGCAGCTGCT TCTGGCCACA CTTCAGGCGG CGCTGCCCTT 540
 GGCGGCGCTG GTGCTGCGGG TGGGCACTGC CCGGGGGGCC CCACTGCCAA GCTATCTACT 600
 TCTGGCCTCC GTGCTGGAGA GTCTGGCCGG CCGCTGTGGC CTGTGGCTGC TTGTCTGTGA 660
 CGCGAGCCAG GCACGGCAGC GTCTGGCAAT GGCCTCTGAG ATCAAGTTCA GGCACAGCCC 720
 TGGTCTCTCT CTCTCTCTGA CTGTGGCGTT TGCACTGAG AACTTGGCCC TGGTGTCTTG 780
 45 GAACAGCCCA CAGTGTGTGT GGGCAAGGGC AGACTTGGGC CAACAGGTTT AGTTTAGCCT 840
 GTGGGTGCTG CGGTATGTGG TCTCTGGAGG GCTGTTTGTG CTGGGTCTCT GGGCCCGTGG 900
 ACTTCTGCCC CAGTCTCTATA CATTGCAAGT TCAAGAAAGG GACCAAGATG TGGAAAGGAG 960
 CCAGGTTCCG TCAGCAGCCC AACAGTCTAC CTGGCGAGAT TTTGGCAGGA AGCTCCGCTT 1020
 CCTGAGTGGC TACTGTGTC CTGAGGGGAG TCCAGCTCTG CAGCTGGTGG TGCTCATCTG 1080
 50 CCTGGGCTCT ATGGGTTTGG AACCGGCACT CAATGTGTGG GTGCCTATAT TCTATAGGAA 1140
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 TTACGTCTTC CTCAAGTTCC TCCAGGGGGG TGGCACTGGC AGTACAGGCT TCGTAGCAA 1260
 CCTGGCACC TTCTGTGGA TCCGGGTGCA GCAGTTCAAG TCTCGGCGGG TGGAGCTGCT 1320
 CATCTTCTCC CACCTGCAGC AGCTCTCACT GCGCTGGCAC CTGGGGCGCC GCACAGGGGA 1380
 55 GGTGCTGGCG ATGCGGATC GGGGCACATC CAGTGTCA CA GGGCTGCTCA GCTACCTGGT 1440
 GTTCAATGTC ATCCCAAGC TGGCCGACAT CATCATGGC ATCATCTACT TCAGCATGTT 1500
 CTTCAACGCC TGGTTTGGCC TCATTGTGTT CCTGTGCATG AGTCTTTACC TCACCCTGAC 1560
 CATTGTGGTC ACTGAGTGA GAACCAAGTT TGGTGTGCT ATGAACACAC AGGAGAACGC 1620
 TACCCGGGCA CGAGCAGTGG ACTCTCTGCT AAACCTCGAG ACGGTGAAGT ATTACAACGC 1680
 60 CGAGAGTTAC GAAGTGAAC GCTATGAGA GGCCATCATC AAATATCAGG GTTTGGAGTG 1740
 GAAGTGGAGC GCTTCACTGG TTTTACTAAA TCAGACCCAG AACCTGGTGA TTGGGCTCGG 1800
 GCTCCTCGCC GGTCCCTGTC TTTGGGCATA CTTGTCTACT GAGCAGAAGC TACAGGTTGG 1860
 GGACTATGTG CTCTTTGGCA CCTACATTAT CCAGCTGTAC ATGCCCTTCA ATTGGTTTGG 1920
 65 CACCTACTAC AGGATGATCC AGACCAACTT CATTGACATG GAGAACATGT TTGACTTGCT 1980
 GAAGAGGAG ACAGAAAGTGA AGGACCTTCC TGGAGCAGGG CCGCTTGGCT TTGAGAGGG 2040
 CCGTATTGAG TTTGAGAACG TGCACTTCAG CTATGCCGAT GGGCGGGAGA CTTGCAAGGA 2100
 CGTGCTTTT ACTGTGATGC CTGGACAGAC ACTTGGCCCTG GTGGGCCCAT CTGGGCGAGG 2160
 GAAGAGCACA ATTTTGGGCC TGCTGTTTGG CTTCTAAGAC ATCAGCTCTG GCTGCATCCG 2220
 70 AATAGATGGG CAGGACATTT CACAGGTGAC CCAGGCTCT CTCCGGTCTC ACATTGGAGT 2280
 TGTGCCCAA GACACTGTCC TCTTTAATGA CACCATGCGC GACAATATCC GTTACGGCCG 2340
 TGTACAGCT GGGAAATGAT AGGTGGAGGC TGCTGCTCAG GCTGCAGGCA TCCATGATGC 2400
 CATTATGGCT TTTCTTGAAG GGTACAGGAC ACAGGTGGGC GAGCGGGGAC TGAAGCTGAG 2460
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 75 TCTGCTGGAT GAGGCAAGCT CAGCGCTGGA TACATCTAAT GAGAGGGCCA TCCAGGCTTC 2580
 TCTGGCCAAA GTCTGTGCCA ACCGCACCAC CATGTAGTGT GCACACAGGC TCTCAACTGT 2640
 GGTCAATGCT GACCAGATCC TCGTCTATCA GGATGGCTGC ATCGTGAGA GGGGACGACA 2700
 CGAGGCTCTG TTGTCGCGAG GTGGGCTGTA TGCTGACATG TGGCAGCTGC AGCAGGACCA 2760
 GGAAGAAACC TCTGAAGACA CTAAGCCTCA GACCATGGAA CGGTGACAAA AGTTTGGCCA 2820
 CTTCCCTTCC AAGACTTAC CCAGAAAGGA ATAAGATGTG TCTCTTTCC CTGGCTTATT 2880
 80 TCATCCTGGT CTTGGGGTAT GGTGCTAGCT ATGGAAGGG AAAGGGACCT TTCGAAAAA 2940
 CATCTTTTGG GGAATAAAAA ATGTGGACTG TGAATAAAAA AAAAAAAAAA AAA 2993

Seq ID NO: C119 DNA Sequence
 Nucleic Acid Accession #: NM_000676
 Coding sequence: 333..1331

1 11 21 31 41 51
5 GGGCAATTG TTAGTTATCC GCGCCACCA AGACGGGCA CGGCGCTGG ACCGAGGGG 60
CCCCGCGCG GCGCAACTT TGGGCTCGG CAGTGGGTG GTGCTCCGCC CAGCCCGAGA 120
CGGCGGGCG GCGGGCCAA TGGGTGCGC CTCTGGCGG CGGGGGGCC CGACCCGTGG 180
GTCCCGGCCA CCAGCGCCCC AGCCCGAGG CTCAGAAGG CGAGGCGAG GCGCGGTCCG 240
GGGCTATGG CCATGCCCGG CGGGTCTCAC GCGGCTGCC CTGCGCCGG GCGCCTTCGG 300
TAGGGGGCG CCGGGGCCA GCTGGCCGG CCATGCTGCT GGAGACACAG GACGCGCTGT 360
10 ACGTGGCGCT GGAGCTGGTC ATCGCGCGC TTTCGGTGG GGGCAACGTG CTGGTGTGCG 420
CGCGGTGGG CACGGCGAAC ACTCTGCAG CGCCACCAA CTACTTCCTG GTGTCCCTGG 480
CTGCGGCGA CGTGGCGGTG GGGCTCTCG CCATCCCTT TGCCATCACC ATCAGCCTGG 540
GCTTCTGCAC TGACTTCTAC GGTGCTCTT TCCTCGCCTG CTCTGCTGCT GTGCTCAOGC 600
AGAGCTCCAT CTTCAGCCTT CTGGCCGTGG CAGTGCACAG ATACCTGGCC ATCTGTGTCC 660
15 CGCTCAGTA TAAAAGTTT GTCAAGGGA CCGAGCAGG AGGGTCAAT GCTGTCTCT 720
GGGTCTTGC CTTTGGCATC GGATTGACTC CATTCTGGG GTGGAACAGT AAAGACAGT 780
CCACCAACAA CTGCACAGAA CCCTGGGATG GAACACGAA TGAAGCTGC TGCCTTGTGA 840
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GTGTTCTGCC CTTAGCTGCT ATAATGCTGG TGATCTACAT TAAGATCTTC CTGGTGGCCT 960
20 GCAGGCACT TCAGGCACT GAGCTGATG ACCATCGAG GACCACCTC CAGCGGAGA 1020
TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTT TGCCCTGTGC TGGTTACCTG 1080
TGCACTGCTG TAACGTGTG ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT 1140
GGGCAATGAA TATGGCCATT CTCTGTGAC ATGCCAATTC AGTTGTCAAT CCCATTGTCT 1200
ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC 1260
25 TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTGGGTG 1320
TGGGCTATG ATCTAGGCTC TCGCTCTTTC CAGGAGAAGA TACAATCCA CAAGAAACAA 1380
AGAGGACAGC GCTGTGTTTC ATTGTGAAG ATAGCTACAC CTCACAAGGA AATGACTGTC 1440
CTCTCTTGGC CACTTCCCTG GAGCTACAC GTATCTAGCT AATATGTATG TGTCTAGTAG 1500
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30 ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTTGT TTTAAAGTC TGCTTGTGTT 1620
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Seq ID NO: C120 DNA Sequence

Nucleic Acid Accession #: NM_052932

Coding sequence: 217..786

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GAGCCACGA GGCTGCCGCA TCCTGCCCTC GGAACAATGG GACTCGGCGC GCGAGGTGCT 240
45 TGGGCGCGCC TGCTCCTGGG GAGGCTGAGC GTGCTAGCGC TGCTGGGGGC CGCCATGAA 300
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AACAGTACTG TGAACCAACC AACTTCAGTT GCCTCAGACT CAGTAATAC AACGGTCACC 420
ACCATGAAC CACAGCGCGC ATCTAATACA ACAACACAG GAGTGGTCTC AACAAATATG 480
ACTTCTACCA CTTTAAAGTC TACACCCAAA ACAACAAGTG TTTACAGAA CACATCTCAG 540
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65 AACTGCAGTG TTTAACAATA TAATGTTTAA AAGACTTAGT TGTCAATATT AAATAATCCT 1560
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ACCACTGGA GTTACTTTAG TTCAATTAAT TTTAATTTTA TATTTTGTGA ATATTTTAAG 1680
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75 AATCCTCTCT CTACTCCAT GCTGAAGGAG AAGTACTCTC AGATGCATTA TGTTAATGGA 2100
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CTGAGTTTGA TGTACTAAC TTGGCCCTGA CTGGTGTGTC AACCATGTCT TCATTTCTTT 2640
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5
10
15

TTCTTGGTAT TTCACTACT CAAGTCAGTC AGAAGTTCGT AGACCGACCT GAAGTTTCTT 2760
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CAGTATATTA TAGTGATAAT TTTGTATTTT CAAMAAAAAA AAAGTTAAAC TCTTCTTTTC 3240
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AATTGTTCTC CTCTAAAAA AAAAAAATA AAAAAA 3338

Seq ID NO: C121 DNA Sequence

Nucleic Acid Accession #: NM_004195

Coding sequence: 1..726

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CTTGGGAGCG GAACGGAGCG GCGCTGCTGC CGGTTCACCA CGACGCGCTG CTGCGCGAT 180
TACCGGGCGG AGGAGTGTCTG TTCCGAGTGG GACTGCATGT GTGTCCAGCC TGAATTCAC 240
TGGGAGAGCC CTGTGTCAC GACCTGCGCG CACCACCTTT GTCCCGCAGG CCAGGGGGTA 300
CAGTCCAGG GGAATTCAG TTTTGGCTTC CAGTGTATCG ACTGTGCTTC GGGGACCTTC 360
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ACTGTGTTC CTGGGAACAA GACCCACAAC GCTGTGTGCG TCCAGGGGTC CCGCGCGGCA 480
GAGCGGCTTG GGTGGCTGAC CGTGGTCTTC CTGGCGGTGG CCGCTGCGT CCTCTCTG 540
ACCTGGGCCC AGCTTGGACT GCACATCTGG CAGCTGAGGA GTCACTGCAT GTGCCCCGA 600
GAGACCCAGC TGTCTGTGGA GGTGCCGCGG TCGACCGAAG ACGCCAGAAG CTGCCAGTTC 660
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GTGTA 726

Seq ID NO: C122 DNA Sequence

Nucleic Acid Accession #: AK091896.1

Coding sequence: 28..1572

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1 11 21 31 41 51

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CAGATCTCTT GGGTCTTCTT CTGCGAGCAG CTCTGCTCTC TGCTGGGCGG CGCCCTCGGG 240
GGGCTTCTCA AAAGGACCTT GGCCCACTCA CTATGGGCCC TGTTCACTTC CTCTCTGGCC 300
ATCTCCCTGG TGTGTGCGGT CATCCCTTTC TGGCGCGAGC TGAAGGTGCT GGCCTCAGTC 360
ATGGCGCTGG CGGGCTTGGC CATGGGCTGC ATCGACACCG TGGCCAACTC GCAGCTGGTA 420
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GGTGTCTGTC TGAGCCCTCT TATTGCTGAC CCTTTCCTGT CTGAGGCCAA CTGCTTGCT 540
GCCAATAGCA CGGCCAACAC CACCTCCGGA GGCACCTGT TCCATGTCTC CAGGGTCTG 600
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CAGAGGAGGC CCTGCTTCT GTCTGCTGAT GAGCTTGCTT TGGAGACACA GCCTCTGAG 840
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Seq ID NO: C123 DNA Sequence

Nucleic Acid Accession #: NM_002203.2

Coding sequence: 43..3588

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	TGTTTGGCCCT	ACAAATGTTGG	TCTCCCGAGAA	GCAAAAATAT	TTTCCGGTCC	TTCAAGTGAA	180
5	CAGTTTGGGT	ATGCAAGTGCA	GCAGTTTATA	AATCCAAAAG	GCAACTGGTT	ACTGGTTGGT	240
	TCACCCCTGGA	GTGGCTTTCC	TGAGAACOGA	ATGGGAGATG	TGTATAAATG	TCCTGTTGAC	300
	CTATCCACTG	CCACATGTGA	AAAACATAAT	TTGCAAACTT	CAACAAGCAT	TCCAAATGTT	360
	ACTGAGATGA	AAACCAACAT	GAGCCTCGGC	TTGATCCTCA	CCAGGAACAT	GGGAACCTGA	420
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10	GGTGTGTGTT	CTGACATCAG	TCCTGATTTT	CAGCTCTCAG	CCAGCTTCTC	ACCTGCAACT	540
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	ACAAAGACAC	AGGTGGGGTT	AATTCAGTAT	GCCAATAATC	CAAGAGTTGT	GTTAACTTGT	720
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	GCCTCTGGTG	GGCGACGAAG	TGCTAGCAAA	GTAATGTTAG	TTGTAATGTA	CGGTGAATCA	900
	CATGATGGTT	CAATGTGAA	AGCTGTGATT	GATCAATGCA	ACCATGACAA	TATACCTAGG	960
	TTTGGCATAG	CAGTTCTTGG	GTACTTAAAC	AGAAACGCC	TTGATACTAA	AAATTTAATA	1020
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20	GAAGCAGCTC	TACTAGAAAA	GGCTGGGACA	TTAGGAGAAC	AAATTTTCAG	CATTGAAGGT	1140
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25	GGAGAAAGCA	CTCACTTTGT	TGCTGGTGTG	CCTCGGGCAA	ATTATACCGG	CCAGATAGTG	1440
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35	CTCTGGTCAC	AAAGTATTGC	TGATGTAGCT	ATAGAAGCTT	CATTTCACAC	AGAAAAATC	2040
	ACTTTGGTCA	ACAAGAATGC	TCAGATAATT	CTCAAACTCT	GCTTCAGTGC	AAAGTTTCAA	2100
	CCTACTAAGC	AAAACAATCA	AGTGGCCATT	GTATATAACA	TCACACTTGA	TGCAGATGGA	2160
	TTTTTCAATG	GAGTAACTCC	CAGGGGGTTA	TTTAAAGAAA	ACAATGAAGG	GTCCCTGCAG	2220
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40	CCCTCTGATG	TGTGCAACTC	TTTGGATTGG	CGTGTGGACA	TCAGTCTGGA	AAACCCCTGGC	2340
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45	GAAGAACTGT	TTTTTGCATC	ATTTCTCCCTA	CGGTTTGTAT	GGACAGAAAT	AAATGCTCAG	2640
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55	GAATTTGAAT	CGAGAACTGC	TTCTGTGATG	AAATGTTACCT	GCTGGTTGAA	AGACGTTTCA	3240
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65	GTAGGGAAAT	AATAGGGAAA	ATACCTATTT	TATATGATGG	GGGAAAAAAA	GTAACTCTTA	3840
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	TCTCTTTAAA	ATATTTGTCT	TTAAACAGCA	ACTACAGAAAG	TGGAAGTGCT	TGATATGTAA	4020
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70	ACAGGTTTTT	TCAATTTATG	CTGCTCATCC	AAAGTTGCCA	CAGATGATAC	TTCCAAATGA	4140
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	CTTCCACACC	CCATCTTGCT	CTAATGATCA	AAACATGCTT	GAATAACTGA	GCITAGAGTA	4260
	TACCTCTCTAT	ATGTCATTTT	AAGTTAGGAG	AGGGGGGOGAT	ATAGAGACTA	AGGCACAAAA	4320
	TTTGTGTTAA	AACTCAGAAAT	ATAACATTTA	TGTAATAATCC	CATCTGCTAG	AAGCCCATCC	4380
75	TGTGCCAGAG	GAAGGAAAG	GAGGAAATTT	CCTTTCTCTT	TTAGGAGGCA	CAACAGTTCT	4440
	CTTCTAGGAT	TGTTTGGCT	GACTGGCAGT	AACTAGTGA	ATTTTGTAAA	GATGAGTAAT	4500
	TTCTTTGGCA	ACCTTCTCTC	TCCTTACTG	AACTACTCTC	CCACTCTCTG	GTGGTACCAT	4560
	TATTATAGAA	GCCCTCTACA	GCTTGAATTT	CTCTCCAGCG	GTCCAAAGTT	ATCCCTCTCT	4620
80	TACCCCTTAA	TCCAAAGTTC	CCACTCTTTC	AGGACAGCTG	CTGTGCATTA	GATATAGGG	4680
	GGGAAAGTCA	TCTGTTTAAAT	TTACACACTT	GCATGAATTA	CTGTATATAA	ACTCCTTAAAC	4740
	TTAGGGGAGC	TATTTTCAAT	TAGTGCTAAA	CAAGTAAGAA	AAATAAGCTA	GAGTGAATTT	4800
	CTAAATGTTG	GAATGTAAAT	AATGTAAAGT	AAAACTCTCT	CAGGATTTCA	4860	
	CCAGAAAGTTA	CAGATGAGGC	ACTGGAACCC	ACCAACCAAT	TAGCAGGTGC	ACCTTCTGTG	4920
	CTGTCTTGT	TTCTCAAGTA	CTTTTCTTTC	CACAAGAGTG	AATTTGACCT	AGGCAAGTTT	4980
	GTTCAAAAGG	TAGATCTCTGA	GATGATTTGG	TCAGATTTGGG	ATAAGGCCCA	GCAATCTGCA	5040

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 Nucleic Acid Accession #: NM_031460
 Coding sequence: 103..1101

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 Nucleic Acid Accession #: NM_004154
 Coding sequence: 309..1295

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 Seq ID NO: C126 DNA Sequence
 Nucleic Acid Accession #: NM_007197
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	TGATGGGCCA	CGAAGACCA	CGCGAGGCAG	CCATCCAGTT	GCAOGAGTTC	GCGCGCTGG	240
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	ATGGAACCA	AGCCAAATGT	ATAGACGTTT	GGACTGATTT	GTGGAAGGGA	GGGGGGAAGA	2580
45	GGGAGAGGA	TCAATTCAAA	GTTACCCAAA	GGGCTTATG	ACTCTTCTTA	TTGTTAAACA	2640
	AATGATTTCC	ACAAACAGAT	CAGGAAGCAC	TAGGTTGGCA	GAGACACTTT	GTCTAGTGTA	2700
	TTCTCTTAC	AGTGCCAGGA	AAGAGTGGT	TCTGCGTGTG	TATATTGTA	ATATATGATA	2760
	TTTTTCATGC	TCCACTATTT	TATTAATAAT	AAAAATATGT	CTTTAAAAAA	A	2811
50	Seq ID NO: C127 DNA Sequence						
	Nucleic Acid Accession #: NM_005761.1						
	Coding sequence: 250..4956						
55	1	11	21	31	41	51	
	GCGAGGAGGA	AACCGTGGCG	GAGCGCGCAG	GGCTTGCTGC	CGCCACCGCC	GCTGCACAGG	60
	CTGCGGAGC	GAGCCTGCGG	CGCGCGCGCC	TCCCGCTCT	CCTTCTGGG	CGAGCTGCGG	120
	GGATGGGGCG	GCGCGGGGAG	CCCGAGCGCG	CGCAGGAACC	GCGCGCGCGG	CCGCGCGGGT	180
	CTCGGTGGC	GCGCGCTTGA	GCGCGCGTGG	CGCGCGCGCG	CCCTGCGCGG	GGCGCGCCCC	240
60	CCAGCCCCA	TGGAGGTCTC	CGGAGGGAAG	GCGCGCGCGC	GCCCCCGCGG	CCCGCGCAGG	300
	CCACTGCCCC	TGCTGCGCTA	TCTGCTGGCA	CTGCGCGCTC	CGGCGCGGGG	CGGGAAGAG	360
	CCCGTGTGGC	GGTGGAGCA	AGCCATCGGA	GCCATCGCGG	CGAGCCAGGA	GGACGCGGTG	420
	TTTGTGGCGA	GCGGCGAGTG	CCTGGACAG	CTGGACTACA	GCTTGGAGCA	CAGCCTCTCG	480
	CGCCTGTACC	GGGACCAAGC	GGGCAACTGC	ACAGAGCGCG	TCTCGCTGGC	GCCCCCGCGG	540
65	CGGCCCCGGC	CGGCGAGCAG	CTTCAGCAAG	CTGCTGCTGC	CCTACCGCGA	GGGGGCGGGC	600
	GGCCTCGGGG	GGCTGCTGCT	CACCGGCTGG	ACCTTCGACC	GGGGCGCTCG	CGAGGTGCGG	660
	CCCCTGGGCA	ACCTGAGCGG	CAACTCCCTG	CGCAACGGCA	CCGAGGTGGT	GTGCTGCCAC	720
	CGCAGGGGCT	CGACGGCGGG	CGTGGGTGAC	CGCGCGGGCC	GGAAACAAAG	CTGGTACCTG	780
	GCGGTGGCG	AGACCTAGCT	GCTGCGTGG	CGGAGAGCGG	CGAGCGCGTG	CAACCCCGCG	840
70	GCATCCGACC	ACGACACGGC	CATCGCGCTC	AAGGACACGG	AGGGGCGCAG	CCTGGGCAAG	900
	CAGGAGCTGG	GGCGCTCAA	GCTGTGCGAG	GGCGGGGCA	GCTGCACTT	CGTGGACGCC	960
	TTTCTCTGGA	ACGGCAGCAT	CTACTTCCCC	TACTACCCCT	ACAACCTATAC	GAGCGGGCGT	1020
	GCCACCGGGT	GGCCAGCAT	GGCGCGCATC	GCGCAGAGCA	CGAGGTGCT	GTTCCAGGGC	1080
	CAGGCATCCC	TGAGCTGCGG	CCACGGCCAC	CCGACCGGCC	GCGCGCTGCT	CCTCTCTCC	1140
75	AGCCTAGTGG	AGGCCCTGGA	CGTCTGGGCG	GGAGTGTCA	GCGCGCGCGC	TGAGAGGGGC	1200
	CAGGAGCGGC	GCTCCCCCAC	CACCACGGCG	CTCTGCGCTC	TCAGAAATGAG	TGAGATCCAG	1260
	GCGCGGCGCA	AGAGGGTCCAG	CTGGGACTTC	AAGACGGCGG	AGAGCCACTG	CAAGAAAGGG	1320
	GATCAACCTG	AAAGAGTCCA	ACCAATCGCA	TCATCTACCT	TGATCCATTC	CGACCTGACA	1380
	TCGCTTATG	GCACCGTGGT	AATGAACAGG	ACTGTTTTAT	TCTTGGGGAC	TGGAGATGGC	1440
80	CAGTTACTTA	AGGTTATCT	TGGTGAGAAT	TTGACTTCAA	ATTGTCCAGA	GTTTATCTAT	1500
	GAAATTAAG	AAGAGACACC	TGTTTTCTAC	AAACTCGTTC	CTGATCTCTG	GAAGATATC	1560
	TACATTTATC	TAACAGCTGG	GAAAGAGGTG	AGGAGAATTC	GTGTTGCAAA	CTGCAATAAA	1620
	CATAAATCCT	GTTCCGAGTG	TTTAAACAGC	ACAGACCCCT	ACTCGGGTTG	GTGCCATTCG	1680
	CTACAAAGGT	GCACCTTTCA	AGGAGATTGT	GTACATTTCAG	AGAACTTGA	AAACTGGCTG	1740
	GATATTTCTG	CTGGAGCAAA	AAAGTGCCCT	AAAATTCAGA	TAATTCGAG	CAGTAAAGAA	1800

	AAGACTACAG	TGACTATGGT	GGGAAGCTTC	TCTCCAAGAC	ACTCAAAGTG	CATGGTGAAG	1860
	AATGTGGACT	CTAGCAGGGA	GCTCTGCCAG	AATAAAAGTC	AGCCCAACCG	GACCTGCACC	1920
	TGTAGCATCC	CAACCAGAGC	AACCTACAAA	GATGTTTCAG	TTGTCAACGT	GATGTTCTCC	1980
5	TTCCGTTCTT	GGAAATTTAT	AGACAGATTTC	AACTTTACCA	ACTGCTCATC	ATTAAAGAA	2040
	TGCCAGCAT	GGGTAGAAAC	TGGCTGCGCG	TGGTGTAAAA	GTGCAAGAA	GTGTATCCAC	2100
	CCCTTCACAG	CTTGCGACCC	TTCTGATTAT	GAGAGAAACC	AGGAACAGTG	TCCAGTGGCT	2160
	GTCCAGAGA	CATCAGGAGG	AGGAAGACCC	AAGGAGAAC	AGGGGAACAG	AACCAACCAG	2220
	GCTTTACAGG	TCTTCTACAT	TAAGTCCATT	GAGCCACAGA	AAGTATCGAC	ATTAGGGAAA	2280
10	AGCAACGTGA	TAGTAACGGG	AGCAAACTTT	ACCCGGGCAT	CGAACATCAC	AATGATCCTG	2340
	AAAGGAACCA	GTACCTGTGA	TAAGGATGTG	ATACAGGTTA	GCCATGTGCT	AAATGACACC	2400
	CACATGAAT	TCTCTCTTCC	ATCAAGCCGG	AAAGAAATGA	AGGATGTGTG	TATCCAGTTT	2460
	GATGGTGGGA	ACTGCTCTTC	TGTGGGATCC	TTATCCTACA	TTGCTCTGCC	ACATTGTTC	2520
	CTTATATTTT	CTGCTACACC	CTGGATCAGT	GGTGGTCAAA	ATATAACCAT	GATGGGCAGA	2580
15	AATTTTGATG	TAAATGACAA	CTTAATCATT	TCACATGAAT	TAAAGGAAA	CATAAATGTC	2640
	TCTGAATATT	GTGTGGGAC	TTACTGCGGG	TTTTTAGCCC	CCAGTTTAAA	GAGTTCAAAA	2700
	GTGCGCACGA	ATGTCACTGT	GAAGCTGAGA	GTACAAGACA	CCTACTGGGA	TTGTGGAACC	2760
	CTGCAGTATC	GCGAGGACCC	CAGATTACCG	GGGTATCGGG	TGGAATCCGA	GGTGGACACA	2820
	GAACTGGAAG	TGAAAATTC	AAAAGAAAAT	GACAACCTCA	ATATTTCCAA	AAAGACATT	2880
20	GAAATTACT	TCTTCCATGG	GGAAAATGGG	CAATTAAATT	GCAGTTTGA	AAATATTACT	2940
	AGAAATCAAG	ATCTTACCAC	CATCCTTTTC	AAAATTAAAG	GCATCAAGAC	TGCAAGCACC	3000
	ATTGCCAAT	CTTCTAAGAA	AGTTCCGGTC	AAGCTGGGAA	ACCTGGAGCT	CTACGTCGAG	3060
	CAGGAGTCAG	TCTCTTCCAC	ATGGTATTTT	CTGATTGTGC	TCCCTGTCTT	GCTAGTGATT	3120
	GTCAATTTTG	CGCCCGTGGG	GGTGACCAGG	CACAAATCGA	AGGAGCTGAG	TCGCAACACG	3180
25	AGTCAACAC	TAGATTGCT	GGAAAGCGAG	CTCCGAAAG	AGATACGTGA	CGGCTTTGCT	3240
	GAGCTGCAGA	TGGATAAATT	GGATGTGGTT	GATAGTTTTC	GAACTGTTC	CTTCTTGAC	3300
	TACAAACATT	TTGCTCTGAG	AACCTTCTTC	CCTGAGTCAG	GTGGCTTCAC	CCACATCTTC	3360
	ACTGAAGATA	TCTAATACAG	AGACGCGAAC	GACAAGAATG	AAAGTCTCAC	AGCTTTGGAT	3420
	GCCTAATCT	GTAATAAAG	CTTCTTGT	ACTGTATCC	ACACCTTGA	AAAGCAGAAG	3480
30	AACCTTCTG	TGAAGGACAG	GTGCTGTGTT	GCCTCTCTCC	TAACCATTCG	ACTGCAAAAC	3540
	AAGCTGGTCT	AGCTGACCAG	CATCCTAGAG	GTGCTGACCA	GGGACTGTAT	GGAACAGTGT	3600
	AGTAACATGC	AGCCGAAACT	CATGCTGAGA	CGCACGGAGT	CGTCTGCGA	AAACTCTCTC	3660
	ACAAACTGGA	TGTCTGCTG	CTTCTCTGGA	TTTCTCCGGG	AGACTGTCCG	AGAGCCCTTC	3720
	TATTTGCTGG	TGACGACTCT	GAACCAGAAA	ATTAACAAGG	GTCCCGTGA	TGTAATCACT	3780
35	TGCAAGACCC	TGTACACACT	TAATGAAGAC	TGGCTGTGTT	GGCAGGTTCC	GGAAATTCAGT	3840
	ACTGTGGCAT	TAAACGTCTG	CTTTGAAAAA	ATCCCGGAAA	ACGAGAGTGC	AGATGTCTGT	3900
	CGGAATATTT	CAGTCAATGT	TCTCGACTGT	GACACCATTG	GCCAAGCCAA	AGAAAAGATT	3960
	TTCCAAAGCAT	TCTTAAGCAA	AAATGGCTCT	CCTTATGGAC	TTTCTGCTTA	TGAAATTGGT	4020
	CTTGAGCTTC	AAATGGGAC	ACGACAGAAA	GAACCTCTGG	ACATCGACAG	TTCTCCGCTG	4080
40	ATTCTTGAAG	ATGGAATCAC	CAAGCTAAAC	ACCAATGGCC	ACTATGAGAT	ATCAATGGA	4140
	TTCCACTATA	AAGTCTTTAA	GAAGATAGCA	AAATTTACTT	CAGATGTGGA	GTACTCGGAT	4200
	GACCACTGCC	ATTGATTTT	ACCAGATTGG	GAAGCATTCC	AAGATGTGCA	AGGAAGAGAA	4260
	CATCGAGGGA	AGCACAAGTT	CAAAAGTAAA	GAATGTATC	TGACAAAGCT	GCTGTGAGCC	4320
	AAGGTGGCAA	TTCTATCTGT	GCTTGAAAAA	CTTTTAGAAA	GCATTTGGAG	TTTACCCAAC	4380
45	AGCAGAGCTC	CATTGTCTAT	AAAATACTTT	TTTGACTTTT	TGGACGCCCA	GGCTGAAAAA	4440
	AAAAAAATCA	CAGATCTGTA	CGTCGTACAT	ATTTGAAAAA	CAACAGCCCT	TCCTCTTGGC	4500
	TTCTGGGTAA	ACATCTCTGA	GAACCTCTAG	TTTGTCTTTG	ACATTAAGAA	GACACCACT	4560
	ATAGACGGCT	GTGTGTCTAGT	GATTGCCAG	GCATTCTAGG	ATGCATTTTC	TCTCAGAGAG	4620
	CAGCAACTAG	GGAAAGGAGC	ACCAACTAAT	AAGCTTCTCT	ATGCCAAGGA	TATCCCAACC	4680
50	TACAAGAGAG	AAGTAAATTC	TTATTACAAA	GCAATCAGGG	ATTGCTCTCC	ATTGTATCC	4740
	TCAGAAATGG	AGAATTTT	AACCTAGGAA	TCTAAGAAAC	ATGAAAATGA	ATTTAATGAA	4800
	GAAGTGGCCT	TGACAGAAAT	TTACAAATAC	ATCGTAAAT	ATTTGATGA	GATTCTAAT	4860
	AAACTAGAAA	GAGAACGAGG	GCTGGAAGAA	GCTCAGAAAC	AACCTCTGCA	TGTAAGAGTC	4920
	TATTTATGAT	AAAAGAGAAA	ATGCAAGTGG	ATGTAAGCAC	TCTGGGGCCT	GGCTTAATCT	4980
55	GGCAAGATT	TTACAGACAC	TTGGGAGCAA	AATGGCTGCT	TGAGCTACTC	TGTGTGTTTA	5040
	ATTTGTGTT	TGCACATAGG	TTCCACTTTG	GGCACTGTCT	TTTTAAGAGA	CCAAGGCACA	5100
	TGCACAGCTT	TTAGAAAGCA	A				5121

Seq ID NO: C128 DNA Sequence

Nucleic Acid Accession #: NM_002185.1

Coding sequence: 23..1402

	1	11	21	31	41	51	
65	CTCTCTCTCT	ATCTCTCTCA	GAATGACAAT	TCTAGGTACA	ACTTTTGGCA	TGGTTTTTTC	60
	TTTACTTCAA	GTGGTTTCTG	GAGAAAGTGG	CTATGCTCAA	AATGGAGACT	TGGAAGATGC	120
	AGAACTGGAT	GACTACTCAT	TCTCATGCTA	TAGCCAGTTG	GAAGTGAATG	GATCGCAGCA	180
	TTCACTGACC	TGTGCTTTTG	AGGACCCAGA	TGTCAACACC	ACCAATCTGG	AATTTGAAAT	240
	ATGTGGGGCC	CTCGTGGAGG	TAAAGTGCC	GAATTTCAAG	AAACTACAAG	AGATATATTT	300
70	CATCGAGACA	AGAATAATCT	TACTGATTGG	AAAGAGCRA	ATATGTGTGA	AGGTTGGAGA	360
	AAAGAGTCTA	ACCTGCAGAAA	AAATAGACCT	AACCACTATA	GTAAACCTG	AGGCTCCTTT	420
	TGACCTGAGT	GTACATCTATC	GGGAAGGAGC	CAATGACTTT	GTGGTGACAT	TTAATACATC	480
	ACACTTGCAA	AGAAGTATG	TAAAGTTTT	AATGCTATG	GTAGCTTACC	GCCAGGAAAA	540
	GGATGAAAA	AAATGGACGC	ATGTGAATTT	ATCCAGCACA	AAGCTGACAC	TCCTGCAGAG	600
75	AAAGCTCCAA	CCGGCAGCAA	TGTATGAGAT	TAAAGTTGGA	TCCATCCCTG	ATCACTATTT	660
	TAAAGGCTTC	TGGAGTGAAT	GGAGTCCAG	TTATTACTTC	AGAACTCCAG	AGATCAATAA	720
	TAGCTCAGGG	GAGATGGATC	CTATCTTACT	AACCATCAGC	ATTTGAGTTT	TTTTCTCTGT	780
	GGCTCTGTTG	GTACTCTTGG	CCTGTGTGTT	ATGGAAGAAA	AGGATTAAAC	CTATCGTATG	840
	CCCGAGTCTC	CCCGATCATA	AGAAGACTCT	GGAACATCTT	TGTAAGAAAC	CAAGAAAAAA	900
80	TTTAAATGTT	AGTTTCAATC	CTGAAAGTTT	CCTGAGCTGC	CAGATTCTAT	GGGTGGATGA	960
	CATTCAGCTG	AGAGATGAAG	TGGAAGGTTT	TCTGCAAGAT	ACGTTTCTCT	AGCAACTAGA	1020
	AGAACTCTGAG	AAGCAGAGGC	TTGGAGGGGA	TGTGCAGAGC	CCCACTGCC	CATCTGAGGA	1080
	TGTAGTCGTC	ACTCCAGAAA	GCTTTGGAAG	AGATTCAATC	CTCACATGCC	TGGCTGGGAA	1140
	TGTCAGTGCA	TGTACCGCCC	CTATTCTCTC	CTCTTCCAGG	TCCCTAGACT	GCAGGGAGAG	1200
	TGGCAAGAA	GGGCTCATG	TGTACCAGGA	CCTCTCTGTT	AGCCTTGGGA	CTACAAACAG	1260

5 CACGCTGCC CCTCCATTTT CTCTCCAATC TGAATCCTG ACATTGAACC CAGTTGCTCA 1320
GGGTCAGCCC ATTCTTACTT CCTGGGGATC AAATCAAGAA GAAGCATATG TCACCATGTC 1380
CAGCTTCTAC CAAAACCAAGT GAAGTGTAAG AAACCCAGAC TGAACCTTACC GTGAGCGACA 1440
AAGATGATTT AAAAGGGAAG TCTAGAGTTC CTAGTCTCCC TCACAGCACA GAGAAGACAA 1500
AATTAGCAAA ACCCCACTAC ACAGTCTGCA AGATTCTGAA ACATTGCTTT GACCACTCTT 1560
CCTGAGTTCA GTGGCACTCA ACATGAGTCA AGAGCATCCT GCTTCTACCA TGTGGATTTC 1620
GTCACAAGGT TTAAGGTGAC CCAATGATTC AGCTATTT 1658

10 Seq ID NO: C129 DNA Sequence
Nucleic Acid Accession #: NM_002722.1
Coding sequence: 15..302

15 1 11 21 31 41 51
ACTCTGGACT CCGGATGGCT GCGGCACGCC TCTGCCTCTC CCGTCTGCTC CTGTCCACCT 60
GCGTGGCTCT GTTACTACAG CCACTGCTGG GTGCCCAGGG AGCCCCACTG GAGCCAGTGT 120
ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCCAAGT TGCAGCTGAT CTCGTAGAT 180
ACATCAACAT GCTGACCAGG CTAAGTATG GGAAGAGCA CAAAGAGGAC ACGCTGGCCT 240
TCTGGAGTG GGGTCCCG CATGCTGCTG TCCCCAGGGA GCTCAGCCCG CTGGAATTAT 300
20 ATGCGACCT TCTGTCTCCT ACGACTCCAT GAGCAGCGCC AGCCAGCTC TCCCTCTGCT 360
ACCTTGGCT CTGGCCAAAG CTGTCTCCT GCTCCACAC AGGCTCAATA AAGCAAGTCA 420
AAGCC 425

25 Seq ID NO: C130 DNA Sequence
Nucleic Acid Accession #: NM_032545.1
Coding sequence: 47..718

30 1 11 21 31 41 51
AAATGATCT TCAATGCACT AAGAGAAGGA GACTCTCAA CCAAAATGA CCTGGAGGCA 60
CCATGTGAGG CTCTGTGTTA CGGTGAGTTT GGCAATACAG ATCATCAATT TGGGAAACAG 120
CTATCAAGGA GAGAAACATA ACGGCGTAG AGAGGAAGTC ACCAAGTTG CCACTCAGAA 180
GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCAATTC GGAGAGGTGA CTGGGAGCGC 240
CGAGGGCTGG GGGCCGGAGG AGCCGCTCCC TACTCCCGG GCTTTCGGAG AGGGTGGCTC 300
35 CGCGCGCCG CGCTGCTGCA GGAACGCGCG TACCTGCGTG CTGGGAGGCT TCTGCGTGTG 360
CCCGCCCAAC TTACCGCGCC GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGCGC 420
CTGGAGCAC GGAGCTGGA CCTTCGCGC CTGCCACCTC TGCAGGTGCA TCTTCGGGCG 480
CCTGCACTGC CTCCCCTCC AGAAGCCTGA CCGCTGTGAC CGGAAAGACT TCCTGGCCTC 540
CCACGCTCAC GGGCCGAGCG CCGGGGCGGC GCCCAGCCTG CTACTCTTGC TGCCCTGCGC 600
40 ACTCTGCAC CGCCTCCTGC GCCCGGATGC GCCCGGCGAC CCGGTGCTCC TGGTCCCTTC 660
CGTCTCCAG CGGGAGCGGC GCCCTCGCGG AAGGCGCGGA CTGGGCGATC GCCTTTAATT 720
TTCTATGTT TAAATAATAG ATGTGTTTAG TTACCGTAA GCTGAAGCAC TGGGTGAATA 780
TTTTTATGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA 840
AAAAAA 846

45 Seq ID NO: C131 DNA Sequence
Nucleic Acid Accession #: NM_006533.1
Coding sequence: 72..467

50 1 11 21 31 41 51
AGGGAGAGAG GGAGGGGAGG AAATTGGAGA CCCCAGCACC CCCTTGCTCA CTCTCTTGCT 60
CACAGTCCAC GATGGCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCTT 120
TCTCCGACAC TGGTGTGACG GGTGGTCTTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180
55 CGGACCAAGA GTGACGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGGCC 240
CCGACTGCGG ATTCTGTACC ATTCACCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300
AGGGCCGTTG GCGGCTCTTC TGGGAGGACA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360
CTGCTCGCCT GGGCTATTTC CCAAGTAGCA TTGTCCGAGA GGAACAGACC CTGAAACCTG 420
60 GCAAGTGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCCTACCG 480
CTGGCCCTGC CGTTTCCCTT CCTTGGGTTT ATGCAATATC AATCAGCCCA GTGCAAAAC 538

65 Seq ID NO: C132 DNA Sequence
Nucleic Acid Accession #: AB064272
Coding sequence: 1..708

70 1 11 21 31 41 51
ATGACACAAG TCACAGAAAA GTCCACAGAA CACCCAGAAA AGACCAGCTC AACCAAGAG 60
AAAACCACAA GAACCCAGAA AAAGCCTAAG CTATACTCAG AGAAGACCAT ATGCACCAAA 120
GGGAAAAACA CACCACTCCC AGAAAAGCCT ACAGAAAACC TGGGSAACAC CACACTGACC 180
ACTGAGACCA TAAAGCCCC AGTAAAGTCC ACAGAAAACC CAGAAAAAAC AGCAGCAGTC 240
ACAAAGACTA TAAACCTTC AGTCAAGGTC ACAGAGACAA AATCTCTCAC TACTACCTCT 300
TCTCATCTAA ATAAACTGA AGTTACTCAT CAGGTGCCCA CTGGTTCTTT CACCTCAT 360
75 ACATCTAGAA CGAAGCTGAG TTCTATCACA TCAGAAGCCA CAGGAAACGA GAGCCATCCA 420
TACCTCAATA AAGATGGCTC ACAGAAAGGT ATCCAAGCTG GACAGATGGG AGAGAATGAT 480
TCATTCCCTG CATGGGCCAT AGTTAATGTG GTCCCTGGTG CTGTGATTCT CCTCCTGGTG 540
TTCTTGGCC TGATCTCTCT GGTCTCCTAT ATGATGCGGA CACGCGCAC ACTAACCCAG 600
80 AACACCCAGT ACAATGATGC AGAGGATGAG GGTGGCCCCA ATCTCTACCC GGTCTACCTG 660
ATGGAGCAGC AGAATCTTGG CATGGGCCAG ATCCCTTCCC CACGGTGA 708

Seq ID NO: C133 DNA Sequence
Nucleic Acid Accession #: NM_080870.1
Coding sequence: 3..710

	1	11	21	31	41	51	
5	AGATGACACA	AGTCACAGAA	AAGTCCACAG	AACACCCAGA	AAAGACCACG	TCAACCACAG	60
	AGAAAAACCC	AAGAACCCCA	GAAAAGCCCTA	OGCTATATCT	AGAGAGAGACC	ATATGCACCA	120
	AAGGGAAAAA	CACACCAGTC	CCAGAAAAGC	CTACAGAAAA	CCTGGGGAAC	ACCACACTGA	180
	CCACTGAGAC	CATAAAAGCC	CCAGTAAAGT	CCACAGAAAA	CCCAGAAAAA	ACAGCAGCAG	240
	TCACAAAGAC	TATAAAACCT	TCAGTCAAGG	TCACAGGAGA	CAAATCTCTC	ACTACTACCT	300
10	CTTCTCATCT	AAATAAAACT	GAAGTTACTC	ATCAGGTGCC	CACTGGTTCT	TTCACCTCA	360
	TTACATCTAG	AACGAAGCTG	AGTTCTATCA	CATCAGAAAC	CACAGGAAAC	GAGAGCCATC	420
	CATACCTCAA	TAAAGATGGC	TCACAGAAAG	GTATCCACGC	TGGACAGATG	GGAGAGAAATG	480
	ATTCAITCCC	TGCATGGGCC	ATAGTTAATG	TGGTCCTGGT	GGCTGTGATT	CTCCTCTCTG	540
	TGTTCTTGG	CCTGATCTTC	TTGGTCTCCT	ATATGATGCG	GACACGCCGC	ACACTAACCC	600
15	AGAACACCCA	GTACAATGAT	GCAGAGGATG	AGGGTGGCCC	CAATTCCTAC	COGCTCTACC	660
	TGATGGAGCA	GCAGAATCTT	GGCATGGGCC	AGATCCCTTC	CCCAOCGTGA	TCTTGGAGTA	720
	GGCGCCACGC	CCTGGCTCTT	CCATGCTCTG	CCCTTTCTCT	GGATGAGGAA	COGGACTCAC	780
	AATTTCTATT	TCOGGGACTA	CAGGAAGGGC	AGAGAATACT	GACGGTTACC	AGTATTAACC	840
	CTTCATCTGT	TCTTGAACCT	GGTTGGGGAA	TGAGGTGATA	AGCAAGGAGG	GTGTAAAGTT	900
20	AGGGGACAAA	GAAGAAAGAA	TGAATAATAC	GAGCAGACAT	TCTCTGTAGA	AGGTAATGGT	960
	CTGAGAATGA	AAAGGTGTTT	GATGGACATG	TTGTGGGGGC	ACCAATGCAG	AACACTGCAC	1020
	TGAGTCTCAA	AGGAAGGACA	GGAGCCTTAT	AGGCAATGCC	CCAGACTGAC	TTGTGAGTGG	1080
	GGTTTATGGG	GAAAGGGAGG	GACTGAGGGC	AGAGTCTCTG	GGTTTCAGGA	CAGCATTATG	1140
	TTAATTCAT	TCACTATTAC	TTAAGAGTTT	GTGTGTAAC	AGGCTCATCT	CTGAGTTCTC	1200
25	AGGACCCCTG	CCCCACCCCT	CATTTTTTTA	ATGAAAAAAA	AAAACAAAA	AAACGGATCC	1260
	AAGAAGAAAA	GAGAATTTAT	TTCTTCTCC	ACTCTCTCCA	TGCCCTGGAG	AAAAAAAAGT	1320
	CCAGAAGAAA	TCATAAATAT	CTCTCATCTA	CATGGTTGCT	TCTCTTCTCT	CCCAATCCCT	1380
	TTAGTTTTC	TAAATGTCTA	CAGTGGACGC	CCTGTTGGTT	TGGCTTGGTG	GGTTTGGGGT	1440
	GGACACGCAA	GGAGGGGATT	TTTATTGGC	CAGCAGTCTC	ACCCACTGAT	CTCCACCCCA	1500
30	GACCTTCCCT	GATTGGTGTG	TCAGCATTTA	TTTTCTCTGC	TCTTCCACCA	AAAGCCAGCT	1560
	GTAGCTTTAT	CTCGTAAAGG	TTACCCATCT	TCTCTACTGT	CCCAATTCTC	TCTCTCCCA	1620
	CCTTCACCCC	AGATTCAAGT	TTTCTCTCTT	GTAGGCATTT	CATCTGTGTG	TGTTTCTCTG	1680
	ATTTTCTCTC	TCTCTTCTTA	TGGCCATTTC	ACCTTATTAC	TGATTGGGTA	GAGGGGAAAA	1740
35	AGGAGAATGA	TGATGATAGT	TTCTTCTGT	CTATTGACCT	TTTTTATAAT	AAAGTATAAC	1800
	ATGTT						1805

Seq ID NO: C134 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..10674

40	1	11	21	31	41	51	
	ATGTGGCCTC	GCCTGGCCTT	TTGTTGCTGG	GGTCTGGGCG	TCGTTTCGGG	CTGGGCGACC	60
45	TTTCAGCAGA	TGTCGCCGTC	GCGCAATTTT	AGCTTCCGCC	TCTTCCCGCA	GACCGCGCCC	120
	GGGGCCCCCG	GGAGTATCCC	OGCGCGGCCC	GCTCCTGGCG	ACGAAGCGGC	GGGGAGCAGA	180
	GTGGAGCGGC	TGGGCCAGGC	GTTCCGGCGA	CGCGTGCGGC	TGCTGCGGGA	GCTCAGCAGG	240
	CGCCTGGAGC	TTGTCTTCTT	GGTGGATGAT	TCGTCCAGCG	TGGGCGAAGT	CAACTTCCGC	300
	AGCGAGCTCA	TGTTCTGTCG	CAAGCTGCTG	TCGCACTTCC	COGTGGTGCC	CACGGCCACG	360
50	CGCGTGGCCA	TCTGTACCTT	CTGTCCAGG	AACTAAGTGG	TGCCGCGCGT	CGATTACATC	420
	TCCACCGGCC	GCGCGCGCCA	GCACAAGTGC	GCGCTGCTCC	TCCAAGAGAT	CCCTGCCATC	480
	TCCTACCGAG	GTGGCGGCAC	CTACACCAAG	GGCGCCTTCC	AGCAGCCGCG	GCAAAITCTT	540
	CTTCATGCTA	GAGAAAACCT	AACAAAAGTT	GTATTTCTCA	TCACTGATGG	ATATTCCAAT	600
	GGGGAGAGCC	CTAGACCAAT	TGCAGCGTCA	CTGGAGAGAT	CAGGAGTGGG	GATCTTCACT	660
55	TTTGCAATAT	GGCAAGGGAA	CATTGAGAG	CTGAATGACA	TGGCTTCCAC	CCCAAAGGAG	720
	GAGCACTGTT	AACCTGCTACA	CAGTTTGTAA	GAATTTGAGG	CTTTAGCTCG	CCGGGCATTG	780
	CATGAAGATC	TACCTTCTGG	GAGTTTATAT	CAAGATGATA	TGGTCCACTG	CTCATATCTT	840
	TGTGATGAAG	GCAAGGACTG	CTGTGACCGA	ATGGGAGACT	GCAATGTGGG	GACACACACA	900
	GGCCATTTTG	AGTGCATCTG	TGAAAAGGGG	TATTAAGGGA	AAGGTCTGCA	GTATGAATGC	960
60	ACAGCTTGCC	CATCGGGGAC	ATACAAACCT	GAAGGCTCAC	CAGGAGGAAT	CAGCAGTTGC	1020
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	GAAGGGTCTA	GTACCAAGTA	TTATTGTGCT	TATGAAGATG	GGGTCTGGAA	ACCAACATAT	2340
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Seq ID NO: C135 DNA Sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..390

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Seq ID NO: C137 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1761

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	TGTGCTTCTG	ACTATCTTCT	CTTCACCAGC	TCTTCAGATC	AATATGGTCC	ATACTGTGGA	480
40	AGTATGACTG	TTCCCAAAGA	ACTCTTGTGG	AACACAAAGT	AAGTAAACCGT	CGGCTTTGAG	540
	AGTGGATCCC	ACATTTCTGG	CCGGGGTTTT	TGCTGACCTT	ATGCGAGCAG	CGAACCATCA	600
	GATTTAATAA	CATGTTTGGA	ACGAGCTAGC	CATTATTTGA	AGACAGAAAT	CAGCAAATTC	660
	TGCCACAGTG	GTGTAGAGAA	CGTAGCAGGA	GACATTTCTG	GGAATATGGT	AGATGGATAT	720
	AGAGATACCT	CTTTATTTGT	CAAAGCTGCC	ATCCATGCAG	GAATAATTGC	TGATGAACATA	780
45	GGTGGCCAGA	TCAGGTGTCT	TCAGCGCAAA	GGGATCAGTC	GATATGAAGG	GATTCTGGCC	840
	AATGGTGTTC	TTTCGAGGGA	TGGTTCCTTG	TCAGACAAGC	GATTTCTGTT	TACCTCCAAT	900
	GGTTGCAGCA	GATCCTTGAG	TTTTGAACCT	GACGGGCAAA	TCAGAGCTTC	TTCTCTCATG	960
	CAGTCGGTCA	ATGAGATGCG	AGACCAAGTT	CAGTGGTCTC	CTGGCCAAAG	CCGACTTCAG	1020
	GACCAAGGCC	CATCATGGGC	TTGCGGCGAC	AGTAGCAACA	ACCACAAACC	ACGAGAGTGG	1080
50	CTGGAGATCG	ATTTGGGGGA	GAATAAGAAA	ATAACAGGAA	TTAGGACCA	AGGATCTACA	1140
	CAGTCGAATC	TCAACTTTTA	TGTTAAGAGT	TTTGTGATGA	ACTTCAAAAA	CAATAATTCT	1200
	AAGTGAAGA	CCATAAAGG	AATTGTGAAT	AATGAAGAAA	AGGTGTTTCA	GGGTAACTCT	1260
	AACCTTTCGG	ACCCAGTGCA	AAACAATTTC	ATCCCTCCCA	TGTTGGCCAG	ATATGTGCGG	1320
	GTGTGCCCCC	AGACATGGCA	CCAGAGGATA	GCCTTGAAGG	TGGAGCTCAT	TGGTTGCCAG	1380
55	ATTACACAAG	GTAATTGATT	ATTGGTGTGG	CGCAAGACAA	GTCAAAGCAC	CAGTGTTCAT	1440
	ACTAAGAAAG	AAGATGAGAC	AATCACAAAG	CCCATCCCTT	CGAAGAAAC	ATCCACAGGA	1500
	ATAAACATTA	CAACGGTGGC	TATTCCATTG	GTGCTCCTTG	TTGTCTGGGT	GTTTGTCTGA	1560
	ATGGGGATCT	TTGCAGCCTT	TAGAAAGAA	AAGAAGAAAG	GAAGTCCGTA	TGGATCAGCA	1620
	GAGGCTCAGA	AAACAGACTG	TTGGAAGCAG	ATTAAATATC	CCTTTGCCAG	ACATCAGTCA	1680
60	GCTGAGTTTA	CCATCAGCTA	TGATAATGAG	AAGGAGATGA	CACAAAGTTT	AGATCTCATC	1740
	ACAAGTGATA	TGGCAGGTTA	A				1761

Seq ID NO: C138 DNA Sequence
Nucleic Acid Accession #: PGENSEH predicted
Coding sequence: 1..2310

65	1	11	21	31	41	51	
	ATGTTCCAGC	GGCAGGAAG	ATTCTCTGAC	TTATCTTCAG	CTGAAGCAGT	GGCAGCTTGG	60
	ATATTACATC	AACATCTCTA	CATTATTAAC	AAAGGTGATG	GCTGTGGACA	CCTAGTGACT	120
70	TATCAGGATA	GTGGCACAAT	GACATCTAAG	AATTATCCCG	GGACCTACCC	CAATCACACT	180
	GTTTGCGAAA	AGACAATTAC	AGTACCAAAG	GGGAAAAGAC	TGATTTCTGAG	GTGTGGAGAT	240
	TTGGATATCG	AATCCAGAC	CTGTGCTTCT	GACTATCTTC	TCTTCAACAG	CTCTTCAGAT	300
	CAATATGGAA	TGCAGAAGGA	GGAGGAGACA	GAAGTGCTTT	GTCTTTCAGT	GGCTGGCGCT	360
	CAGAGAGTGG	ACATTCTCTG	GCAGCTGTTG	CCGAGCTTCC	TGGAAGGGTG	GAAGGGTCAT	420
75	GCTGATGCAA	GAGGTTCATA	CTGTGGAAGT	ATGACTGTTC	CCAAAGAACT	CTTGTGTAAC	480
	ACAAGTGAAG	TAAACGTCGG	CTTTGAGAGT	GGATCCACCA	TTTCTGGCCG	GGGTTTTTTG	540
	CTGACCTATG	CGAGCAGGGA	CCATCCAGAT	TTAATAACAT	GTTTGGAAAG	AGCTAGCCAT	600
	TATTTGAAGA	CAGAATACAG	CAAAATCTGC	CCAGCTGGTT	GTAGAGAGCT	AGCAGGAGAC	660
80	ATTCTTGGGA	ATATGGTAGA	TGATATATAGA	GATACCTCTT	TATTTGTCAA	AGCTGCCATC	720
	CATGCAGGAA	TAATGCTGTA	TGAAGTGGT	GGCCAGATCA	GTGTGCTTCA	GGCAGAAAGG	780
	ATCAGTCGAT	ATGAAGGGAT	TCTGGCCAAT	GGTGTCTTCT	CGAGGGATGG	TTCCCTGTCA	840
	GACAAAGCAT	TCTGCTTAC	CTCCAATGGT	TGCAGCAGAT	CAATTGAGTTT	TGAACCTGAC	900
	GGGCAATCA	GAGCTTCTTC	CTCATGGCAG	TGCGTCAATG	AGAGTGGAGA	CCAAGTTTAC	960

5 TGGTCTCCTG GCCAAGCCCG ACTTCAGGAC CAAGGCCCAT CATGGGCTTC GGGCGACAGT 1020
 AGCAACAACC ACAAACCACG AGAGTGGCTG GAGATCGATT TGGGGGAGAA AAAGAAAATA 1080
 ACAGGAATTA GGACCACAGG ATCTACACAG TCGAACTTCA ACTTTTATGT TAAGAGTTTT 1140
 GTGATGAAC TCAAAAACAA TAATTCTAAG TGAAGACCT ATAAAGGAAT TGTGAATAAT 1200
 GAAGAAAAGG TGTTCAGGG TAACTCTAAC TTTCGGGACC CAGTGC AAAA CAATTTTCATC 1260
 CCTCCATCG TGGCCAGATA TGTGCGGTT GTCCCCAGA CATGGCACC CAAGATAGCC 1320
 TTGAAGGTGG AGCTCATTTG TTGCCAGATT ACACAAGGTA ATGATTCAAT GGTGTGGCGC 1380
 AAGACAAGTC AAAGCACCAG TGTTCACAT AAGAAAGAA ATGAGACAAT CACAAGGCC 1440
 ATCCCTCGG AAGAAACATC CACAGATGCC ATGCCAGTGC AGATTGTGG AGACCATACC 1500
 10 CAGATGATCT CACAAGGGA GAATCTGGGA CCTGATGAGG GCAAAATACC TTTTAAAGGC 1560
 ACAGGGGAAA GCATGGTTAG AGTAGTGTGT GCTGTGTGG TTAATGACCT TGGCATGCTG 1620
 TTCTTAGCAC ACACACCTGA GGAGGACATT GATCACTACT GTTGAAGCA GATTAAATAT 1680
 CCCTTTGCCA GACATCAGTC AGCTGAGTTT ACCATCAGCT ATGATAATGA GAAGGAGATG 1740
 ACACAAAAGT TAGATCTCAT CACAAGTAT ATGGCAGATT ACCAGCAGCC CCTCATGATT 1800
 15 GGCACCGGGA CAGTCAAGAG GAAGGGCTCC ACCTTCGGGC CCATGGACAC GGATGCCGAG 1860
 GAGGCAGGGG TAGCACCAGA TGCCGGCGGC CACTATGACT GCCCGCAGCG GGC CGGCGCG 1920
 CACGAGTACG CGCTGCCCTT GCGCGCCCG GAGCCCGAGT ACGCCACGCC CATCGTGAG 1980
 CGGCACGTGC TCGCGGCCA CACGTCTCT GCGCAGAGCG GCTACCGGT CCCAGGGCCC 2040
 CAGCCCGGCC ACAAACACTC CCTCTCTCG GCGCGCTTCT CCCCGTAGC GGGTGTGGGC 2100
 20 GCCCAGGACG GAGACTATCA AAGGCCACAC AGCGCACAGC CTGCGGACAG GGGCTAAGAC 2160
 CGGCCCAAG CTGTACGCGC CCTCGCCACC GAAAGCGGCG ACCCTGACTC TCAGAAAGCCC 2220
 CCAAGCATC CGGGACGAG TGACAGCTAT TCTGCCCA GAGACTGCCT CACACCCCTC 2280
 AACCAGCGG CCATGACTGC CCTTTGTGA 2310

25 Seq ID NO: C139 DNA Sequence
 Nucleic Acid Accession #: NM_004616.2
 Coding sequence: 180..893

30 1 11 21 31 41 51
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 AGTGCCCCAG GAGCTATGAC AAGCAAAGGA ACATACTTGC CTGGAGATAG CCTTTGCGAT 60
 ATTTAAATGT CCGTGGATAC AGAAATCTCT GCAGGCAAGT TGCTCCAGAG CATATTGCAG 120
 GACAAGCCTG TAACGAATAG TTAATTCAC GGCATCTGGA TTCTTAATCC TTTCCGAAA 180
 35 TGGCAGGTGT GAGTGCGCTG ATAAAATATT CTATGTTTAC CTTCACCTC TTGTCTTGGC 240
 TATGTGGTAT CTGTATCCTA GCATTAGCAA TATGGGTACG AGTAAGCAAT GACTCTCAAG 300
 CAATTTTGGG TTCTGAAGAT GTAGGCTCTA GCTCCTACGT TGCTGTGGAC ATATTGATTG 360
 CTGTAGGTGC CATCATCATG ATTCTGGGCT TCCTGGGATG CTGCGGTGCT ATAAAGAAA 420
 GTGCTGCAAT GCTTCTGTGG TTTTTCATAG GCTTGTCTCT GATCCTGCTC CTGCAGGTGG 480
 CGACAGGTAT CCTAGGAGCT GTTTTCAAT CTAACTCTGA TCGCATTTGT AATGAACTC 540
 40 TCTATGAAA CACAAGCTT TTGAGCGCCA CAGGGGAAAG TGAAAAACAA TTCCAGGAAG 600
 CCATAATGT GTTTCAGAA GAGTTTAAAT GCTGCGGTTT GGTCAATGGA GCTGCTGATT 660
 GGGGAAATAA TTTTCAACAC TATCCTGAAT TATGTGCTG TCTAGATAAG CAGAGACCAT 720
 GCCAAAGCTA TAATGGAAAA CAAGTTTACA AAGAGACCTG TATTTCTTTC ATAAAGACT 780
 TCTTGGCAA AATTTTGAAT ATAGTTATG GAATATCATT TGGACTGGCA GTTATTGAGA 840
 45 TACTGGTTT GGTGTTTCTT ATGCTCCTGT ATTGCCAGT CGGGAACAAA TGAATCTGTG 900
 GATGCATCAA CCTATGCTA GTCAAACCCC TTTAAATGT TGCTTTGGCT TTGTAAATTT 960
 AAATATGTAA GTGCTATATA AGTCAGGAGC AGCTGTCTTT TTAATATGTC TCGGCTAGCT 1020
 AGACCAAGA TATCTTCTAG ACATATTGAA CACATTTAAG ATTTGAGGGA TATAAGGAA 1080
 AATGATATGA ATGTGTATTT TTACTCAAAA TAAAGTAAC TGTTTACGTT AAAAAAATA 1140
 50 AAAAAAATA AAAAAAATA 1159

55 Seq ID NO: C140 DNA Sequence
 Nucleic Acid Accession #: NM_004617.2
 Coding sequence: 232..840

60 1 11 21 31 41 51
 | | | | |
 CTTCAAGTCA GGGAGAATGT ATAAATGTCC ATTGCCATCG AGGTTCTGCT ATTTTGTAGA 60
 AGCTGAGCA ACTCCAAGGA CACAGTTTAC AGAAATTTGG TTCTCAGCCC CAAAATACTG 120
 ATTGAATTGG AGACAATTAC AAGGACTCTC TGGCCAAAAA CCTTGAAGA GGCCCGTGA 180
 AGGAGGCAGT GAGGAGCTTT TGATTGCTGA CCTGTGTGCT ACCACCCAG AATGTGCACT 240
 GGGGGCTGTG CCAGATGCCT GGGGGGGACC CTCATTCCCC TTGCTTTTTC TGGCTTCTCG 300
 GCTAACATCC GTTTATTTT TCCTGGAGGA AAAGTGATAG ATGACAAOGA CCACCTTTCC 360
 65 CAAGAGATCT GGTTTTTCGG AGGAATATTA GGAAGCGGTG TCTTGATGAT CTTCCTGCG 420
 CTGGTGTCT TGGGCTGAA GAACAATGAC TGCTGTGGGT GCTGCGGCA CGAGGGCTGT 480
 GGGAGGAGAT TTGCGATGTT CACCTCCACG ATATTGCTG TGGTTGGATT CTGGGAGCT 540
 GGATACCTGT TTATCATCTC AGCCATTTC AACAACAGG GTCCATAATG CCTCATGGCC 600
 AATAGTACAT GGGGCTACCC CTTCACGAC GGGGATTATC TCAATGATGA GGCCTTATGG 660
 70 AACAGTGCC GAGAGCTCT CAATGTGTT CCTTGAATC TGAACCTCT CTCCATCTCG 720
 CTGGTCTGAG GAGGAATCCA GATGTTCTC TGGGCCATCC AGGTGGTCAA TGGCCTCTCG 780
 GGGACCTCT GTGGGACTG CCAGTGTGT GGTGCTGTG GGGGAGATGG ACCCGTTAA 840
 ACCTCCGAGA TGAGCTGCTC AGACTCTACA GCATGACGAC TACAATTTCT TTTCATAAAA 900
 CTCTCTCT CTCTGGAAT ATTAATCTCT ATCTGCTTCC TAGCTGATA AGCTTAGAAA 960
 75 AGGCAGTTAT TCCCTCTTC CAACAGCTT TGCTGAGTT AGAATTTTGT TATTTTCAAA 1020
 TAAAAAATAG TTTGGCCACT TAACAAATTT GATTATATAA TCTTTCAAT TAGTTCTCTT 1080
 TTAGAATTTA CCAACAGGTT CAAAGCATAC TTTTCATGAT TTTTATTA CAAATGTAAA 1140
 ATGTATAAAG TCACATGTAC TGCCATACTA CTCTTTGTA TATAAGATG TTTATATCTT 1200
 TGAAGATTTT ACATAAATCA AAGGAAGAAA GCACATTTAA AATGAGAAAC TAAGACCAAT 1260
 80 TTCTGTTTTT AAGAGGAAAA AGAATGATG ATGTATCTTA AGTATTGTTA TTTGTGTCT 1320
 TTTTGTGCTG CCTTGTCTGA GTTGTGTGT ACTGATCTTT TGAGGCTGTC ATCATGGCTA 1380
 GGTTCCTTT ATGTATGTTA AATTAAAAAC TGAATTCAGA GGTAACTG 1428

Seq ID NO: C141 DNA Sequence
 Nucleic Acid Accession #: NM_002381.2

Coding sequence: 64..1524

	1	11	21	31	41	51	
5	AAATCCGAGC	CTGCGTGGG	CTCCTGGCCC	CGAAGGACA	CCACGAGGCC	CACGAGAGCC	60
	ACCATGCCGC	GCCCGGCCCC	CGCGCGCCGC	CTCCCGGGAC	TCTCTCTGCT	GCTCTGGCCG	120
	CTGCTGCTGC	TGCCCTCCGC	CGCCCCCGAC	CCCGTGGCCC	GCCCGGGCTT	CCGAGGGCTG	180
	GAGACCGGAG	GTCCCGGGGG	CAGCCCTGGA	CGCGCCCTCT	CTCCTGCGGC	TCCCGACGGC	240
	GCGCCGCTT	CGGGGACCA	CGAGCCTGGC	CGCGCCCGCG	GTGCAGGTGT	TTGCAAGAGC	300
10	AGACCCCTTG	ACCTGGTGT	TATCATTGAT	AGTTCTCGTA	GCGTACGGCC	CCTGGAATTC	360
	ACCAAGTGTA	AACTTTTGT	CTCCCGGATA	ATCGACATCT	TGGACATTGG	GCCAGCGGAC	420
	ACGCGGTGG	CAGTGGTGAA	CTATGCTAGC	ACTGTGAAGA	TGAGTTTCCA	ACTCCAGGCC	480
	TACACAGATA	AGCAGTCCCT	GAAGCAGGCT	GTGGGTGAA	TCACACCTTT	GTCAACAGGC	540
	ACCATGTCAG	GCCTAGCCAT	CCAGACAGCA	ATGGACGAAG	CCTTCACAGT	GGAGGCAGGG	600
15	GCTCGAGAGC	CCTCTTCTAA	CATCCCTAAG	GTGGCCATCA	TTGTTACAGA	TGGAGGGCCC	660
	CAGGACCAAG	TGAATGAAGT	GGCGGCTCGG	GCCCAAGCAT	CTGGTATTGA	GCTCTATGCT	720
	GTGGGTGGG	ACCGGGCAGA	CATGGGCTCC	CTCAAGATGA	TGGCCAGTGA	GCCCTTAGAG	780
	GAGCATGTTT	TCTACGTGGA	GACCTATGGG	GTCAATTGAGA	AACTTTCCTC	TAGATTCCAG	840
	GAAACCTTCT	GTGGCTGGA	CCCTGTGTG	CTTGAACAC	ACCAAGTGCA	GCACTCTGTC	900
20	ATCAGTGATG	GGGAAGGCAA	GCACCACTGT	GAGTGTAGCC	AAGGATACAC	CTTGAATGCC	960
	GACAAAGAAA	CGTGTTCAGC	TCTTGATAGG	TGTGCTCTTA	ACACCCACGG	ATGTGAGCAC	1020
	ATCTGTGTGA	ATGACAGAAG	TGGCTCTTAT	CATTGTGAGT	GCTATGAAGG	TTATACCTTG	1080
	AATGAAGACA	GGAAACTTGG	TTCACTCAAA	GATAAATGTG	CTTTGGGTAC	CCATGGGTGT	1140
	CAGCACATTT	GTGTGAATGA	CAGAACAGGG	TCCCATCATT	GTGAATGCTA	TGAGGGCTAC	1200
25	ACTCTGAATG	CAGATAAAAA	AACATGTTCA	GTCCGTGACA	AGTGTGCCCT	AGGCTCTCAT	1260
	GGTGGCCAGC	ACATTTGTGT	GAGTGATGGG	GCCGCATCCT	ACCAGTGTGA	TTGCTATCCT	1320
	GGCTACACTT	TAAATGAGGA	CAAGAAAACA	TGTTCAAGCA	CTGAGGAAGC	AOGAAGACTT	1380
	GTTCACACTG	AAGATGCTTG	TGGATGTGAA	GCTACACTGG	CATTCCAGGA	CAAGGTGAGC	1440
	TGATATCTTC	AAAGACTGAA	CACTAAACTT	GATGACATTT	TGGAGAAGTT	GAAAAATAAT	1500
30	GAATATGGAC	AAATACATCG	TTAAATTGCT	CCAATTCTC	ACCTGAAAT	GTGCACAGCT	1560
	TGGTGTACTT	AATACTCATG	CATTCTTTTG	CACACCTGTT	ATTGCCAATG	TTCTCTGCTAA	1620
	TAATTTGCCA	TATCTGTAT	TAATGCTTGA	ATATTACTGG	ATAAATTGTA	TGAAGATCTT	1680
	CTGCAGAAAT	AGCATGATTT	TTCCAGGAA	ATACATATGC	AGATACTTAT	TAAGAGCAAA	1740
35	CTTTAGTGTC	TCTAAGTTAT	GACTGTGAAA	TGATTGGTAG	GAAATAGAAT	GAAAAGTTTA	1800
	GTGTTTCTTT	ATCTACTAAT	TGAGCCATTT	AAATTTTAAA	TGTTTATATT	AGATAACCAT	1860
	ATTACAAATG	GAACTTTTAA	GTCTAGTTTC	TTTTGATAGT	ATTATATAAT	TAAATCAATC	1920
	TTATTACTGA	GAGTGCAAAAT	TGTACAAGGT	ATTACACAT	ACNACTTCAT	ATAACTGAGA	1980
	TGAATGTAAT	TTTGAAGTGT	TTAACACTTT	TTGTTTTTTG	CTTATTTTGT	TGGAGTATTA	2040
40	TTGAAGATGT	GATCAATAGA	TTGTAATACA	CATATCTAAA	AATAGTTAAT	ACAGATCAAG	2100
	TGAACATTAT	ATTGCCATTT	TTAATTCTAT	CTGGTCTTTG	AAAGAAATGT	ACTACTAAAG	2160
	AGCACTAGTT	GTGAATTTAG	GGTGTAAAC	TTTTTACCAG	GTACAAAAT	CCCAAAATCA	2220
	CTTTATTATT	TTGCTTCAGG	ATCCAAGTGA	CAAAGTTATA	TATTTATAAA	ATTGCTATAA	2280
	ATCGACAAAA	CTTAATGTTG	TCCTTTTAA	TTTAGTGATC	CACCTGCCCT	AGCCTCCCAA	2340
45	AGTGTCTGGG	TTACAGGCTT	GAAAGTCTAA	CTTTTCTTTA	CTTATATATT	TGATACATAT	2400
	AATTTCTTTG	GCTTTGAAAC	TTGCAACTTT	GAGAACAAAA	CAGTCCCTTA	AAATTTGCAC	2460
	TGCTCAATTC	TGTTTTCGT	TTGCATTGTC	TTTAATATAA	TAAAGTTTAT	TACCTTTACA	2520
	TATTATCATG	TCTATTTTGG	ATGACTCATC	AATTTTGTCT	ATTAAGATA	TTTCTTTAAA	2580
	TTAAAAAAA	AAAAAAA					2599

Seq ID NO: C142 DNA Sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

55	1	11	21	31	41	51	
	GCGGCGGGCG	CAGACAGCGG	CGGGCGCAGG	ACGTGCACTA	TGGCTCGGGG	CTGCTGCGC	60
	CGGTTCCTGC	GGCTCCTCGT	GCTGGGGCTC	TGGCTGGCGT	TGCTGCGCTC	CGTGGCGGGG	120
	GAGCAGCGCG	CAGGACCGCG	CCCTGCTCC	CGCGGCAGCT	CCTGGAGCGC	GGACCTGGAC	180
60	AAGTGCATCG	ACTGCGGTC	TTGCAGGCGG	CGACCGCACA	GCGACTTCTG	CCTGGGCTGC	240
	GCTGCAGCAC	CTCCTGCCCC	CTTCCGGCTG	CTTTGGCCCA	TCCTTGGGGG	CGCTCTGAGC	300
	CTGACCTTCG	TGCTGGGGCT	GCTTCTGCGC	TTTTTGTCT	GGAGACGATG	CGCAGGAGAG	360
	GAGAAGTTCA	CCACCCCAT	AGAGGAGACC	GGCGGAGAGG	GCTGCCCGAG	TGTGGGCTGC	420
	ATCCAGTGAC	AATGTGCCCG	CTGCCAGCGG	GGGCTCGCCC	ACTCATCAT	CATTATCCCA	480
65	TTCTAGAGCC	AGTCTCTGCC	TCCAGAGCGC	GGCGGGAGCC	AAGCTCTCTC	AAACCAAGAG	540
	GGGGTGGGGG	GCGGTGAATC	ACCTCTGAGG	CCTGGGCCCA	GGGTTCAGGG	GAACCTTCCA	600
	AGGTGTCTGG	TTGCCCTGCC	TCTGGCTCCA	GAACAGAAAG	GGAGCCTCAC	GCTGGCTCAC	660
	ACAAAACAGC	TGACACTGAC	TAAGGAACCTG	CAGCATTTGC	ACAGGGGAGG	GGGGTGCCCT	720
70	CCTTCTCTAG	GACCTGGGGG	CCAGGCTGAC	TTGGGGGGCA	GACTTGACAC	TAGGCCCCAC	780
	TCACTCAGAT	GTCTGAAAT	TCCACCACGG	GGGTCAACCT	GGGGGGTTAG	GGACCTATTT	840
	TTAACTACTAG	GGCTGGGGCC	ACTAGAGGGG	CTGGCCCTAA	GATACAGACC	CCCCCACTC	900
	CCCAAGCGCG	GGAGGAGATA	TTTATTTTGG	GGAGAGTTTG	GAGGGGAGGG	AGAAATTTATT	960
	AATAAAGAA	TCITTAACCT	TAAAAAATA	AAAAAATA			998

Seq ID NO: C143 DNA Sequence
Nucleic Acid Accession #: NM_001819
Coding sequence: 113..2146

80	1	11	21	31	41	51	
	CCAGGAGGCA	CGCTGGTTTT	CGGGGGCGGC	TCCATCGCGC	CTTCTCTCTG	CGCCTCGCTT	60
	CTCCGGTCCA	GCGCCCATCT	TCCTTTCCGC	ACAGGGGCGG	CGAGCGGGGG	CCATGCAGCC	120
	AACGCTGCTT	ATCCACTCTC	TGGGAGCCGT	GGGGCTGGGG	GCTGTCAATT	CCATGCCAGT	180
	GGATAACAGG	AACACCAATG	AAGGAATGTT	GACTCGCTGC	ATCATTGAGG	TCCTCTCAAA	240

5 TGCCCTTGTC AAGTCCAGCG CTCACCCAT CACCCCTGAG TGCCGCCAAG TCCTGAAGAC 300
 GAGTAGAAAA GACGTCAAAG ACAAAGAGAC AACTGAAAT GAAAAACAA AGTTTGAAGT 360
 AAGATTGTTA AGAGACCCAG CTGATGCCCTC GGAAGCCAC GAGTCTCCA GCAGGGGAGA 420
 GGCAGGAGCC CCAGGGGAGG AGGACATCCA AGGCCAACA AAGGCAGACA CAGAGAAATG 480
 GGCAGAGGGA GCGGGGCACA GCGAGAGCG AGCGGATGAG CCCCAGTGA GCTCTATCC 540
 CTCGACAGC CAAGTCTCTG AAGAAGTGAA GACACGCCAT TCTGAGAAGA GCCAGAGAGA 600
 GGATGAGAGG GAGGAGGAGG GAGAGAACTA TCAAAAAGGG GAGCGAGGGG AAGATAGCAG 660
 TGAAGAGAAA CACCTTGAAAG AGCCAGGAGA GACACAAAC GCTTTTCTCA ATGAAAGAAA 720
 GCAGGCTTCA GCTATAAAAA AAGAGGAGTT AGTGGCCAGA TOGGAACAC ATGCTGCCGG 780
 10 GCATTCTCAG GAGAAGACAC ATAGCCGAGA GAAGAGTAGC CAGGAGAGTG GAGAGGAGGC 840
 AGGGAGCCAG GAGAATCACC CCCAGGAGTC TAAAGGCCAA CCCCAGAGCC AGGAAGAATC 900
 TGAGGAAGGT GAGGAAGATG CCACCTCTGA GGTGGACAAA CGACGCACGA GGCCAGACA 960
 CCACCAAGGG AGGAGCAGGC CCGACAGGTC CTCTCAAGGA GGGAGTCTTC CCTCTGAGGA 1020
 AAAGGGACAC CCCAGGAGG AATCTGAGGA GTCAAACGTC AGCATGGCCA GTTTAGGGGA 1080
 15 AAAGAGGGAC CACCATTCAA CCCACTACAG GGCTTCAGAG GAAGAACCTG AATATGGAGA 1140
 AGAAATAAAG GGTATCCAG GCGTCCAGGC CCCTGAGGAC CTGAGTGGG AGCGCTATAG 1200
 GGGCAGAGGA AGTGAAGAAT ACAGGGCTCC AAGACCTCAG AGTGAGGAGA GTTGGGATGA 1260
 GGAGGACAAG AGAAACTACC CCAGCTTAGA GCTTGATAAG ATGCCACATG GATATGGTGA 1320
 AGAAAGTGAG GAAGAGAGGG GCCTTGAGCC GGGAAAGGGA CGCCATCACA GAGGCAGGGG 1380
 20 AGGGGAGCCA CGTGCCATT TCAATGCTGA CACAGAGAAA GAGAAAAGGT TCTTGGGTGA 1440
 AGGACACCAC CGTGTCCAAG AAAACCCAGAT GGACAAAGCA AGGAGGCAAT CACAAGGTGC 1500
 TGGGAAGGT CTGGACAGAA ATTATCTCAA CTACGGTGAG GAAGGAGCCC CAGGGAAGTG 1560
 GCAGCAGCAG GGAGACCTGC AGGACACTAA AGAAAACAGG GAGGAAGCTA GGTTCACAGA 1620
 25 TAAACAATAT AGCTCCATC ACACAGCTGA AAAGAGGAAG AGATTAGGGG AACTGTTCAA 1680
 CCCATAGTAC GACCCCTCC AGTGGAAAGAG CAGCCATTTT GAAAGAAGAG ACAACATGAA 1740
 TGACAAATTT CTCGAGGGTG AGGAGGAAAA TGAGCTGACC TTGAACGAGA AGAATTTCTT 1800
 CCCAGAATAC AACTATGACT GGTGGGAGAA AAGCCCTTC TCTGAGGATG TGAATCGGGG 1860
 GTATGAGAAG AGAAACCTCG CCAGGGTCCC CAAGCTGGAC CTGAAAAGGC AATATGACAG 1920
 30 GGTGGCCCAA CTGGACACGC TCCTTCACCTA CAGGAAGAG TCAGCTGAGT TTCCAGACTT 1980
 CTATGATPCT GAGGAGCCGG TGAGCACCCA CCAGGAGGCA GAAAAAGAAA AGGACAGGGC 2040
 TGACCAGACA GTCTGACAG AGGACGAGAA AAAAGAACTC GAAAACTTGG CTGCAATGGA 2100
 TTTGAACTA CAGAGATAG CTGAGAAATT CAGCCAAAGG GGTGACTGT CATTTGGAGC 2160
 GTGGGCACTG TTAAGAAGCA GCCATCACAT GATCTGTTTT TCACCCTTC ACTGAAAGAC 2220
 35 ACCATTTATA TACCAGAGGG CAGAAAGTAG AACTTACTAT TCATTAAATG TTTGACACAA 2280
 TTGGAATTGT CTTTAATTC TGTCAGAAAT CTATTGAAAA TGTAATTTGC ATGACTTTGA 2340
 GCATATCTT TCTGCAAAA TAGACATATT AACATGCTTA TGACAATGAC TGTGCTACTG 2400
 TCTTTGGAAA AATGTTTGT CAGTTGGAA ATAATAAAG ATTACCTGA GACC 2454

40 Seq ID NO: C144 DNA Sequence
 Nucleic Acid Accession #: XM_093082.1
 Coding sequence: 93..1988

45 1 11 21 31 41 51
 CTTCTGTGG TAGGGACCTC TCCTCAGTAT TTGAACTAA CCAGCATCTG ACAGATTTCG 60
 AATTGTGAAA AAATACCCCTC GAAGATTTCAG GAATGAAGCT TCTGTGTGAA GGATTAAGAC 120
 AGCCCAACTG TGTATTACAG ACATTGAGGT GGTACCGGTG CCTTATCTCT TCTGCTTCTT 180
 GTGGGGCTCT AGCAGCTGTT CTTAGCACCA GTCACTGGCT CACTGAACCT GAATTTAGTG 240
 50 AGACAAAATC GGAAGCTTCA GCTTTGAAAT TGCTCTATGG AGGCTTAAAA GATCCAAATT 300
 GCAAATTAAC GAAGCTCAAC TTGCAGTTTT CTATTCTGT AACCGCTGCA AAACCTCCAG 360
 TTGSAATGGT TGGAAATGT TCTGGTTTCT CGGGATCAIT GGTGCAATCT CATTTGGCT 420
 ACTGTGCGCA CAGTCTCTTC AAATGTGATC TTTGTAAAGT GCTCTGCGCT TCCACAGAG 480
 55 TTGCTGTCTG AAAGGATTGT GGGAGTCCCTA AGTCCCTTCT ATCAGAAAGG CTGAACTGGG 540
 CAGGAGACT TGAGGAGTGT GAGGAGGTTT TGGGGTTGGG GGTGCTTGTG CAGCCCGGTG 600
 ACCCAGCATC TCAGGGTGGG GGCATTGTG AAAACTATGG GTCTTTTAGA GACTTGGTGG 660
 ACTTAGAAGT CAAGGCAGAA CCAAGCCTGA GAAAAGGTGG TATGGATCTC CAGAGACCCA 720
 CCTTACAAGT TGCTCTCTCT TGCAAAATCT TCTCCCTCAA ACTATTCTC TTTATTGCAT 780
 60 TGCTTAATTC TCCTGGTCAG GTTAGTGTGG TGCAAGTGAC CATCCAGAC GGTTCGTGTA 840
 AGTGACTGT TGGATCTAAT GTCACTCTCA TCTGCATCTA CACCAACACT GTGGCCTCCC 900
 GAGAACAGCT TTCCATCCAG TGTCTTTTCT TCCATAAGAA GGAGATGGAG CCAATTTCTT 960
 CTCCTTGGGA GGAGGGGAGG TGGCCAGATG TTGAGGCTGT GAAGGGCACT CTGTATGGAC 1020
 AGCAGGCTGA ACTCCAGATT TACTTTTCTC AAGGTGGACA AGCTGTAGCC ATCGGGCAAT 1080
 65 TTAAGATCG AAATTACAGG TCCAACGATC CAGGTAATGC ATCTATCACT ATCTCGCATA 1140
 TGCAGCCAGC AGACAGTGGG ATTTACATCT GCGATGTTAA CAACCCCCA GACTTCTCG 1200
 GCCAAACCA AGGCATCCTC AAGGTCAAGT TGTAGTAGAA ACCTTCTAAG CCCCTTTGTA 1260
 GCGTTCAAGG AAGACAGAA ACTGGCCACA CTATTTCCCT TTCTGTCTC TCTGCGCTTG 1320
 GAACACCTTC CCTGTGTAC TACTGGCATA AACTTGAAGG AAGAGACATC GTGCCAGTGA 1380
 AAGAAAATTT CAACCAACC ACCGGGATT TGGTCATTGG AAATCTGACA AATTTGAAC 1440
 70 AAGGTTATTA CAGTGTACT GCCATCAACA GACTTGGCAA TAGTCTCTGC GAAATCGATC 1500
 TCACTTCTC ACATCCAGAA GTTGAATCA TGTGTGGGC CTGTATTGGT AGCCTGGTAG 1560
 GTGCGCCCAT CATCATCTCT GTTGTGTGCT TCGCAAGGAA TAAGGCCAAA GCAAGGCCAA 1620
 AAGAAAGAAA TTCTAAGACC ATCGCGGAAC TTGAGCCAAT GACAAAGATA AACCAAGGG 1680
 75 GAGAAAGGGA AGCAATGCCA AGAGAAGAGC CTACCCAACT AGAAGTAACT CTACATCTT 1740
 CCATTATGA GACTGGCCCT GATACCATCC AAGAACCCGA CTATGAGCCA AAGCCTACTC 1800
 AGGAGCTCGC CCAGAGCCT GCCCCAGGAT CAGAGCCTAT GGCAGTGCCT GACCTTGACA 1860
 TCGAGCTGGA GCTGGAGCCA GAAACGCAGT CGGAATTGGA GCCAGAGCCA GAGCCAGAGC 1920
 CAGAGTCAGA GCCTGGGGTT GTAGTTGAGC CCTTAAGTGA AGATGAAAAG GGAGTGGTTA 1980
 AGGCATAG

80 Seq ID NO: C145 DNA Sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1242

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	ATGGTGTTCG		CATTTTGGAA		GGTCTTTCTG		ATCCTAAGCT		GCCTTGCAGG		TCAGGTTAGT	60
	GTGGTGCAGG		TGACCATCCC		AGACGGTTTC		GTGAACGTGA		CTGTTGGATC		TAATGTCAC	120
	CTCATCTCGA		TCTACACAC		CACGTGCGCC		TCCCGAGAAC		AGCTTTCCAT		CCAGTGGTCT	180
	TTCTTCOCAT		AGAAGGAGAT		GGAGCCAAAT		TCTTCTCCTT		GGGAGGAGGG		GAGTGGCCA	240
	GATGTTGAGG		CTGTGAAGGG		CACCTCTGAT		GGACAGCAGG		CTGAATCCA		GATTTACTTT	300
	TCTCAAGGTG		GACAAGCTGT		AGCCATCGGG		CAATTTAAAG		ATCGAATTAC		AGGGTCCAAC	360
	GATCCAGGTA		ATGCATCTAT		CACATCTCG		CATATGCAGC		CAGCAGACAG		TGGAATTTAC	420
	ATCTGCGATG		TTAACAAACC		CCCAGACTTT		CTCGGCCAAA		ACCAAGGCAT		CCTCAACGTC	480
	AGTGTGTTAG		TGAAACCTTC		TAAGCCCTTT		TGTAGCGTTC		AAGGAAGACC		AGAAACTGGC	540
	CACACTATTT		CCCTTTCTCG		TCTCTCTCG		CTTGGAAAC		CTTCCCTGTT		GTACTACTGG	600
	CATAAACTTG		AGGGAAGAGA		CATCGTGCCA		GTGAAAGAAA		ACTTCAACCC		AACCAACGGG	660
	ATTTTGTGTA		TTGGAATCT		GACAAATTTT		GAACAAGGTT		ATTACCAATG		TACTGCCATC	720
	AACAGACTTG		GCAATAGTTC		CTGCGAAATC		GATCTCACTT		CTTCACATCC		AGAAGTTGGA	780
	ATCATTGTTG		GGGCTTGTAT		TGGTAGCCTG		GTAGGTGCCG		CCATCATCAT		CTCTGTTGTG	840
	TGCTTGGCAA		GGAATGAAGC		AAAAGCAAAG		GCAAAAGAAA		GAAATTTCTA		GACCATCGCG	900
	GAACCTTAGG		CAATGACAAA		GATAAACCCA		AGGGGAGAAA		GCGAAGCAAT		GCCAGAGAAA	960
	GACGCTACCC		AACTAGAAGT		AATCTACCA		TCTTCCATTC		ATGAGACTGG		CCCTGATACC	1020
	ATCCAAGAAC		CAGACTATGA		GCCAAAGCCT		ACTCAGGAGC		CTGCCCCAGA		GCCTGCCCCA	1080
	GGATCAGAGC		CTATGGCAGT		GCCTGACCTT		GACATCGAGC		TGGAGCTGGA		GCCAGAAACG	1140
	CAGTCGGAAT		TGGAGCCAGA		GCCAGAGCCA		GAGCCAGAGT		CAGAGCCTGG		GGTGTAGTGT	1200
	GAGCCCTTAA		GTGAAGATGA		AAAGGGAGTG		GTTAAGGCAT		AG			1242

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Seq ID NO: C146 DNA Sequence
Nucleic Acid Accession #: NM_003020.1
Coding sequence: 29..664

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	CGCTCCTCGG		GCTGCCCTCT		GGTTGACAAT		GGTCTCCAGG		ATGGTCTCTA		CCATGCTATC	60
	TGGCCTACTG		TTTTGGCTGG		CATCTGGATG		GACTCCAGCA		TTTGCTTACA		GCCCCGGGAC	120
	CCCTGACCGG		GTCTCAGAAG		CAGATATCCA		GAGGCTGCTT		CATGGTGTTA		TGGAGCAATT	180
	GGGCATTGCC		AGGCCCCGAG		TGGAATATCC		AGCTCACCAG		GCCATGAATC		TTGTGGGCCC	240
	CCAGAGCATT		GARGGTGGAG		CTCATGAAGG		ACTTCAGCAT		TTGGGTCTTT		TTGGCAACAT	300
	CCCCAACATC		GTGGCAGAGT		TGACTGGAGA		CAACATTCCCT		AAGGACTTTA		GTGAGGATCA	360
	GGGGTACCCA		GACCCCTCCA		ATCCCTGTCC		TGTTGGAAAA		ACAGATGATG		GATGCTTAGA	420
	AAACACCCCT		GACACTGCAG		AGTTCACTCG		AGAGTTCACG		TTGCACCAGC		ATCTCTTTGA	480
	TCCGGAACAT		GACTATCCAG		GCTTGGGGCA		GTGGAACAAG		AAACTCCTTT		ACGAGAAGAT	540
	GAGGGGAGGA		GAGAGACGAA		AGCGGAGGAG		TGTCATATCCA		TATCTACAAG		GACAGAGACT	600
	GGATAATGTT		GTGCAAAAGA		AGTCTGTCCC		CCATTTTTC		GATGAGGATA		AGGATCCAGA	660
	GTAAAGAGAA		GATGCTAGAC		GAAACCCAC		ATTACCTGTT		AGGCTCAGC		ATGGCTTAGT	720
	TGCACGTGTA		ATGGAGTCC		CTGTGAATGA		CAGCATGTTT		CTTACATAGA		TAATTATGGA	780
	TACAAAGCAG		CTGTATGTAG		ATAGTGTATT		GTCTTCACAC		CGATGATTCT		GCTTTTGTCT	840
	AAATTAGATT		AAGAGCTTTT		TTGTTTCTTG		GGTTTTTAAA		ATGTGAATCT		GCAATGATCA	900
	TAAAAATTAA		AATGTGAATG		TCAACAATAA		AAAGCAAGAC		TATGAAAGGC		TCAGATTTCT	960
	TGCAGTTTAA		AATGGTGTCT		GAGGTGTGAC		TATTTTGGCC		AAGTCTGTAG		AAAGCTGTCA	1020
	TTTGATTTTG		ATTATGTAGT		TCATCCAGCC		CTTGGGCATT		GTATACACCC		AGTAAAGAAG	1080
	GCTGTACTCA		AGAGGAGGAG		CTGACACATT		TCACCTGGCT		GGTCTTAAAT		AAACATGAAT	1140
	GCAAGCATTG		GC									1152

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Seq ID NO: C147 DNA Sequence
Nucleic Acid Accession #: NM_024021.2
Coding sequence: 144..806

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	AACATTCCTG		CAAATGGTTT		CAATATATGC		AGATGTCTCG		ATATAGGAAT		GAAATTACGT	60
	CTTTGGAACA		ACTTAAATAA		GTCAAATATA		CTTGGAGCTT		TAAAAATTAA		AAGGAGAGAG	120
	ATTGAGACAC		CTTTTCTGCT		GCCATGACAA		OCATGCAAGG		AATGGAACAG		GCCATGCCAG	180
	GGGCTGGCCC		TGGTGTGCCC		CAGCTGGGAA		ACATGGCTGT		CATACATTCA		CATCTGTGGA	240
	AAGGATTGCA		AGAGAAGTTC		TTGAAGGGAG		AAACCAAGT		CCTTGGGGTT		GTGCAGATTC	300
	TGACTGCCCT		GATGAGCCTT		AGCATGGGAA		TAACAATGAT		GTGTATGGCA		TCTAATACTT	360
	ATGGAAGTAA		CCCTATTTC		GTGTATATCG		GGTACACAAT		TTGGGGGTCA		GTAATGTTTA	420
	TTATTTTCAGG		ATCCTTGTC		ATTGCAGCAG		GAATTAGAAC		TACAAAGGC		CTGGTCCGAG	480
	GTAGTCTAGG		AATGAATATC		ACCAGCTCTG		TACTGGCTGC		ATCAGGGATC		TTAATCAACA	540
	CATTTAGCTT		GGGCTTTTAT		TCAATCCATC		ACCCCTACTG		TAACACTAT		GGCAACTCAA	600
	ATAATTGTCA		TGGGACTATG		TCCATCTTAA		TGGGTCTGGA		TGGCATGGTG		CTCCTCTTAA	660
	GTGTGCTGGA		ATTCTGCATT		GCTGTGTCCC		TCTCTGCCCT		TGGATGTAAA		GTGCTCTGTT	720
	GTACCCCTGG		TGGGGTTGTG		TTAATTTCTG		CATCACATTC		TCACATGGCA		GAAACAGCAT	780
	CTCCACACCC		ACTTAATGAG		GTTTGAGGCC		ACCAAAAGAT		CAACAGACAA		ATGCTCCAGA	840
	AATCTATGCT		GACTGTGACA		CAAGAGCCTC		ACATGAGAAA		TTACCAATAT		CCAACTTCCA	900
	TACTGATGTA		CTTGTGATA		TTATTATTAT		ATGTAATCCA		ATTATGAATC		GTGTGTGTAT	960
	AGAGAGATAA		TAAATTCAAA		ATTATGTTCT		CAITTTTTTTC		CCTGGAATCT		AATAACTCAT	1020
	TTCACTGGCT		CTTTATCGAG		AGTACTAGAA		GTTAAATTAA		TAAATTAATG		ATTTAATGAG	1080
	GCAACAGCAC		TGTAAAGTTT		TTCACTCATC		ATAAGAACTT		TATATAAAGG		CATTACATG	1140
	GCAAAATAGG		TTTGAAGACA		GAAGAGCAAA		AAAAAGATAT		TGTTAAATG		AGGCTCCCAT	1200
	GCAAAACACA		TACTTCCCTC		CCATTTATTT		AACTTTTTTT		TTCTCCTACC		TATGGGGACC	1260
	AAAGTCTTTT		TTCTTTCAGG		AAGTGGAGAT		GCATGGCCAT		CTCCCTCTCC		CTTTTCTCTT	1320
	CTCCGTCTTT		TCTTTCCCCA		TAGAAAGTAC		CTTGAAGTAG		CACAGTCCGT		CCTTGCATGT	1380
	GCAAGAGCTA		CTATTGAGT		AAAAGTATAC		ATGGAGTAAA		AATCATATTA		AGCATCAGAT	1440
	TCAACTATATA		TTTTCTATTT		CATCTTCTTC		CTTTCCTCTC		TCCCACTCTC		TACTGGGCAT	1500
	AATTATATCT		TATCATATATA		TGGAAATGTG		CAACATATGG		TATTTGTTAA		ATACGTTTGT	1560
	TTTTATTGCA		GAGCAAAAAA		AAATCAAAT		AGAGCAATA		AAAAAAAATA		AAAAAAAATA	1619

Seq ID NO: C148 DNA Sequence
Nucleic Acid Accession #: NM_002091.1
Coding sequence: 56..502

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AGTCTCTGCT CTTCCTCAGCC TCTCCGGGCG GCTCCAAGGG CTTCCTCGTG GGACCATGCG 60
CGCCAGTGGC CTCCCGCTGG TCTGCTGGC GCTGGTCTCT TGCTTAGCGC CCGGGGGGCG 120
AGCGGTCCCG CTGCTCTGGG GCGGAGGGAC CGTGCTGACC AAGATGTACC CGCGCGGCCA 180
CCACTGGGCG GTGGGGCACT TAATGGGGAA AAGAGCACA GGGGAGTCTT CTTCGTGTTT 240
TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
GAATTGCTG GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCACCCAA 360
GGCCTTGGCG AATCAGCAGC CTTCGTGGGA TTCAGAGGAT AGCAGCAACT TCAAAGATGT 420
AGGTTCAAAA GGCAAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
CCCCAGCTG AACCAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC 540
TAAGAGACTG AGTTCTGCAA GCATCAGTTC TACGGATCAT CAACAAGATT TCCTGTGCA 600
AAATATTGA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTATTTT CAAGCAGCAT 660
CTTCGTGTTT AAACCTGTTT GCTGTGAACA ATTGTGAAA AGAGTCTTCC AATTATGCT 720
TTTTTATATC TAGGCTACCT GTTGGTTAGA TTCAAGGCC CGAGCTGTGA CCATTACAA 780
TAAAGCTTA AACACAT 797

Seq ID NO: C149 DNA Sequence
Nucleic Acid Accession #: NM_012261.1
Coding sequence: 203..1045

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GATTGTCTCT GCCAGCAGCT GTGGGTGCGG CGCTCGACAC CGAGTCTAG CTAGGGCGTC 60
ACAGATACCG CGCTCCCTCC CTCCCTCTTC TCTGTCCCCC GCCTCTGCT CAACCCGGCC 120
CACTCCAGCG GGCATTGTA GGGATTCCCT CTCTGGGCGC CTCTGACGA GCACAGCCGG 180
CCTCATTGGG GGCATGCGA GTATGGATCT CCAAGGAAGA GGGGTCCCC GCATGACAG 240
ACTTCGAGTT CTCTGTATGT TGTTCCATAC AATGGCTCAA ATCATGGCAG AACAAAGAGT 300
GGAAATCTCT TCAGGCCTTT CCACTAACCC TGAAAAAGAT ATATTGTGG TGCGGGAAAA 360
TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATT ATGTACCTT ATGATGTGTG 420
GGCCAGCAAC TACGTAGATC TGATCACAGA ACAGGCCGAT ATCGCATTGA CCGGGGGAGC 480
TGAGGTGAGG GGCCTGCTGG GCCACAGCCA GTCCGAGCTG CAAGTGTCTT GGGTGGATCG 540
CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAAGCCAC AACATGTCCA AGGGACCTGA 600
GGCGACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660
CAAGAAGCCA GTCAGTGCTG GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCCTTGGT 720
CACCCCGCTT GGAAGTCTCT ATGAGTGTCA AGCTCAACAA ACCATTTTAC TGGCCTCTAG 780
TGATCCGACG AAGACGCTCA CCTATGATCT GTCTGCGGTC CACATCCAAC CTTTGTGACT 840
TATCTCAGTT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGATGAGC GGGAGCAACT 900
GGAAGAAACC TTGCCCTGTA TTTTGGGGCT CATCTTGGGC CTGTCATCA TGTAAACACT 960
CGCGATTATC CACGTCACCC ACAAAATGAC TGCCAAACAG GTGCAGATCC CTCGGGACAG 1020
ATCCAGTAT AAGACATAGG GCTAGAGGCC GTTAGGCAGG CACCCCTAT TCCTGCTCCC 1080
CCAACCTGAT CAGGTAGAAC AACAAAAGCA CTTTTCATC TTGTACAGA GATACACAA 1140
CATAGCTACA ATCAAACAGG CCTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200
AACCCACGGA AGGGGGAGAC TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC 1260
ATGCTGGGGA GGAGGGGAGG AGGGTCTCAG ACAGCTTTGG TGCTCATGGT GGCTTGGCTT 1320
TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGGCCCCAA AGTTTAGGGA 1380
TTGAAACATG GCTTCTTGA GGAGGAAACC CCTTTAGGTT CAGAAGAATA TGGGGTGCTT 1440
TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAACC 1500
TCATGCTCCC TGCAGCAAGA CCCCTGAAAG TGATTCTATG TTCTGCTGG CATTCTGCAT 1560
GTTTAGTGAT TGCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG 1620
AAAACGACTA ATGTAACAT GCAGAGTTGT TTGGACTTCT TCCTGTGACA GGTCCAAGTC 1680
GGGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTC AATGAAATA AAACACACTA 1740
TTCTCTGGC 1745

Seq ID NO: C150 DNA Sequence
Nucleic Acid Accession #: NM_003226.1
Coding sequence: 2..226

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GATGCTGGGG CTGCTCTCGG CCTTGTGTC CTCCAGCTCT GCTGAGGAGT ACGTGGGCTT 60
GTCTGCAAAC CAGTGTGCGG TGCCGGCCAA GGACAGGGTG GACTGCGGCT ACCCCCATGT 120
CACCCCAAG GAGTGAACA ACCGGGCTG CTGCTTTGAC TCCAGGATCC CTGGAGTGCC 180
TTGGTGTGTT AAGCCCCGTA CTAGGAAGAC AGAATGCACC TTCTGAGGCA CCTCCAGCTG 240
CCCTGGGAT GCAGGCTGAG CACCTTGCC CGGCTGTGAT TGCTGCCAG CACTGTTTAT 300
CTCAGTTTTT CTGTCCCTTT GCTCCCGGCA AGCTTTCTGC TGAAGTTCA TATCTGGAGC 360
CTGATGTCTT AACGAATAAA GGTCCCATGC TCCACCCG 398

Seq ID NO: C151 DNA Sequence
Nucleic Acid Accession #: NM_002993.1
Coding sequence: 64..408

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GGCAGGAGCC AGTCTCCGCG CCTCAACCA GCTCAGGAAC CCGGAACCC TCTCTTGACC 60
ACTATGAGCC TCCCGTCCAG CCGCGCGGCC CGTGTCCCGG GTCTTCCGG CTCCTTGTGC 120
GCGTGTCTG CGCTGTGCT CCTGTGACG CCGCGGGGCG CCTCGCCAG CGCTGTGCT 180
GTCTCTGCTG TGCTGACAGA GCTGCGTTGC ACTTGTTCAC GCGTTACGCT GAGAGTAAC 240

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CCCCAAACGA TTGGTAAACT GCAGGTGTTT CCCGAGGCC CGCAGTGCTC CAAGGTGGAA 300
GTGGTAGCCT CCCTGAAGAA CGGGAAGCAA GTTGTCTGG ACCCGGAAGC CCCTTTTCTA 360
AAGAAAGTCA TCCAGAAAAT TTGGACAGT GGAAACRAAG AAAACTGAGT AACAAAAAAG 420
ACCATGCATC ATAAATTGTC CCAGTCTTCA GCGAGCAGT TTCTGGAGA TCCCTGGACC 480
CAGTAAGAAAT AAGAAGGAAG GGTGGTTTT TTCCATTTT CTACATGGAT TCCCTACTTT 540
GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CCTGAAGTTT ACAGCTCAGC TAATGAAGTA 600
CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCCCTTGG 660
CAATTGACCA TATTGTGAGC AAAGAATCAC TGGTTATTAG TCTTTCAATG AATATTGAAT 720
TGAAGATAAC TATTGTATT CTATCATACA TTCTTAAAG TCTTACCGAA AAGGCTGTGG 780
ATTTCTGATG GAAATAATGT TTTATTAGTG TGCTGTTGAG GGAGGTATCC TGTGTCTCTT 840
ACTCAGCTCT CTCATAAAAT AGGAAATATT TTAGTTCTGT TTCTTGGGG AATATGTTAC 900
TCITTAACCT AGGATGCTAT TTAAGTTGTA CTGTATTAGA ACACGGGTG TGTACATCCG 960
TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AATTTAAGT TCTGTAAGGG 1020
CTAATATATT CTCTTCTAT GGTTTAGAT GTTTGATGTC TTCTTAGTAT GGCATAATGT 1080
CATGATTTAC TCATTAAACT TTGATTTTGT ATGCTATTTT TTCATATAG GATGACTATA 1140
ATTCTGGTCA CTAATATATC ACTTTAGATA GATGAAGAAG CCAAAAAACA GATAAATTC 1200
TGATTGCTAA TTACATAGA AATGTATTCT CTGGTTTTT TAAATAAAG CAAAAATTAAC 1260
AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTGAA CAATTGAAT ATAAATTCAT 1320
CATTTAGTTC TCMAATATA TACAGATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
TTTAAAGGTT TTAACGATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
AAATTGCACT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCAAT 1500
TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAA AAAA 1547
  
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 Seq ID NO: C152 DNA Sequence
 Nucleic Acid Accession #: NM_005242.2
 Coding sequence: 148..1341

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1 11 21 31 41 51
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CGGCCCGCCC TGGGGAGGCG CGCAGCAGAG GCTCCGATTC GGGGCAGGTG AGAGGCTGAC 60
TTTCTCTCGG TCGCTCCAGT GGAGCTCTGA GTTTCGAATC GGTGGCGGCG GATTCGCCGC 120
GCGCCCGGCG TGGGGGCTTC CAGGAGGATG CGGAGCCCCA GCGCGGCGTG GCTGCTGGGG 180
GCGGCCATCC TGCTAGCAGC CTCTCTCTCC TGCAGTGGCA CCATCCAAGG AACCAATAGA 240
TCCTCTAAG GAAGAAGCCT TATTGGTAAG GTTGATGGCA CATCCACGCT CACTGGAAAA 300
GGAGTTACAG TTGAAACAGT CTITTCGTGT GATGAGTTT CTGCATCTGT CCTCACTGGA 360
AAACTGACCA CGGTCTTCT TCCAATTGTC TACAATTTG TGTGTGTGGT GGGTTTGCCA 420
AGTAACGGCA TGGCCCTGTG GGTCTTTCTT TTCCGAAC TAAGAAGACA CCTGCTGTG 480
ATTTACATGG CCAATCTGGC CTGGCTGAC CTCTCTCTG TCATCTGGTT CCCCTGAAG 540
ATTGCTATC ACATACATGC CAACAACGAG ATTATGCGG AAGCTCTTTG TAATGTGCTT 600
ATTGGCTTTT TCATGGAACA CATGTACTGT TCCATCTCT TCATGACCTG CCTCAGTGTG 660
CAGAGGTATT GGTTCATGTT GAACCCCATG GGGCACTCCA GGAAGAAGGC AACATTGCC 720
ATTGGCATCT TCGTGGCAAT ATGGCTGCTG ATTCGTCTGG TCACCATCCC TTTGTATGTC 780
GTGAAGCACA CCATCTTCAT TCCTGCCCCG AACATCAACA CCTGTCAATG TGTTTGCTCT 840
GAGCAGCTCT TGGTGGGAGA CATGTTCAAT TACTTCTCT CTCGCGCAT TGGGGTCTTT 900
CTGTTCCGAG CCTTCTCTAC AGCCTCTGCC TATGTGCTGA TGATCAGAAT GCTGCGATCT 960
TCTGCCATGG ATGAAAACTC AGAGAAGAAA AGGAAGAGGG CCATCAAACT CATTGTCACT 1020
GTCTGGGCCA TGTACTCTAT CTGCTTCACT CCTAGTAACT TTCTGCTTGT GGTGCATTAT 1080
TTTCTGATTA AGAGCCAGGG CCAGAGCCAT GTCTATGCC TGTACATTGT AGCCCTCTGC 1140
CTCTCAACC TTAACAGCTG CATCGACCCC TTGTCTTATT ACTTTGTTT ACATGATTTT 1200
AGGGATCATG CAAGAAGCGC TCTCCTTTGC CGAAGTGTCC GCACTGTAAA GCAGATGCAA 1260
GTATCCCTCA CCTCAAGAAA ACACCTCCAG AAATCCAGCT CTTACTCTTC AAGTTCGAAC 1320
ACTGTTAAGA CCTCTCTATT AGTTTCCAG GTCTCTCAGT GGGAAATGCA CAGTAGGATG 1380
TGGAACTGTT TTAATGTTAT GAGGACGTGT CTGTTATTTC CTAATCAAAA AGGTCTCACC 1440
ACATACCACC G 1451
  
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60
 Seq ID NO: C153 DNA Sequence
 Nucleic Acid Accession #: NM_003469.2
 Coding sequence: 92..1945

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GAAACGGCCC GAGAAGCTCG CCGGAGAAC GGGGAGGAAT ATGCTGTGGA GCTCCTCTGC 60
CATATAAACA AAAAGAGGAA ATCTTTCAAA CATGGCTGAA GCAAGAGACC ACTGGCTTGG 120
AGCAGCCCTG TCTCTTATCC CTTTAATTTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT 180
TCAGAGAAAC CAGCTGCTTC AGAAAGAAC AGACCTCAGG TTGGAAAATG TCCAAAAGTT 240
TCCAGTCTCT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCCGAC AACAGCTCA 300
TAAGGAAGAA AGCAGCCAG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCTTCAGCA 360
AAAAGAAAAA GCGATGAAA GCCACTTGCC CGAGAGGGAT TCACTGAGTG AAGAAGACTG 420
GATGAGAATA ATACTCGAAG CTTTGAGACA GGCTGAAAAT GAGCCTCAGT CTGCACCAAA 480
AGAAAATAG CCCTATGCC TGAATTGAGA AAAGAACTTT CCAATGGACA TGAGTGATGA 540
TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCTATGTA 600
TGAAGAGAA TCCAGGGATA ACCCCTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA 660
TACTCTCTCA AGCCTTGCTA CATTGGAATC TGTCTTCCAA GAGCTGGGGA AACTGACAGG 720
ACCAAAACAC CAGAAACGTC AGAGGATGGA TGAGGAGCAA AAACCTTATA CGGATGATGA 780
AGATGATATC TACAAGGCTA ATAACATTGC CTATGAAGAT GTGGTGGGG GAGAAGACTG 840
GAACCCAGTA GAGGAGAAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAGA 900
GAATATAGGA AAAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGSC AGCTTGGCAT 960
CCAGGAAGAA GATCTTCGGA AAGAGAGTAA AGACCAACTC TCAGATGATG TCTCCAAGT 1020
AATTGCCAT TTTGAAAGGT TAGTAAATGC TGCAAGAGT GGGAGGTTAC AGAATGGGCA 1080
AAATGGGGAA AGGGCCACCA GGCTTTTGA GAAACCTCTT GATTCTCAGT CTAATTTATCA 1140
GCTGATTGAA ATCTCAAGGA ATTTACAGAT ACCCCAGAA GACTTAATTG AGATGCTCAA 1200
AATCGGGGAG AAGCCGAATG GATCAGTGGG ACCGGAGCGG GAGCTTGACC TTCTGTGTA 1260
CCTAGATGAC ATCTCAGAGG CTGACTTAGA CCATCCAGAC CTGTTCCAAA ATAGGATGCT 1320
  
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5	CTCCAAGAGT	GGCTACCCCTA	AAACACCTGG	TGGTGTGGG	ACTGAGGCCC	TACCAGACGG	1380
	GCTCAGTGTT	GAGGATATTT	TAAATCTTTT	AGGGATGGAG	AGTGCAGCAA	ATCAGAAAAC	1440
	GTCGTATTTT	CCCAATCCAT	ATAACACGGA	GAAAGTTCCT	CCAAGGCTCC	CTTATGGTGC	1500
	TGGAAGATCT	AGATCGAACC	AGCTTCCCAA	AGCTGCCTGG	ATTCCACATG	TTGAAAAACAG	1560
	ACAGATGGCA	TATGAAAACC	TGAACGACAA	GGATCAAGAA	TTAGGTGAGT	ACTTGGCCAG	1620
	GATGCTAGTT	AAATACCCCTG	AGATCATTA	TTCAAACCAA	GTGAAGCGAG	TTCTGGTCA	1680
	AGGCTCATCT	GAAGATGACC	TGCAGGAAGA	GGAACAAATT	GAGCAGGCCA	TCAAAGAGCA	1740
	TTTGAATCAA	GGCAGCTCTC	AGGAGACTGA	CAAGCTGGCC	CCGCTGAGCA	AAAGGTTCCG	1800
10	TGTGGGGCCC	CCGAAGAATG	ATGATACCCC	AAATAGGCAG	TACTGGGATG	AAGATCTGTT	1860
	AATGAAAGTG	CTGGAATACC	TCAATCAAGA	AAAGGCAGAA	AAGGGAAGGG	AGCATATTGC	1920
	TAAGAGAGCA	ATGGAATAA	TGTAAGCTGC	TTTCATTAA	TACCTACTT	TCATTCTCTC	1980
	CACCCCAAGC	AAATCCCAAC	ATTCTCTTC	AGTGTGTTGA	CTTCTATCCT	GTAAACACTG	2040
	TAATATCTTT	AAATGATGTA	CAGGCAGATG	AAACCAGGTC	ACTGGGAGT	CTGCTTCATT	2100
15	TCTCTGAGC	TGTTATCTTG	TGTATGGATA	TGTGTAATG	TTATGACTCC	TTGATAAAAA	2160
	ATTTATTATG	TCCATTATTC	AAGAAAGATA	TCTATGACTG	TGTTAATAG	TATATCTAAT	2220
	GGCTGTGGCA	TTGTTGATGC	TCACATATGA	TAAAAAAGTG	TCCTATAATT	CTATTGAAAG	2280
	TTTTTAATAT	TTATTGAATT	ATTTTGTAC	TGTCGTAGC	GTTTGTGGA	GTAATGGACC	2340
	AAAAAATAA	AGCATTATAA	ATATA				2365
20	Seq ID NO: C154 DNA Sequence Nucleic Acid Accession #: NM_030955 Coding sequence: 327..5108						
25	1	11	21	31	41	51	
	GAATTCGGG	AGCGGGCGGG	CTGCGAGGCC	CGGGGGCATG	CGGGAGGCGG	AGGGGTGGGA	60
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	CCTTTTAGGA	GGAGGGAGGG	GGAAAAGGTG	TCTAGCTAAT	TTCTGCTTAA	AAAAGCACAG	180
30	GAGATCGCGG	GTCAGCTTTG	CAGTCGCTGC	CTTCTCGCGC	CTGACCATGC	ACCCCTGCAT	240
	CTTCTGCTGC	GGCAGAGCGG	AGCGCTTTAT	TTCTGGAGCT	GAGGGCTAAA	ACTTTTTTCA	300
	CTTTCTCTCT	CCTCAACATC	TGAATCATGC	CATGTGCCCA	GAGGAGCTGG	CTTGCAAAAC	360
	TTTCCGRTGT	GGCTCAGCTC	CTTAACCTTG	GGGCGCTTTG	CTATGGGAGA	CAGCCTCAGC	420
	CAGGCCCGGT	TGCTTTCCCG	GACAGGAGGC	AAGAGCATTT	TATCAAGGGC	CTGCCAGAAT	480
35	ACCACGTGGT	GGGTCCAGTC	CGAGTAGATG	CCAGTGGGCA	TTTTTTGTCA	TATGGCTTGC	540
	ACTATCCCAT	GAAGATGAGC	AGGAGGAAGA	GAGATTGGA	TGGCTCAGAG	GACTGGGTGT	600
	ACTACAGAA	TTCTCAGCAG	GAGAAGGACC	TGTTTTTAA	CTTGACGCTC	AATCAAGGAT	660
	TTCTTTCCAA	TAGCTACATC	ATGGAGAAGA	GATATGGGAA	CCTCTCCCAT	GTTAAGATGA	720
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40	TTGGGACGCG	AGCCCTCAGT	GCCTGCCATG	GACTGACTGG	ATTTTCCCAA	CTACCACATG	840
	GAGACTTTTT	CATTGAACCC	GTGAAGAAGC	ATCCACTGGT	TGAGGGAGGG	TACCACCCGC	900
	ACATCGTTTA	CAGGAGGCGG	AAAGTTCCAG	AAACCAAGGA	GCCAACTGT	GGATTAAAGG	960
	ACAGTGTFAA	CATCTCCCG	AAGCAAGAGC	TATGGCGGGA	GAAGTGGGAG	AGGCACAAC	1020
	TGCCAAGCAG	AAGCCTTCTC	CGCGTTTCCA	TCAGCAAGGA	GAGATGGGTG	GAGACACTGG	1080
45	TGGTGGCGGA	CACAAGATG	ATTGAATACC	ATGGGAGTGA	GAATGTGGAG	TCCTACATCC	1140
	TCACCATCAT	GAACATGGTG	ACTGGGTGT	TCCATAACCC	AAGCATTTGG	AATGCAATTC	1200
	ACATTGTGT	GGTTCCGCTC	ATTCTACTCG	AAGAAGAAGA	GCAAGGACTG	AAATAGATTC	1260
	ACCATGCAGA	AAAGACACTG	TCTAGCTTCT	GCAAGTGGCA	GAAGAGTATC	AATCCCAAGA	1320
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50	CTGGTTTCAA	TGCCCCCTGC	GAGACCTCGG	GCCTGTCTCA	CCTTTCAAGG	ATGTGTGAGC	1440
	CTCACCGCAG	TTGTAACATC	AATGAAGATT	CGGGACTTCC	TCTGGCTTTC	ACAATTGCCG	1500
	ATGAGCTAGG	ACACAGCTTC	GGCATCCAGC	ATGATGGGAA	AGAAAATGAC	TGTGAGCCTG	1560
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	GGTCCAGAGT	GACGAGAGG	TACATCACCC	GCTTCTTGA	CCGAGGCTGG	GGGTTCTGTC	1680
55	TTGATGACAT	ACCTAAAGAG	AAAGGCTTGA	AGTCCAAAGT	CATTGCCCCC	GGAGTGATCT	1740
	ATGATGCTCA	CCACCACTGC	CAGCTACAAT	ATGGACCCAA	TGCTACCTTC	TGCCAGGAAG	1800
	TAGAAAACGT	CTGCCAGACA	CTGTGGTGCT	CGGTGAAGGG	CTTTTGTGCG	TCTAAGCTGG	1860
	AGCTGTCTGC	AGATGGAAC	CAATGTGGTG	AGAAGAGATG	GTGTATGGCA	GGCAAGTGCA	1920
	TCACAGTGGG	GAGAAACCA	GAGAGCATTC	CTGAGGCTG	GGGCGGCTGG	TCACCTGGT	1980
60	CCCACTGTTC	CAGGACCTGT	GGGGCTGGAG	TCCAGAGCGC	AGAGAGGCTC	TGCAACAAAC	2040
	CCGAGCCAAA	GTTTGGAGGG	AAATATTGCA	CTGGAGAAAG	AAAACGCTAT	CGCTTGTGCA	2100
	ACGTCCACCC	CTGTCTGCTA	GAGGCACCAA	CATTTCGGCA	GATGCAGTGT	AGTGAATTGT	2160
	ACACTGTTC	CTACAAGAT	GAACTCTACC	ACTGGTTTCC	CATTTTTAAC	CCAGCACATC	2220
	CTTGTGAGCT	CTACTGCCGA	CCCATAGATG	GCCAGTTTTC	TGAGAAATG	CTGGATGCTG	2280
65	TCATTGATGG	TACCCCTTGC	TTTGAAGGCG	GCAACAGCAG	AAATGTCTGT	ATTATATGCA	2340
	TATGTAAGAT	GGTTGGCTGT	GACTATGAGA	TGATTTCCAA	TGCCACCGAG	GATCGCTGCG	2400
	GTGTGTGCGT	GGGAGATGGC	TCTTCTGCTC	AGACTGTGAG	AAAGATGTTT	AAGCAGAAGG	2460
	AAGGATCTGG	TTATGTTGAC	ATTGGGCTCA	TTCCAAAAGG	AGCAAGGGAC	ATAAGAGTGA	2520
	TGGAAATTGA	GGGAGCTGGA	AACCTTCTGG	CCATCAGGAG	TGAAGATCCT	GAAAAATATT	2580
70	ACCTGAATGG	AGGGTTTATT	ATCCAGTGGG	ACGGAACTA	TAAGCTGGCA	GGGACTGTCT	2640
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	CTGTGTGGAT	CCAGCTTCTA	TTCCAGGTGA	CTAACCTTGG	CATCAAGTAT	GAGTACACAA	2760
	TCCAGAAAGA	TGGCCTTGAC	AATGATGTTG	AGCAGATGTA	CTTCTGGCAG	TACGGCCACT	2820
	GGACAGATGG	CAGTGTGACC	TGCGGACAG	GTATCCGCG	CCAACTGCC	CATTGCATAA	2880
75	AGAAGGGCCG	CGGATGTTG	AAAGCTACAT	TCTGTGACCC	AGAAACACAG	CCCAATGGGA	2940
	GACAGAAAGA	GTGCCATGAA	AAGGCTTGTG	CACCCAGGTG	GTGGGCGAGG	GAGTGGGAAG	3000
	CATGCTGGCG	GACATGGCGG	CCCAACGGGG	AGAAGAAGCG	AACCGTCTG	TGCATCCAGA	3060
	CCATGTCTCT	TGACGAGCAG	GCTCTCCCGC	CCACAGACTG	CCAGCACCTG	CTGAAGCCCA	3120
	AGACCTCTCT	TCTCTCAAC	AGAGACATCC	TGTGCCCTTC	GGACTGGACA	GTGGGCAACT	3180
80	GGAGTGAGTG	TTCTGTTTCC	TGTGGTGGTG	GAGTGGGAT	TGCGAGTGTG	ACATGTGCCA	3240
	AGAACCATGA	TGAACCTTGC	GATGTGACAA	GGAACCCCAA	CAGCCGAGCT	CTGTGTGGCC	3300
	TCCAGCAATG	CCCTTCTAGC	CGGAGAGTTC	TGAACCCAAA	CAAGGCACT	ATTTCCAATG	3360
	GAAAAAACCC	ACCAACACTA	AAGCCCGTCC	CTCCACCTAC	ATCCAGGCCG	AGAATGCTGA	3420
	CCACACCCAC	AGGGCCTGAG	TCTATGAGCA	CAAGCACTCC	AGCAATCAGC	AGCCCTAGTC	3480
	CTACACACAG	CTCCAAAGAA	GGAGACCTGG	GTGGGAAACA	GTGGCAAGAT	AGCTCAACCC	3540

AACCTGAGCT GAGCTCTCGC TATCTCATT CCACTGGAAG CACTTCCCAG CCCATCCTCA 3600
 CTTFCCCAATC CTTGAGCATT CAGCCAAAGT AGGAAAATGT TTCCAGTTCA GATACTGGTC 3660
 CTACCTGGGA GGGAGGCCCT GTAGCTACAA CAACAAGTGG TTCTGGCTTG TCATCTTCCC 3720
 5 GCAACCCCTAT CACTTGGCCT GTGACTCCAT TTTACAATAC CTTGACCAAA GGTCCAGAAA 3780
 TGGAGATTCA CAGTGGCTCA GGGGAAGAAA GAGAACAGCC TGAGGACAAA GATGAAAGCA 3840
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 AARTGCCACT TGCACCTCCA CTAACACCAAG ATCTCAGCAG GGAGTCTGG TGGCCACCCT 3960
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 10 CACCCAGAGT TGAGGGGATG GTTACTGAAA AGCCAGCCAA CACTCTGCTC CCTCTGGGAG 4080
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 TGATTACTGA GGGCTTTTGT CTAATGCCT CCAATTACAA GCAGCTCACA AACGGCCACG 4260
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 15 CCTACTGGAA AAGGGTGGAG TGCACACCC AGATGGATTG TGACTGTGCG GCCATCCAGA 4380
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 GGAGCAAGTG CTCAGAAAC TGCAGTGGGG GCTTCAAGAT ACGCAGATT CAGTGCCTGG 4500
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 20 GCCAGTGCTC CAGGTCTCTGT GGAGGTGGAG TTCAGGAGAG AGGAGTGTTC TGTCCAGGAG 4680
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 25 AAAGTGCCGA TTTACTTTGC ACTAAGGACA AACTGTCAAG CAGTTTCTGC CAGACACTGA 4980
 AAGCCATGAA GAAATGTTCT GTGCCACCG TGAGGGCTGA GTGCTGCTC TCGTGTCCCC 5040
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Seq ID NO: C155 DNA Sequence
 Nucleic Acid Accession #: NM_001062.1
 Coding sequence: 76..1380

1 11 21 31 41 51
 35 GCTCTCATT CCTTCTGCC ATCACTTAAT AAATAGCCAG CCAATTCATC AACATTCTGG 60
 TACACTGTTG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTACTGTGTT 120
 TCTTTTATTC CAAGCCAACT ATGCGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC 180
 CTAAAACTTC TGTGAAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTG 240
 40 AATGTTGTGT TGTCCCTCAA ACTTGTGGA ATCCAGATCC AAACCTGAT GCAAAAGATG 300
 ATCCAACAAA TCAATACAA TGTGAAAAGC AGATTGTGAG ATGTAGCTC GGGAGAGCTT 360
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAACGCTG AGGAAAACCT AATATATGAT 420
 TACCACCTGA CTGACAGCT AGAAAAATAA TTCCAGCAG AAATTGAAAA TATGGAAGCA 480
 CACAATGGCA TCCTCCCTGAC TAACTACTAC CAGCTCAGCC TGGACGTTT GGCCTTGTGT 540
 45 CTGTTCAATG GGAACACTC AACCCGCGAA GTTGTCAACC ACTTCACTCC TGAATAATAA 600
 AACTATTATT TTGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTG CTGCGCTCTG 660
 ACCTGTGTGA AGAAGAGTCT AATAAATGGG CAGATCAAAG CAGATGAAGG CAGTTTAAAG 720
 AACATCAGTA TTTATACAAA GTCACTGTGA GAAAAGATTC TGTCTGAGAA AAAAGAAAAA 780
 GGTCTGATTC GAAACACATT TAGCACAGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA 840
 50 GACTATTATA ATGAAAATGA CTGGAATTGC CAACAACTC TGAATACAGT GCTCACGGAA 900
 ATTTCTCAAG GAGCATTTCG TAATCCAAAC GCTGCAGCCC AGGCTTTACC TGCCCTGATG 960
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 AACATCTCCG CTGATGAGCC TATAACTGTG ACACCTCCTG ACTCACAATC ATATATCTCC 1080
 GTCAATTACT CTGTGAGAAAT CAATGAAACA TATTTACCA ATGTCACTGT GCTAAATGGT 1140
 55 TCTGTCTTCC TCAGTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACTAT ATTTGTTTTC 1200
 ACAATGGAGG AGCGCTCATG GGGGCCCTAT ATCACCCTGA TTCAGGGCCT ATGTGCCAAC 1260
 AATAATGACA GAACCTACTG GGAACCTCTG AGTGGAGGCG AACCACTGAG CCAAGGAGCT 1320
 GGTAGTTACG TTGTCCGCAA TGGAGAAAAC TTGGAGGTTG CCTGGAGCAA ATACTAATAA 1380
 60 GCCAAACTT TCCTCAGCTG CATAAAATCC ATTTGCAGTG GAGTTCCATG TTTATTGTCC 1440
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 TCTCTCATG TTCAATAAAA GTTGTGAAA GATTAAAC 1537

Seq ID NO: C156 DNA Sequence
 Nucleic Acid Accession #: NM_004591
 Coding sequence: 59..349

1 11 21 31 41 51
 65 CACTCCCAAA GAATGGGTA CTCAACACTG AGCAGATCTG TTCTTTGAGC TAAAAACCAT 60
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 CGGCGAATCA GAAGCAGCAA GCAACTTTGA CTGCTGTCTT GGATACACAG ACOGTATTCT 180
 70 TCATCCTAAA TTTATTGTGG GCTTCACAG GCAGCTGGCC AATGAAGGCT GTGACATCAA 240
 TGTCTATATC TTTCACACAA AGAAAAGTT GTCTGTGTGC GCAATCCAA AACAGACTG 300
 GGTGAATAT ATTTGCGCTC TCCTCAGTAA AAAAGTCAAG AACATGTAAG AACTGTGGCT 360
 75 TTTCTGGAAT GGAATTGGAC ATAGCCCAAG AACAGAAAGA ACCTTGTCTG GGTGGAGGTT 420
 TTCACTTGCA CATCATGGAG GGTTAGTGTG TTATCTAATT TGTGCTCAC TGGACTGTG 480
 CAATTAAGA AGTTGATTCA TATTGCATCA TAGTTTGCTT TGTTTAAGCA TCACATTAAA 540
 GTTAAACGT ATTTTATGTT ATTTATAGCT GTAGGTTTTC TGTGTTAGC TATTTAATAC 600
 TAATTTTCCA TAAGCTATTT TGGTTTAGTG CAAAGTATAA AATTATATTT GGGGGGGAAT 660
 80 AAGATTATAT GGACTTTCTT GCAAGCAACA AGCTATTTTT TAAAAAATC ATTTAAACAT 720
 CTTTGTGTTA TATTGTTTGT TCTCTAAAT TGTGTGAATT GCATTATAAA ATAAGAAAAA 780
 CATTATAAG ACATAATT 799

Seq ID NO: C157 DNA Sequence
 Nucleic Acid Accession #: NM_013271.1

Coding sequence: 27..809

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      CCGGGGGCGT CCGCCTTTTG GTGCTGTGTC TGCTCGGCCT GTTTCGGCCG CCCCCCGGCG 120
      TCTGGCGCGG GCGCGTAAAG GAAACCCGCG GCCTAAGCGC AGOGTCTCG CCCTTGGCTG 180
      AGACTGGCGC TCCTCGCCGC TTCGGCGGGT CAGTGCCCGG AGGTGAGGCG GCGGGGGCGG 240
      TGCAGGAGCT GCGCGGGCGG CTGGGSCATC TGCTGAGGCG CGAACSTCAG GAGCGGGGCG 300
10     GGGCCGAGGC GCAGGAGGCT GAGGATCAGC AGGCGGCGCT CCTGGCGCAG CTGCTGCGCG 360
      TCTGGGGCGC CCCCCGCAAC TCTGATCCGG CTCTGGGCCT GGAACGACGAC CCGACGCGCG 420
      CTGCAGCGCA GCTCGCTGCG GCTCTGTCTC GCGCCCGGCT TGAACCTGCC GCCCTAGCAG 480
      CCCAGCTTGT CCCCOCGCCG GTCCCGCGCG CGGCGCTCCG ACCCGGGCCC CCGGTCTACG 540
      ACGACGGCCC GCGGGGCCCC GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600
15     CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG 660
      TGGCAGCCCC GCGCGGCTCT CGCCGTGCGG CCGAACCGA TGTGGGCTCT GAGCTGCCCG 720
      CTGAGGGCGT CTGGGGGGCG CTGCTGCGTG TGAACCGCT AGAGACCCCG GCGCCCCAGG 780
      TGCTGTCACG CCGCCTCTTG CCACCCTGAG CACTGCCCCG ATCCCGTGCA CCCTGGGACC 840
      CAGAAGTGCC CCGCCATACC CGCCACCAGG ACTTCTCCCC GCCAGCAGCT CCAGAGCAAC 900
20     TTACCCCGGC CAGCCAGCCC TCTCACCCGA GGATCCCTAC CCCCTGGCCC ACAAATAACAT 960
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Seq ID NO: C158 DNA Sequence

Nucleic Acid Accession #: NM_002245.2

Coding sequence: 183..1193

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      GCGGGCGGGA GCGAGGCCCG GCGGGGGGCG GGGGCGGGCG GGCCAGAAGA GCGGGCGGGC 120
      CGCGCTCCGG CCGGTCTGCG GCGTTGGCCT TGGCTTTGGC TTTCGGCGCG GCGGTGGAGA 180
      AGATGCTGCA GTCCCTGGCC GGCAGCTCGT GCGTGGCGCT GGTGGAGCGG CACCGCTCGG 240
      CTGGTGCTTT GCGCTTCTTG GTGCTGGGCT ACTTGCTCTA CCTGTCTTTC GGCGCAGTGG 300
      TCTTCTCCTC GGTGGAGCTG CCCTATGAGG ACCTGCTGCG CCAGGAGCTG CGCAAGCTGA 360
35     AGCGAGCGTT CTGGAGGAGC CACGAGTGCC TGTCTGAGCA GCAGCTGGAG CAGTTCTGGG 420
      GCGGGGTGCT GGAGGCCAGC AACTACGCGG TGTGCGTGCT CAGCAACGCC TCGGGCAACT 480
      GGAACGTGGA CTTCACCTCC GCGCTCTTCT TCGCCAGCAC CGTGTCTTCC ACCACAGGTT 540
      ATGGCCACAC CGTGCCCTTG TCAGATGGAG GTAAGGCCTT CTGCATCATC TACTCCGTCA 600
      TTGGCATTCC CTTCACCCCTC CTGTTCTGTA CGGCTGTGGT CCAGCGCATC ACCGTGCAAG 660
40     TCACCCGCGG GCGGCTCCTC TACTTCCACA TCGCTGGGG CTCTTCCAAG CAGGTGGTGG 720
      CCATCGTCCA TGCCGTGCTC CTGGGGTTTG TCACGTGTGC CTGCTTCTTC TTCATCCCGG 780
      CCGCTGTCTT CTAGTCCCTG GAGGATGACT GGAACCTTCT GGAATCCTTT TATTTTGTGT 840
      TTATTTCCCT GAGCACCAAT GGCCTGGGGG ATTATGTGCC TGGGGAAGGC TACAATCAAA 900
      AATTCAGAGA GCTCTATAAG ATTGGGATCA CGTGTACCT GCTACTTGGC CTATTGGCCA 960
45     TGTGTGTAAG TCTGGAACCC TTCTGTGAAC TCCATGAGCT GAAAAAATTC AGAAAAATGT 1020
      TCTATGTGAA GAAGGACAAAG GACGAGGATC AGGTGCACAT CATAGAGCAT GACCAACTGT 1080
      CCTTCTCCTC GATCACAGAC CAGGCAGCTG GCATGAAAGA GGACCAAGAG CAAAATGAGC 1140
      CTTTGTGGC CACCCAGTCA TCTGCTGCG TGGATGGCCC TGCAAAACCAT TGAGCGTAGG 1200
      ATTTGTGCA TTATGCTAGA GCACCAAGGT CAGGGTGCA GGAAGAGGCT TAAGTATGTT 1260
50     CATTTTATC AGAATGCAAA AGCGAAAATT ATGTCACTTT AAGAAATAGC TACTGTTTGC 1320
      AATGTCTTAT TAAAAAACA CAAAAAAGA CACATGGAAC AAAGAAGCTG TGACCCGAGC 1380
      AGGATGCTTA ATATGTGAGG AATGAGATG TCCACCTAAA ATTCAATATG GACAAAATTA 1440
      TCTGAGCTTT ACATAGGAGG AGAATACTTG AAGCAGTATG CTGCTGTGGT TAGAAGCAGA 1500
      TTTTATACTT TTAATGGAA ACTTTGGGGT TTGCATTTAG ATCATTTAGC TGATGGCTAA 1560
55     ATAGCAAAAT TTATATTTAG AAGCAAAAAA AAAAAAGCATA GAGATGTGTT TTATAAATAG 1620
      GTTTATGTGT ACTGTTTTC ATGTACCCAC CCAAAATGAT TATTTTGA GAATCTAAGT 1680
      CAAACTCACT ATTTATAATG CATAGGTAAC CATTAACTAT GTACATATAA AGTATAAATA 1740
      TGTTTATAT CTGTATATAT GGTTAGGTC ACCAGATCCT AGTGTAGTTC TGAAACTAAG 1800
      ACTATAGATA TTTTGTTTCT TTTGATTTCT CTTTATACTA AAGAATCCAG AGTTGCTACA 1860
60     ATAAATAAAG GGAATAATA AACTTGAGAG TGAATAACCA T 1901
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Seq ID NO: C159 DNA Sequence

Nucleic Acid Accession #: NM_005472.1

Coding sequence: 93..404

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      CCGAGTCTTC CCGCACTTCA ATCCCTGTTC CTATGGAGAC TACCAATGGA ACGGAGACCT 120
      GGTATGAGAG CCGCATGCCC GTGCTGAAGG CTCTAAATGC CACTCTTAC AGCAATTTCG 180
      TCTGCGCGCC AGGGCCAGGG CTGGGGCCAG ACAACAGAC TGAAGAGAGG CCGGCCAGCC 240
      TACCTGGCCG TGATGACAA CTTACATGT ACATTCTCTT TGTCATGTTT CTATTGCTG 300
      TAACTGTGGG CAGCTCATC CTGGGATACA CCGCTCCCG CAAAGTGAGC AAGCGTAGTG 360
      ACCCTATCA TGTGTATATC AAGAACCCTG TGTCTATGAT CTAAACGAG AGGGCTGGGA 420
75     CCGTGAAGA CCAAGACACC TGGGATGTC GTCTGGGGCC TCCAGAACTC TGCTGTGGAC 480
      TGCATCAGGT CT
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Seq ID NO: C160 DNA Sequence

Nucleic Acid Accession #: NM_005245.1

Coding sequence: 187..13959

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80     |      |      |      |      |      |
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	ACGCGCGAGC	CCGCGGAGGC	CCCAGCAGGC	CCGTCCCTGC	TCGGGGGGGC	GCTGAGACGG	120
	CGGTGAGCT	CCACGAGAGC	GCCGTGCGCA	CTTCGGGCGA	ACTTTGCGAT	TCCCGACAGT	180
	TAAGCAATGG	GGAGACATTT	GGCTTTGCTC	CTGCTTCTGC	TCCTTCTCTT	CCAACATTTT	240
5	GGAGCAGTGG	ATGGCAGGCC	ACGACTTGAA	CAGACTCCTC	TGCAGTTTAC	ACACCTCGAG	300
	TACAACGTCA	CCGTGCAGGA	GAACTCTGCA	GCTAAGACTT	ATGTGGGGCA	TCCTGTCAAG	360
	ATGGGTGTTT	ACATTACACA	TCCAGCGTGG	GAAGTAAGGT	ACAAAATGT	TTCCGGAGAC	420
	AGTGAAAACC	TGTTCAAAGC	TGAAGAGTAC	ATTCTCGGAG	ACTTTTGCTT	TCTAAGAATA	480
	AGGACCAAAG	GAGGAAATAC	AGCTATTCTT	AATAGAGAAG	TGAAGGATCA	CTACACATTG	540
	ATAGTGAAG	CACTTGAAAA	AAATACTAAT	GTGGAGGGCG	GAACAAAGGT	CAGGGTGCAG	600
10	GTGCTGGATA	CAAATGACTT	GAGACCGTTA	TTCTCACCCA	CCTCATAACG	CGTTTCTTTA	660
	CCTGAAAAAC	CAGCTATAAG	GACCACTATC	GCAAGAGTCA	GCGCCACGGA	TGCAGACATA	720
	GGAAACCAAC	GGGAATTTTA	CTACAGTTT	AAAGATCGAA	CAGATATGTT	TGCTATTTCAC	780
	CCAACCAAGT	GTGTGATAGT	GTTAACTGGT	AGACTTGATT	ACCTAGAGAC	CAAGCTCTAT	840
	GAGATGGAAA	TCTTCGCTGC	GGACCGTGGC	ATGAAGTTGT	ATGGGAGCAG	TGGCATCAGC	900
15	AGCATGGCAA	GACTAACGGT	GCACATCGAA	CAGGCCAATG	AATGTGCTCC	GGTGATAACA	960
	GCAGTGACAT	TGTCAACATC	AGAAGCTGGC	AGGGACCCAG	CATATGCAAT	TGTGACAGTG	1020
	GATGACTGCG	ATCAGGGTGC	CAATGGTGAC	ATAGCATCTT	TAAGCATCGT	GGCAGGTGAC	1080
	CTTCTCCAGC	AGTTTAGAAC	AGTGAGGTCC	TTTCCAGGGA	GTAAGGAGTA	TAAAGTCAAA	1140
20	GCCATCGGTG	ACATTGATTG	GGACAGTCT	CCTTTCGGCT	ACAATCTCAC	ACTACAGGCT	1200
	AAAGATAAAG	GAATCCGCGC	CCAGTTCTCT	TCTGTTAAAG	TCATTCACTG	GACTTCTCCA	1260
	CAGTTCAAAG	CCGGGCGAGT	CAAGTTTGAA	AAGGATGTTT	ACAGAGCAGA	AATAAGTGAA	1320
	TTTGTCTCTC	CCAACACACC	TGTGGTCATG	GTAAGGCCCA	TTCTGCTTAA	TTCCCATTTG	1380
	AGGTATGTTT	TAAAAGGAC	ACCTGGAAAA	GCTAAATTCA	GTTTAAATTA	CAACACTGGT	1440
25	CTCATTTCTA	TTTTAGAAC	AGTTAAAAGA	CAGCAGGCG	CCCATTTTGA	ACTTGAAGTA	1500
	ACAACAAGTG	ACAGAAAAGC	GTCCACCAAG	GTCTTGGTGA	AAGTCTTAGG	TGCAAAATAGC	1560
	AATCCCCCTG	AATTTACCCA	GACAGCGTAC	AAAGCTGCTT	TTGATGAGAA	CGTGCCCAT	1620
	GGTACTACTA	TCATGAGCTT	GAGTGCCGTA	GACCTGATG	AGGGTGAGAA	TGGGTACGTG	1680
	ACATACAGTA	TGCAAAATTT	AAATCATGTG	CCGTTTGCGA	TTGACCATTT	CAGTGGTGCC	1740
30	GTGAGTACGT	CAGAAAACTT	GGACTACGAA	CTGATGCCTC	GGGTTTATAC	TCTGAGGATT	1800
	CGTGCACTAG	ATCTGGGCTT	GCCGTACCGC	CGGGAAGTCG	AAGTCTTAGG	TGCAAAATAGC	1860
	CTCAATTAAT	TGAATGACAA	CACACCTTTG	TTTGAGAAAA	TAAATTTGTA	AGGGACAATT	1920
	CCAGAGATAT	TAGGCGTGGG	AGAGCAAAAT	ACCACTGTTT	CTGCTATTGA	TGCAGATGAA	1980
	CTTCAGTTGG	TACAGTATCA	GATTGAAGCT	GGAAATGAAC	TGGATTGTTT	TAGTTTAAAC	2040
35	CCCAACTCGG	GGGTATTGTC	ATTAAGCGGA	TGCTTAATGG	ATGCTTTAGG	TGCAAAAGGTG	2100
	TCTTTCCACA	GCTTGAGAA	CACAGCTACA	GATGGAGAAA	ATTTTGCCAC	ACCAATATAT	2160
	ATCAACATAA	CAGTGGCTGC	CAGTCACAA	CTGTTAAACT	TGCAGTGTGA	AGAGACTGGT	2220
	GTTCGCAAAA	TGCTGGCAGA	GAAGCTCTCG	CAGGCAAAAT	AATTAACAAA	CCAGGGAGAG	2280
	GTGGAGGATA	TTTTCTTCCA	TTCTCACTCT	GTCATGCTC	ACATACGCGA	GTTTAGAAGC	2340
40	ACTCTTCCGA	CTGGTATTCA	GGTAAAGGAA	AACACGCTCG	TGGGTTCCAG	TGTAATTTTC	2400
	ATGAATCCCA	CTGACCTTGA	CAGTGGCTTC	AATGGAAGAA	TGGTCTATGC	TGTTTCTGGA	2460
	GGAAATGAGG	ATAGTTGCTT	CATGATTGAT	ATGGAAACAG	GAATGCTGAA	AATTTTATCT	2520
	CCTCTTGACC	GTGAAACAAC	AGACAAATAC	ACCTGAATA	TTACCGTCTA	TGACCTTGGG	2580
	ATACCCCGAG	AGGCTCGGTG	CGCTCTTCTA	CATGTCGTGG	TTGTGATGTC	CAATGATAAT	2640
45	CCACCCGAGT	TTTTACAGGA	GAGCTATTTT	GTGGAAAGTA	GTGAAGACAA	GGAGGTACAT	2700
	AGTGAATACT	TCCAGGTTGA	AGCCACAGAT	AAAGACCTGG	GGCCCAACGG	ACACGTGACG	2760
	TACTCAATTC	TTACAGACAC	AGACACATTT	TCAATTGACA	CGGTGACGGG	TGTTGTTAAC	2820
	ATCGCACGCC	CTCTGGATCG	AGAGCTGCAG	CATGAGCACT	CCTTAAAGAT	TGAGGCCAGG	2880
50	GACCAAGCCA	GAGAAGAGCC	TCAGCTGTTC	TCCACTGTGC	TTGTGAAAGT	ATCACTAGAA	2940
	GATGTTAATG	ACAACCCACC	TACATTATTT	CCACCTAATT	ATCGTGTGAA	AGTCCGAGAG	3000
	GATCTTCCAG	AAGGAACCGT	CATCATGTGG	TTAGAAGCCC	ACGATCCTGA	TTTAGTTCAG	3060
	TCGTGTCAGG	TGAGATACAG	CCTTCTGGAC	CACGGAGAAG	GAAACTTCGA	TGTGGATAAA	3120
	CTCAGTGGAG	CAGTTAGGAT	CGTCCAGCAG	TTGGACTTTG	AGAAGAAGCA	AGTGATATAAT	3180
	CTCAGTGGTA	GGGCCAAAGG	CAAGGGAAAG	CCAGTTTCTC	TGCTCTCTAC	TTGCTATGTT	3240
55	GAAGTTGAGG	TGGTGTGATG	GAATGAGAAC	CTGCACCCAC	CCGTGTTTTT	CAGCTTTGTG	3300
	GAAAAGGGGA	CAGTGAAAGA	AGATGCACCT	GTTGGTTTCT	TGGTAATGAC	GCTGTCCGCT	3360
	CATGATGAGG	ACGCGGGGAG	AGATGGGGAG	ATCGATACCT	CCATTAGAGA	TGGCTCTGGC	3420
	GTTGGTGTTT	TCAAAATAGG	TGAAGAGACA	GGTGTCTATG	AGACGTGAGA	TGACTCTGGC	3480
	CGTGAATCGA	CCTCCCAITTA	TTGGCTAACA	GTCTTTGCAA	CGATCAGGGG	TGTGCTGCCT	3540
60	CTTTTATCGT	TCATAGAGAT	CTACATAGAG	GTTGAGGATG	TCAATGACAA	TGCACACAG	3600
	ACATCAGAGC	CTGTTTATTA	CCCAGAAATC	ATGGAAAAAT	CTCCTAAAGA	TGTATCTGTG	3660
	GTCCAGATCG	AGGCATTTGA	TCCAGATTGG	AGCTCTAATG	ACAAGCTCAT	GTACAAAAT	3720
	ACAAGTGGAA	ATCCACAAGG	ATTCTTTTCA	ATACATCCTA	AAACAGGTCT	CATCACAACT	3780
	ACGTCAAGGA	AGCTAGACCG	AGAACAGCAA	GATGAACACA	TATTAGAGGT	TACTGTGACA	3840
65	GACATGTTGA	GTCCCCCCTA	ATCAACCAT	GCAAGAGTCA	TTGTGAAAT	CCTGTATGAA	3900
	AATGACAACA	AACCTCAGTT	TCTGCAAAAG	TTTACAAAA	TCAGACTCCC	TGAGCGGGAA	3960
	AAGCCAGACC	GAGAAAGAAA	TGCCAGACGG	GAGCGCTCT	ATCGGTCAT	AGCCACCGAC	4020
	AAGGATGAGG	GCCCCAATGC	AGAAATCTCC	TACAGCATCG	AAGACGGGAA	TGAGCATGGC	4080
	AAATTTTCTA	TGGAACCGAA	AACCTGGAGT	GTTTGTGCTA	AGAGGTTTTT	AGCAGCTGGA	4140
70	GAATATGATA	TTCTTTCAAT	TAAGGCAGTT	GACAAATGGT	GCCCTCAAAA	GTCATCAACC	4200
	ACCAGACTCC	ATATTGAATG	GATCTCCAAG	CCCAACAGT	CCCTGGAGCC	CATTTTATTT	4260
	GAAGAAATAT	TTTTTACCTT	TACTGTGATG	GAAAGTGACC	CGTTGCTCTA	CATGATTGGA	4320
	GTAATATCTG	TGGAGCCTCC	TGGCATACCC	CTTTGGTTTG	ACATCACTGG	TGGCAACTAC	4380
	GACAGTCACT	TGATGTGGA	CAAGGGAAT	GGAACCATCA	TTGTTGCCAA	ACCTCTTGAT	4440
75	GCAGAACAGA	AGTCAAACTA	CAACCTCACA	GTCCAGGCTA	CAGATGGAAC	CACCACTATC	4500
	CTCACTCAGG	TATTCATCAA	AGTAATAGAC	ACAAATGACC	ATCGTCTCA	GTTTCTTACA	4560
	TCAAAGTATG	AAGTTGTTAT	TOCTGAAGAT	ACAGGCGCAG	AAACAGAAAT	TTTGCAAAATC	4620
	AGTGCTGTGG	ATCAGGATGA	GAAAAACAAA	CTAATCTACA	CTCTGCAGAG	CAGTAGAGAT	4680
	CCACTGAGTC	TCAAGAAAT	TGCTCTTGAT	CCTGCAACCG	GCTCTCTCTA	TACTCTTGAG	4740
80	AAACTGAGAT	ATGAAGCTGT	TTCAACAGCA	CACCTCAAGG	TCAATGATCG	AGATCAAGAT	4800
	GTGCTGTGAA	AAAGCAACTT	TGCAAGGATT	GTGGTCAATG	TGAGCGACAC	GAATGACCAAC	4860
	GCOCCTGGGT	TCACGCTTTC	CTCCTACAAA	GGGCGGTTT	ATGAATCGGC	AGCCGTTGGC	4920
	TCAGTGTGTT	TGCAAGGTGAC	GGCTCTGGAC	AAGGACAAAG	GGAAGAAATG	TGAAGTGTGC	4980
	TACTCGATCG	AGTCAGGAAA	TATTGGAAT	ATTGGAAT	CTTTTATGAT	TGATCTCTGC	5040
	TTGGGCTCTA	TAAAACCTGC	CAAGAATA	GATCGAAGTA	ACCAAGCGGA	GTAATGATTA	5100

	ATGGTAAAG	CTACAGATAA	GGGCAGTCCA	CCAATGAGTG	AAATAACTTC	TGTGCGTATC	5160
	TTTGTACAAA	TTGCTGACAA	CGCCTCTCCG	AAGTTTACAT	CAAAAGAATA	TTCTGTTGAA	5220
	CTTAGTGAAA	CTGTGACGAT	TGGGAGTTTC	GTGGGATGG	TTACAGCCCA	TAGTCAATCA	5280
5	TCAGTGGTGT	ATGAAATAAA	AGATGGAAAT	ACAGGTGATG	CTTTTGATAT	TAATCCACAT	5340
	TCTGGAACATA	TCATCACTCA	GAAAGCCCTG	GACTTTGAAA	CTTTGCCCAT	TTACACATTG	5400
	ATAATACAAG	GAACATAACAT	GGCTGGTTTG	TCCACTAATA	CAACGGTTCT	AGTTCACTTG	5460
	CAGGATGAGA	ATGACAAACGC	GCCAGTTTTT	ATGCAGGCAG	AATATACAGG	ACTCATTAGT	5520
	GAATCAGCCT	CAATTAACAG	CGTGGTCCCTA	ACAGACAGGA	ATGTCCCACT	GGTGATTGCA	5580
10	GCAGCTGATG	CTGATAAAGA	CTCAAAATGCT	TTGCTTGAT	ATCACATTGT	TGAACCATCT	5640
	GTACACACAT	ATTTTGCTAT	TGATTCTAGC	ACTGGTGCTA	TTCATACAGT	ACTAAGTCTG	5700
	GACTATGAAG	AAACAAGTAT	TTTTCACTTT	ACCGTCCAAG	TGCATGACAT	GGGAACCCCA	5760
	CGTTATTGTT	CTGAGTATGC	AGCGAATGTA	ACAGTACATG	TAATTGACAT	TAATGACTGC	5820
	CCCCCTGTGT	TTGCCAAGCC	ATTATATGAA	GCATCTCTTT	TGTTACCAAC	ATACAAAGGA	5880
15	GTAAAGATCA	TCACAGTAAA	TGCTACAGAT	GCTGATTCAA	GTGCATTCTC	ACAGTTGATT	5940
	TACTCCATCA	CCGAAGGCAA	CATCGGGGAG	AAGTTTCTTA	TGGACTACAA	GACTGGTGCT	6000
	CTCACTGTCC	AAAACAACAC	TCAGTTAAGA	AGCCGCTACG	AGCTAACCGT	TAGAGCTTCC	6060
	GATGGCAAGT	TTGCCGCGCT	TACCTCTGTC	AAAATTAATG	TGAAAGAAAG	CAAGAGAAAT	6120
	CACCTAAAGT	TTACCCAGGA	TGTCTACTCT	GCGGTAGTGA	AAGAGAATTC	CAOCCAGGCC	6180
20	GAAACATTAG	CTGTCACTTAC	TGCTATTGGG	AGTCCAATCA	ATGAGCCCTT	GTTTTATCAC	6240
	ATCCTCAACC	CAGATCGCAG	ATTTAAATAA	AGCCGCACTT	CAGGGGTTCT	GTCAACCACT	6300
	GGCAGCGCCT	TCGATCGTGA	GCAGCAGGAG	CGGTTTGATG	TGGTTGTAGA	AGTGATAGAG	6360
	GAACTAAGC	CTTCTGCACT	GGCCCAAGTT	GTGTTGAAGG	TCATTGTAGA	AGACCAAAAT	6420
	GATAATGCGC	CGGTGTTTGT	CAACCTTCCC	TACTACGCCG	TTGTTAAAGT	GGACACTGAG	6480
25	GTGGGCCATG	TCATTGCTTA	TGTCACCTGCT	GTAGACAGAG	ACAGTGGCAG	AAACGGGGAA	6540
	GTGCATTACT	ACCTCAAGGA	ACATCATGAA	CACTTTCAAA	TTGGAACCTT	GGGTGAAAT	6600
	TCACGTGAAA	AGCAATTGGA	GCTTGACACC	TTAAATAAAG	AATATCTTGT	TACAGTGGTT	6660
	GCAAAAGATG	GAGGGAACCC	GGCCTTTTCA	GCGGAAGTTA	TCGTTCCGAT	CACGTGCTAG	6720
	AATAAAGCCA	TGCTGTGTTT	TGAAAACCTT	TTCTACAGTG	CAGAGATTGC	AGAGAGCATC	6780
30	CAGGTGCACA	GGCCTGTGGT	CCACGTGACG	GCTAACAGCC	CGGAAGGCCCT	GAAAGTGTTC	6840
	TACAGCATCA	CCGACGGAGA	CCCTTTACAG	CAGTTCACTA	TTAACTTCAA	TACTGGAGTT	6900
	ATCAATGTCA	TAGTCTCTCT	GGACTTTGAG	GCCCAACCCG	CATATAAGCT	GAGCATACGC	6960
	GCAACTGACT	CCTTGACGGG	CGCTCATGCT	GAAGTATTG	TGGACATCAT	AGTAGACGAC	7020
	ATCAATGATA	ACCCTCTGTT	GTGCTGCTAG	CAGTCTTATG	CGGTGACCTT	GTCTGAGGCA	7080
35	TCTGTAAATG	GAACTCTGTT	TGTTCAAGTT	AGAGCCACCG	ATTCGTATTC	AGAACCAGAT	7140
	AGAGGAATCT	CATACCCAGAT	GTGTTGGGAT	CACAGCAAGA	GTCAATGATCA	TTTTCATGTA	7200
	GACAGCAGCA	CTGSCCTCAT	CTCACTACTC	AGAACCTCTG	ATTACGAGCA	GTCCCGGCAG	7260
	CACACGATTT	TTGTGAGGGC	AGTTGATGGT	GGTATGCCCA	CGCTGAGCAG	TGATGTGATT	7320
	GTCAACGGTG	ACGTTACCGA	CCTCAATGGT	AATCCACCAC	TCMTTGAACA	ACAGATTAT	7380
40	GAAAGCCAGAA	TTAGCGAGCA	CGCCCTCAT	GGGCATTTCG	TGACCTGTGT	AAAAGCCTAT	7440
	GATGCAGACA	GTTCAGACAT	AGACAAGTTG	CAGTATTCCT	TTCTGTCTGT	CAATGATCAT	7500
	AAACATTTTG	TCATTGACAG	TGCAACAGGG	ATTATCACCC	TCTCAACCTT	GCACCGGCAC	7560
	GGCCTGAAGC	CATTTTACAG	TCTTAACCTG	TCAGTGTCTG	ATGAGATTTT	TAGAAGTTCC	7620
45	ACCCAGGTTT	ATGCTAACTG	AATTGGAGGC	AATTGACACA	GTCCGTCTTT	CCTTCAGAAC	7680
	GAATATGAAG	TGGAACTAGC	TGAAAACGCT	CCCTACATA	CCCTGGTGAT	GGAGGTGAAA	7740
	ACTACGGATG	GGGATCTCTG	TATTTATGGT	CACGTTACTT	ACCATAITGT	AAATGACTTT	7800
	GCCAAAGACA	GATTTTACAT	AAATGAGAGA	GGACAGATAT	TTACTTTGGA	AAAACCTGAT	7860
	CGAGAAACCC	CGGCGAGAGA	AGTGATCTCA	GTCCGTTTAA	TGCGTAAGGA	TGCTGGAGGA	7920
50	AAAGTTGCTT	TCGTACCCGT	GAATGTCTAT	CTTACAGATG	ACAATGACAA	TGCACCAACA	7980
	TTTCAGACAA	CCAAATACGA	AGTGAATATC	GGGTCCAGTG	CTGCTAAAGG	GACTTCAGTC	8040
	GTAAAGTCTG	CAAGTGATGC	CGATGAGGGC	TCCAATGCCG	ACATCACCTA	TGCCATTGAA	8100
	GCAGACTCTG	AAAGGTGATA	AGAGAATTTG	GAAATTAACA	AACTGTCCGG	CGTAATCACT	8160
	ACAAAGGAGA	GCCTCATTTG	CTTGGAAAAT	GAAATCTTCA	CTTCTTTTGT	TAGAGCTGTG	8220
	GATAATGGGT	CTCCATCAAA	AGAACTCTGT	GTCTCTGTCT	ATGTTAAAT	CCTTCCACCG	8280
55	GAAATGCAGC	TTCCAAATTT	TTCAAGACCT	TTCTATACCT	TTACAGTGTC	AGAGGACGTG	8340
	CCTGTTGGAA	CAGAGATAGA	TCTCATCCGA	GCAGAACATA	GTGGGACTGT	TCTTTACAGC	8400
	CTGGTCAAG	GGAAATACCT	AGAAAGCAAT	AGGGATGAGT	CCTTTTGATG	TGACAGACAG	8460
	AGCGGGAGAC	TGAAGTTGGA	GAAAGTCTT	GATCATGAGA	CAACTAAGTG	GTATCAGTTT	8520
60	TTCACTACTG	CCAGGTGAC	TCAAGATGAC	CATGAGATGG	TGGCTTCTGT	AGATGTTAGT	8580
	ATCCAAGTGA	AAGATGCAAA	TGACAACAGC	CCGCTCTTTG	AATCTAGTCC	ATATGAGGCA	8640
	TTCAATTGTT	AAAACCTGCC	AGGGGGAAGT	AGAGTAATTC	AGATCAGGGC	ATCTGATGCT	8700
	GACTCAGGAA	CCAACGGCCA	AGTTATGTAT	AGCCTGGATC	AGTCACAAAG	TGTGGAAGTC	8760
	ATTGAATCTC	TTGCCATTAA	CATGGAACA	GGCTGGATTA	CAACTTTAAA	GGAACTTGAC	8820
	CATGAAAAGA	GAGACAAATTA	CCAGATTAAA	GTGGTTGCAT	CAGATCATGG	TGAAAAGATC	8880
65	CAGCTATCCT	CCACAGCCAT	TGTGGATGTT	ACCGTCAACG	ATGTCAACGA	TAGTCCACCA	8940
	CGATTCAACG	CCGAGATCTA	TAAAGGGACT	GTGAGTGAGG	ATGACCCCA	AGGTGGGGTG	9000
	ATTGCCATCT	TAAGTACCAC	GGATGCTGAT	TCTGAAGAGA	TCAACAGACA	AGTTACATAT	9060
	TTCAATACAG	GAGGGGATCC	TTTAGGACAG	TTTGGCGTTG	AACTATATCA	GAATGAATGG	9120
	AAGGTATATG	TGAAGAAACC	TCTAGACAGG	GAAAAAAGGG	ACAATTACCT	TCTTACTATC	9180
70	ACGGCAACTG	ATGGCACCTT	CTCATCAAAA	GCGATAGTTG	AAGTGAAAGT	TCTGGATGCA	9240
	AATGACAACA	GTCCAGTTTG	TGAAAAGACT	TTATATTTCG	ACACTATTCC	TGAAGAOGTC	9300
	CTTCTGGAAA	AATTGATCAT	GCAGATCTCT	GCTACAGACG	CAGACATCCG	CTCTAACGCT	9360
	GAAATTAATT	ACAGTTTATT	GGGTTCAGGT	GCAGAAAAT	TCAACTATAA	TCCAGACACA	9420
	GGTGAATCTA	AAACGTCAAC	CCCCCTTGAT	CGTGAGGAGC	AAGCTGTTTA	TCATCTTCTC	9480
75	GTCAAGGCCA	CAGATGGAGG	AGGAAGATTG	TGCCAAGCCA	GTATTGTGCT	CAGCTAGAAA	9540
	GATGTGAACG	ATAACGCCCC	CGAATTCTCT	GCGATCTCTT	ATGCCATCAC	CGTGTGTTGA	9600
	AACACAGAGC	CGGGAACGCT	GCTGACAAGA	GTGCAGGCCA	CAGATGCGCA	CGCAGGATTA	9660
	AATCGGAAGA	TTTTATACCT	ACTGATTGAC	TCTGCTGATG	GGCAGTTCTC	CATTACAGAA	9720
	TTATCTGGAA	TTATTCAGTT	AGAAAAACCT	TTGGACAGAG	AACTCCAGGC	AGTATACACC	9780
80	CTCTCTTTGA	AATTCTGGGA	TCAAGGCTTG	CCAAGGAGGC	TGACTGCCAC	TGGCACTGTG	9840
	ATTGTATGAT	TTCTTGACAT	AAATGACAAC	CCCCCTGTGT	TTGAGTACCG	TGAATATGGT	9900
	CGCACCGTGT	CGGAGACAT	TCTTGTGGGA	ACTGAAGTTC	TTCAAGTGTG	TGCAGCAAGT	9960
	CGGGATATTG	AAGCAAAATG	AGAAATCAC	TACTCAATAA	TAAGTGGAAA	TGAACATGGG	10020
	AAATTCAGCA	TAGATTCTAA	AACAGGGGCC	GTATTTATCA	TTGAGAAATC	GGATTATGAG	10080
	AGCTCTCATG	AGTATTACCT	AACAGTAGAG	CCCACTGATG	GAGGCACGCC	TTCACTGAGC	10140

	GACGTTGCCA	CTGTGAACGT	TAATGTAACA	GATATCAACG	ATAATACCCC	TGTGTTACAG	10200
	CAAGACACCT	ACACGACAGT	CATCAGTGAA	GATGCCGTTT	TTGAGCAGTC	TGTCATCAGG	10260
	GTATGCGCCG	ATGATGCGCG	TGGACCTTCC	AACAGCCACA	TCCACTACTC	AATTATAGAT	10320
	GGCAACCAAG	GAAGCTCGTT	CACAATTGAC	CCCGTCAGGG	GAGAAGTCAA	AGTGACCCAA	10380
5	CTTCTCGACC	GAGAAACGAT	TTCAAGTTAC	ACGCTCAACG	TTCAAGCTTC	TGATAATGGC	10440
	AGTCCACCCA	GAGTCAACAC	GACGACCGTG	AACATCGATG	TGTCCGATGT	CAATGACAAC	10500
	GCGCCGCTCT	TCTCCAGGGG	AAACTACAGT	GTCTATTATC	AGGAAAATAA	GCCAGTGGGC	10560
	TTCCAGCTGC	TGCAGCTGGT	AGTAACAGAT	GAGGATTCTT	CCCTAAACGG	TCCACCCCTC	10620
10	TTCTTTACTA	TTGTAACCTG	AAATGATGAG	AAGGCTTTTG	AAGTTAACCC	GCAAGGAGTC	10680
	CTCCTGACAT	CATCTGCCAT	CAAGAGGAAG	GAGAAAGATC	ATTACTTACT	GCAGGTGAAG	10740
	GTGGCAGATA	ATGGAAGGCC	TCAGTTGTCA	TCTTTGACAT	ACATTGACAT	TAGGGTAATT	10800
	GAGGAGAGCA	TCTATCOGCC	TGCGATTTTG	CCCTGGGAGA	TTTTTCATCA	CTCTTCTGGA	10860
	GAAGAATACT	CAGGTGGCGT	CATTGGGAAG	ATCCATGCCA	CAGACCAGGA	CGTGTATGAT	10920
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	GGCAAGCTGA	TAGCACACAA	AAAGCTAGAC	ATAGGGCAAT	ACCTTCTCAA	TGTCAGCGTA	11040
	ACAGATGGGA	AGTTCAOGAC	GGTGGCCGAC	ATCAGAGTGC	ATATCAGACA	AGTCACACAG	11100
	GAGATGTGGA	ACCAACCCAT	CGCGATCCGC	TTTGCCAAAC	TCACTCCGGA	AGAATTGGTT	11160
	GGTGACTACT	GGCGCAACTT	CCAGCGAGCT	TTACGGAAAC	TCCCTGGGTG	GAGGAGGAAC	11220
20	GACATACAGA	TTGTTAGTTT	CGAGTCCCTC	GAACCTCACC	CACATCTGGA	CGTCTTACTT	11280
	TTTGTAGAGA	AACCAGGTAG	TGCTCAGATC	TCAACAAAAC	AACCTCTGCA	CAAGATTAAC	11340
	TCTTCCGTGA	CTGACATTGA	GGAAATCATT	GGAGTTAGGA	TACTGAATGT	ATTCCAGAAA	11400
	CTCTGCGCGG	GACTGGACTG	CCCTCGGAAG	TTCTGCGATG	AAAAGGTGTC	TGTGGATGAA	11460
	AGTGTGATGT	CAACACACAG	CACAGCCAGA	CTGAGTTTGT	TGACTCCCGG	CCACCAACAG	11520
25	GCAGCGGTGT	GTCTCTGCAA	AGAGGGGAAG	TGCCCACTCG	TCCACCATGG	CTGTGAAGAT	11580
	GATCCGTGCG	CTGAGGGATC	CGAATGTGTG	TCTGATCCCT	GGGAGGAGAA	ACACACCTGT	11640
	GTCTGTCCCA	GCGGCGAGTT	TGCTCAGTGC	CCAGGGAGTT	CATCTATGAC	ACTGACTGGA	11700
	AACAGCTACG	TGAAATACCG	TCTGACGGAA	AATGAAAACA	AATTAGAGAT	GAAACTGACC	11760
	ATGAGGCTCA	GAACATATTC	CACGCAATCG	GTGTGTCATG	ATGCTCGAGG	AACTGACTAT	11820
30	AGCATCTTGG	AGATTTCATC	TGGAAGGCTG	CAGTACAAGT	TTGACTGTGG	AAGTGGCCCT	11880
	GGAAATGTCT	CTGTTTCAGAG	CATTCAAGTC	AATGATGGGC	AGTGGCAACG	AGTGGCCCTG	11940
	GAAGTGAATG	GAAACTATGC	TGCGTTGGTT	CTAGACCAAG	TTCACTATGC	ATCGGGCACA	12000
	GCCCCAGGGA	CTCTGAAAAC	CCTGAACCTG	GATAACTATG	TGTTTTTTGG	TGGCCACATC	12060
	CGTCAGCAGG	GAACAAGGCA	TGGAAGAAGT	CCTCAAGTTG	GTAATGGTTT	CAGGGGTTGT	12120
35	ATGGACTCCA	TTTATTGTAA	TGGGCAGGAG	CTCCCTTTAA	ACAGCAAAAC	CAGAAGCTAT	12180
	GCACACATCG	AAGAGTCGGT	GGATGTATCT	CACGCGTCTC	TCTGGAOCGG	CACGGAAGAC	12240
	TGCGCCAGCA	ACCCTTGCCA	GAATGGAGGC	GTTCGCAATC	CGTCACCTGC	TGGAGGTTAT	12300
	TACTGCAAA	GCAGTGCCCT	GTACATAGGG	ACCCACTGTG	AGATAAGCGT	CAATCCGTGT	12360
	TCTTCCAAAC	CATGCCCTTA	TGGGGGCACG	TGTGTGTGCG	ACAAOCGAGG	CTTGTGTTGC	12420
40	CAGTGTAGAG	GATTATATAC	TGGTCAGAGG	TGTCAGCTTA	GTCCATCTAG	CAAAGATGAA	12480
	CCCTGTAAAG	CTGTTTCAGAC	AGTTTGGATG	GCGCGGTTTG	TCAAGTGTAT	12540	
	TGCGGTTTAA	GGGAGAAAAG	GTGTGACAGT	GATATCGACG	AGTGTCTTGG	AAACCCCTGC	12600
	CTGCACGGGG	CCCTCTGTGA	GAACAOCGAC	GGCTCCTATC	ACTGCAACTG	CAGCCACGAG	12660
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45	ATTGGGTGCG	CGGAGGAAGT	TGGAATCGTT	GTGTTTGTGT	CAGGGATATT	TTTACTGGTG	12780
	GTGGTGTGTT	TTCTCTGCGG	TAAGATGATT	AGTCGGAATA	AGAAGCATCA	GGCTGAACCT	12840
	AAAGACAAGC	ACCTGGGACC	CGCTACGGCT	TTCTTGCAAA	GACCGTATTT	TGATTCCAA	12900
	CTAAATAAGA	ACATTACTCT	AGACATACCA	CCCGAGGTGC	CTGTCCGGCC	TATTTCTTAC	12960
	ACCCCGGAGT	TTCCAAGTGA	CTCAAGAAAC	AATCTGGACC	GAAATTCCTT	OGAAGGATCT	13020
50	GCTATCCCG	AGCATCCCGA	ATTCAAGCACT	TTTAAACCCG	AGTCTGTGCA	OGGGCACCGA	13080
	AAAGCAGTGG	CGGTCTGACG	CGTGGCCCCA	AACCTGCCTC	CCCCACCCCC	TTCAAACCTC	13140
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Seq ID NO: C165 DNA Sequence
 Nucleic Acid Accession #: AK027843.1
 Coding sequence: 193..1731

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	AACGTGACCA	TTATGGATAT	AGACAGTCTG	TACGATATGC	ATGTAATAAA	GGATTACCA			840
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Seq ID NO: C167 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..2651

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Seq ID NO: C168 DNA Sequence
 Nucleic Acid Accession #: NM_003667.2
 Coding sequence: 49..2772

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30 Seq ID NO: C169 DNA Sequence
 Nucleic Acid Accession #: NM_003506.1
 Coding sequence: 259..2379

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Seq ID NO: C170 DNA Sequence
 Nucleic Acid Accession #: NM_000582
 Coding sequence: 88..990

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Seq ID NO: C171 DNA Sequence
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 50 CCATTGTCTT CATCAAGCAG CGTCTCTCCC AGGATGCACT GCAGGGGCGC CGGGCGCTGC 300
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 60 CCCAGGAGGT GGTAGTAGCG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC 900
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 AGAAGGGCCA CGAGCTGGTG TTGGCCAATA TTGCTGAAAG TGATGCTGTT GTCTACACCT 1320
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 70 TGCCCTCCTG GCTGAAGAAG CCCCAAGACA GCCAGCTGGA GGAGGGCAAA CCGGCTACT 1440
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5	AAGCCAAGCG	GCTGCAGAAG	CAGCCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCCTCAACG	2400
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	GCTTGGGCTC	GGGCCCCGCG	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
	TCCCACGGTC	TAGCTCGCAG	CCCATCACCA	CGCTGGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580
	TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCTTGTTA	CTTGTGAAGA	2640
	GCCTGCAGAC	GAAGGATGAG	CAGCAGCAGC	TGGACTTCCG	GAGGGAGTTG	GAGATGTTTG	2700
	GGAAAGCTGAA	CCACGCCAAC	GTGGTGGCGC	TCCTGGGGCT	GTGCCGGGAG	GCTGAGCCCC	2760
	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCCTG	AGGATTTCCA	2820
10	AGAGCAAGGA	TGAAAAATTG	AAGTCACAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
	GCACCCAGGT	AGCCCTGGGC	ATGGAGCACC	TGTCCACAA	CCGCTTTGTG	CATAAGGACT	2940
	TGGCTGCGCG	TAACTGCCTG	GTCACTGCCG	AGAGACAAGT	GAAGGTGTCT	GCCCTGGGCC	3000
	TCAGCAAGGA	TGTGTACAAC	AGTGAGTACT	ACCACTTCCG	CCAGGCCTGG	GTGCCGCTGC	3060
	GCTGGATGTC	CCCCGAGGCC	ATCCTGGAGG	GTGACTTCTC	TACCAAGTCT	GATGTCTGGG	3120
	CCTTGGGTGT	GTGATGTGG	GAAGTGTTTA	CACATGGAGA	GATGCCCAT	GGTGGGCAGG	3180
15	CAGATGATGA	AGTACTGGCA	GATTTGCAGG	CTGGGAAGGC	TAGACTTCTC	CAGCCCGAGG	3240
	GCTGCCCTTC	CRAACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCAGC	CCCAAGGACC	3300
	GGCCCTCCTT	CAGTGAGATT	GCCAGCGCCC	TGGGAGACAG	CACCGTGGAC	AGCAAGCCGT	3360
	GAGGAGGGAG	CCCGCTCAGG	ATGGCTGGG	CAGGGGAGGA	CATCTCTAGA	GGGAAGCTCA	3420
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20	TTGTGAGGT	CTGAGCAGGG	CCTGGCCCTT	CCTCCTCTTC	CTCACCTCA	TCCTTTGGGA	3540
	GGCTGACTTG	GACCCAAACT	GGGCGACTAG	GGCTTTGAGC	TGGGCACTTT	CCCTTGCCAC	3600
	CTCTCTCTCT	ATCAGGGGACA	GTGTGGGTGC	CACAGGTAAC	CCCAATTTC	GGCCTTCAAC	3660
	TTCTCCCTCT	GACCGGGTCC	AACTCTGCCA	CTCATCTGCC	AATTTTGCCT	GGGGAGGGCT	3720
	AGGCTTGGGA	GCTGATGGGT	TTGTGGGGAG	TTCTTAATA	TTCTCAAGTT	GGGGCACAC	3780
25	AGGGTAAATG	AGTCTCTTGC	CCACTGGTCC	ACTTGGGGGT	CTAGACCAGG	ATTATAGAGG	3840
	ACACAGCAAG	TGAGTCTCTC	CCACTCTGGG	CTTGTGCACA	CTGACCCAGA	CCCAAGTCTT	3900
	CCCCACCTCT	CTCTCCTTTC	CTCATCCTAA	GTGCCCTGGCA	GATGAAGGAG	TTTTCAGGAG	3960
	CTTTTGACAG	TATATAAACG	GCCTTTTGTG	TATGCACCAC	GGGCGGCTTT	TATATGTAAT	4020
	TGCAGCGTGG	GGTGGGTGGG	CATGGGAGGT	AGGGGTGGGC	CCTGGAGATG	AGGAGGGTGG	4080
30	GCCATCCTTA	CCCCACACTT	TTATTGTGTG	CGTTTTTGTG	TTGTTTTGTT	TTTTTGTTTT	4140
	TGTTTTTGTG	TTTACACTCG	CTGCTCTCAA	TAAATAAGCC	TTTTTTTA		4187

Seq ID NO: C172 DNA Sequence

Nucleic Acid Accession #: NM_002309.2

Coding sequence: 65..673

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	ATGTCAACAAC	AACCTCATGA	ACCAGATCAG	GAGCCAACTG	GCACAGCTCA	ATGGCAGTGC	240
	CAATGCCCTC	TTTATTCTCT	ATTACACAGC	CCAGGGGGAG	CCGTTCCTCA	ACAACTTGGA	300
	CAAGCTATGT	GGCCCCAACG	TGACGGACTT	CCCGCCCTTC	CACGCCAACG	GCACGGAGAA	360
45	GGCCAAAGCTG	GTGGAGCTGT	ACCGCATAGT	CGTGTACCTT	GGCACTCTCC	TGGGCAACAT	420
	CACCGCGGAC	CAGAAGATCC	TCAACCCAGC	TGCCCTCAGC	CTCCACAGCA	AGCTCAACGC	480
	CACCGCGGAC	ATCCTGGGAG	GCCTCTTAG	CAACGTGCTG	TGCCGCTCTG	GCAGCAAGTA	540
	CCAAGTGGGC	CATGTGGAGC	TGACCTACGG	CCCTGACACC	TGGGTAAAG	ATGTCTTCCA	600
	GAAGAGAAG	CTGGGCTGTC	AACTCTGGGG	GAAGTATAAG	CAGATCATCG	CGTGTGTGGC	660
50	CACAGGCTTC	TAGCAGGAGG	TCTTGAAGTG	TGCTGTGAAC	CGAGGGATCT	CAGGAGTTGG	720
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	GGGGGCTGCT	GCCAGACCCC	GAGGGTGCTC	GGCCAGTCCA	CTCCACTCTG	GGCTGGGCTG	840
	TGATGAAGCT	GAGCAGAGTG	GAAACTTCCA	TAGGGAGGGA	GCTAGAAGAA	GGTGCCCTTT	900
	CTCTCTGGAG	ATGTGTGAGT	GGGGAGGGTG	GGCTGGGACT	CTGCCTCTAC	TTGTCCCTTT	960
55	GGCCCCCTTG	TCACTTTGTG	CAGTGAACAA	ACTACACAAG	TCACTTACAA	GAGCCCTGAC	1020
	CACAGGGTGA	GACAGCAGGG	CCAGGGGAG	TGGACCAACC	CCCAGCAAT	TATCACCATC	1080
	TGTGCTTTTG	CTGCCCTTTA	GGTTGGGACT	TAGTGGGCC	AGAGGGGCTA	GGATCCCAAA	1140
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	AGGCTGTCTT	CTTTTGAGGA	TGATCAGAGA	ACTTGGGCTT	AGGAACAATC	TGGCAGAAGT	1260
60	TTCCAGAAGG	AGGTCACTTG	GCATTCAAGC	TCTTGGGGAG	GCAGAGAAGC	CACCTTCAGG	1320
	CTTGGGAAGG	AAGACACTGG	GAGGAGGAGA	GGCCTGGAAA	GCTTTGGTAG	GTTCCTTGTT	1380
	CTCTTCCCG	TGATCTTCCC	TGCAGCCTGG	GATGGCCAGG	GTCTGATGGC	TGGACCTGCA	1440
	GCAGGGGTTT	GTGGAGGTGG	GTAGGGCAGG	GGCAGGTTCG	TAACTCAGGT	GCAGAGGTTC	1500
65	TGAGGAGACC	AGGCTCTTCC	TCTGGGTAAA	GGTCTGTAA	AAGGGGCTGG	GGTAGCTCAG	1560
	AGTAGCAGCT	CACATCTGAG	GCCCTGGGAG	GTCTTGTGAG	GTACACAGAG	GGTACTTGAG	1620
	GGGACTTGA	GGCGTCTCT	GGTCCCGAG	GCAAGGGAAC	AGCAGAACTT	AGGGTCAGGG	1680
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	CACGTGTCTT	GGGGGCCCA	GCATTGTGTT	GTGAGGGCGA	CTGTCTCTGG	CAGATATTGT	2160
75	GCCCCCTTGA	GCAGTGGGCA	AGACAGTCC	TGTGGGCCAC	CCTGTCTCTG	TTTCTGTGTC	2220
	CCCATGCTGC	CTCTGAAATA	GCGCCCTGGA	ACAACCTTGC	CCCTGCACCC	AGCATGCTCC	2280
	GACACAGCAG	GGAAGCTCTC	CCTGTGGCCC	GGACACCCAT	AGACGGTGGG	GGGGCCCTGG	2340
	CTGGGGCCAA	CCCAAGGAAG	GTGGGGTAGA	CTGGGGGGAT	CAGCTGCCCA	TTGCTCCCAA	2400
	GAGGAGGAGA	GGGAGGCTGC	AGACGCTTGG	GACTCAGACC	AGGAAGCTGT	GGGCCCTCCT	2460
80	GCTCCACCCC	CATCCCACTC	CCACCATGT	CTGGGCTCCC	AGGCAGGGAA	CCCGATCTCT	2520
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	TGAGCGGGCT	GCGGGCTTCC	AAGTCTCTCC	GACAAGATGA	TGGTACTAAT	TATGGTACTT	2700
	TTCACTCACT	TTGCACCTTT	CCCTGTGCT	CTCTAAGCAC	TTTACTTGA	TGGCGCGTGG	2760

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	GCTGATTCCA CCGGGGGGGC CCGGCTGACT CGCCCATCAC CTATCTCCCC TGTGGACTTG 3060
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Seq ID NO: C173 DNA Sequence
Nucleic Acid Accession #: XM_097508
Coding sequence: 44..2788

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30	CACAGAGCTT	CAGCTCGGCC	TCTTCCACCA	CGCTGGCTCT	TTGGAGGAGC	TGCGTCTCTC	180
	TGGGAACCAT	CTCTCACACA	TCCCAGGACA	AGCATTCTCT	GGTCTCTACA	GCCTGAAAA	240
	CCTGATGCTG	CAGAACATCT	AGCTGGGAGG	AATCCCCGCA	GAGGCGCTGT	GGGAGCTGCC	300
	GAGCTTCAGT	TGCTGCGGCC	TAGATGCCAA	CCTCATCTCC	CTGGTCCCGG	AGAGGAGCTT	360
	TGAGGGGCTG	TCCTCCCTCC	GCCACTCTCG	GCTGGAAGAC	AATGCACTCA	CGGAGATCCC	420
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	ACTAGACCTG	AATTATAACA	AGCTGCAGGA	GTTCCTCTGT	GCCATCCGGA	CCTGGGCGAG	660
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40	GGGGAACCTT	CTGTACAGCA	CGATACACTT	TTATGATAAC	CCAATCCAGT	TTGTGGGAAG	780
	ATCGGCAATC	CAGTACCTGC	CTAAACTCCA	CACACTATCT	CTGAATGGTG	CCATGGACAT	840
	CCAGGAGTTT	CCAGATCTCA	AAGGCACCA	CAGCCTGGAG	ATCCTGACCC	TGACCCGCGC	900
	AGGCATCCGG	CTGCTCCCAT	CGGGGATGTG	CCAAACAGCT	CCGAGGCTCC	GAGTCTGTGA	960
	ACTGTCTCAC	AATCAAAATT	AGGAGCTGCC	CAGCCTGCAC	AGGTGTGAGA	AATTGGAGGA	1020
45	AATGGGCTTC	CAACACAACC	GCATCTGGGA	AATTGGAGCT	GACACCTTCA	GCCAGCTGAG	1080
	CTCCCTGCAA	GCCTCGGATC	TTAGCTGGAA	CGCCATCCGG	TCCATCCACC	CCGAGGCTTT	1140
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	CCTGGCTGGA	CTTGGGGGCT	TGATGCATCT	GAGCTCAA	GGGAACTCTG	CTCTCTCCCA	1260
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	AGTTTGTGTA	GGTGGGATTG	CAGGCGCCAA	CACCTTGACT	GGCAATTTCT	GTGGCCTTCT	1740
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60	GAAGTCCCCC	TCCTTGGGCA	CGGTTCCAGC	AGGGGTCTTA	GGCTGCTCTG	CACCTGGCAGG	1980
	CTGGGCCGCC	GCGCTGCCCC	TGGCCTCAGT	AGGAGAAATAC	GGGGCTTCCC	CACCTTGCTC	2040
	GCCCTACGCG	CCACCTGAGG	GTCAGCCAGC	GGGAGTGGGC	TTCACGTTGG	CCCTGTGTAT	2100
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	TTCACTTGA	TACTGGGCTT	CTTCCCTTGT	ATGTCTGAAG	CTGTGGACCA	GAGACCTGGA	3060
	CTTTGTCTG	CTTAAGGGAA	ATGAGGGAAG	TAAAGACAGT	GAAGGGGTGG	AGGGTTGATC	3120
80	AGGGCAGAGT	GGACAGGGAG	ACCTCACAGA	GAAAGGCTG	GAGGCTGATT	TCCCGTGTGA	3180
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Seq ID NO: C174 DNA Sequence
Nucleic Acid Accession #: NM_130849

Coding sequence: 101..2044

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10 TGTGGAGGAC GGCCTGGGCC TGGGCGAGCC TGAGGGGTCA GGGCTGCCCC CGGGCCCGGT 360
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Seq ID NO: C175 DNA Sequence

Nucleic Acid Accession #: NM_018971

Coding sequence: 1..1128

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Seq ID NO: C176 DNA Sequence

Nucleic Acid Accession #: NM_005631

Coding sequence: 290..2653

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40	CCTGCTCGAG	CGCAACGGCT	CCTTTGCCAA	CTTCTCTGCG	AACATATGCC	CCGATGAGGA	2640
	CCAAGGCGAC	CTGAGGAGCA	GCTGGACCGC	GTGGGAAGGT	GCAGAGGATA	AGGAGGCACT	2700
	GCTGATTGAA	GACACACTCA	GCAACCAAC	GGATCTGACA	GACAAATGAT	CAGTCACTTA	2760
	TGTGGTCCAG	AAGCACTTTA	TGAGACAGCT	GAGTGCCCTG	TCTCTAGATG	GGGAGGGACA	2820
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45	GAAGGCAGAT	GGGGCACTGA	CCCAGSAGGA	GAAAGCAGCC	ATTGGCACTG	TGGAGCTCAG	2940
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	TGTGTGTGAT	GAGGTCTTGG	CCCTGTCTAT	CCTCATGTCT	CTCAATTCTT	TCTTCAACGC	3360
	CATCTCCACT	CTTGTGGTCA	TCTATGGCCAG	CAGCGCGCTC	TTCACTGTGG	TCTCTCTGCC	3420
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55	GGCGCTGGAA	TCACTGAGCC	GCTCACTTAT	CTACTCCAC	TTTTCGGAGA	CAGTGACTGG	3540
	TGCCAGTGTG	TCCCGGGCTT	ACAAACGCG	CGGGATTTT	GAGATCATCA	GTGATACTAA	3600
	GGTGATGACC	AACAGAGAG	GCTGTACCC	CTACATCATC	TCCAACCGGT	GGCTGAGCAT	3660
	CGGAGTGGAG	TTGTTGGGGA	ACTGCGTGGT	GCTCTTGTCT	GCACTATTTG	CCGTGATCGG	3720
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60	ATTTGCTCTG	AACCTGGATG	TACGAATGAT	GTGAGATTGG	GAATCTAACA	TGCTGGCTGT	3840
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70	CGAGCCCTCG	CTCCGCAAGA	GCGCATCTCT	GGTTTTAGAC	GAGGCCACAG	CTGCCATCGA	4440
	CCTGGAGACT	GACAACTTCA	TCCAGGCTAC	CATCCGACCC	CAGTTTGATA	CCTGCACTGT	4500
	CCTGACCATC	GCAACCGGCG	TTAACACTAT	CATGGACTAC	ACCAGGGTCC	TGGTCTGGGA	4560
	CAAAGGAGTA	GTAGCTGAAT	TTGATTCTCC	AGCCAACTCT	ATTGCAGCTA	GAGGCATCTT	4620
	CTACGGGATG	CCAGAGAGTG	CTGGACTTGC	CTAAATATATA	TTCTGTAGAT	TTCTCTCTGG	4680
75	CCTTTCTCTGG	TTTTCTATCAG	GAAGGAAATG	ACACCAATA	TGTCCGAGAG	ATGGACTTGA	4740
	TAGCAAAAC	TGGGGGCACC	TTAAGATTTT	GCACTGTGAA	AGTGCCCTTAC	AGGGTAACTG	4800
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	ACAGAGAGCA	GCTGCTGGGT	CAGGCCACCC	CTAGGAACCT	AGTCTGTGAC	TCTGGGGTGC	5100
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Seq ID NO: C180 DNA Sequence

Nucleic Acid Accession #: NM_004626
Coding sequence: 124..1188

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10 AACGAGACGC AACACTGCAA GCAGCTGGAG GGTCTGGTGT CTGCACAGGT GCAGCTGTGC 300
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15 TCGCGCCCGG TCCAGGTGA GCCACCGCGG CCGGGGAACC GCTGGGGAGG ATGTGCGGAC 600
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CCTGACTTCT GCATGAAGAA TGAGAAGGTG GGTCTCCACG GGACACAAGA CAGGCACTGC 1020
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25 ACCTGCCGCA GGTGTGAGCG TACGTGGAG CGCTATGTCT GCAAGTGAGG CCTTGCCTTC 1200
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CCAGGCA 1927

40 Seq ID NO: C181 DNA Sequence
Nucleic Acid Accession #: NM_031866
Coding sequence: 6..2090

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ACTACAAGAA GCGCTGCGCG CCTTGCCTCT CGTGTGCGA GCGCGCCAG GCGGCTGCG 360
CGCGCTCATC CGGCCAGTAC GGCTTGCCTT GGCCTGACCG CATGCGCTGC GACCGGCTGC 420
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55 GCAGCGGCCA CGCGCGCGCG CGCGGGGCGA GCGCCCGGCA CCGCGAGGCG GCGAGGGGCG 600
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65 TGGGCGCGGT GGAAGCAGCA GTGCGCTACG AGACCAACCG CCGCGCGCTG TGCAAGGTGG 1200
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70 TCAGCTCGGT GGAAGCGGCG CCGGTGGCGG GCATCTGCTA CTGCGGCAAC CAGAGCCTGG 1440
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Seq ID NO: C182 DNA Sequence
 Nucleic Acid Accession #: XM_050625
 Coding sequence: 222..1109

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 25 GCACCCAGCG AAGAGAGCGG GCGCGGGACA AGCTCGAACT CGGCGCCCTT GCGCCCTTCC 180
 CGGCTCGCTT CCCTCTGCCC CCGCGGGTTC GCGCGCCAC GATGCTGCGG GCGCCCTGCT 240
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 30 TGCAGCTGTG TACTTGTAA GAATACCAAG ACATGCGGCT GCCCAACCTG CTGGGCCAGC 420
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 45 TCCTAGCTGC TCAGTCTTCA GCGTGGGCGG CTTCGCCCTG CCTTTGTCAC GTTTGCTATC 1260
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 TT 1382

Seq ID NO: C183 DNA Sequence
 Nucleic Acid Accession #: NM_001306.1
 Coding sequence: 199..861

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 75 ACCACCCCGT CGAGCCCATC CGGGCGGCTG CCGCATGCTC GCGCTGGGCA GGGACCGGCA 1200
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Seq ID NO: C184 DNA Sequence
 Nucleic Acid Accession #: NM_012449.1
 Coding sequence: 66..1085

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 GGAGAAATTT AGAAGAAGAC GATTATTTGC ATAAGGACAC GGGAGAGACC AGCATGCTAA 180

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CTAATATAGC ATCTCTGACT TTTCTTTACA CTCTTCTGAG GGAAGTAATT CACCCITTAG 360
CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCAATCAAC AAAGTCTTGC 420
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AGATTAGACA TGGTTGGGAA GACGTCAACA AAATTAACAA AACTGAGATA TGTTCACAGT 1080
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20
Seq ID NO: C185 DNA Sequence
Nucleic Acid Accession #: NM_001775.1
Coding sequence: 70..972

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CTCTCTCAGG GAGCCCAACT CTGTCTTGGC GTCACTATCC TGGTCTGTAT CCTGCTCGTG 180
GTGCTCGCGG TGGTGTGCCC GAGGTGGCGC CAGACGTGGA GCGGTCCGGG CACCACCAAG 240
CGCTTTCCCG AGACCTGCTT GCGCGATGCG GTCAAGTACA CTGAATTTCA TCCTGAGATG 300
AGACATGTAG ACTGCCAAAG TGTATGGGAT GCTTTCAAGG GTGCATTTAT TTCAAAACAT 360
CCTTGCAACA TTAAGTGAAG AGACTATCAG CCACTAATGA AGTTGGGAAC TCAGACCGTA 420
CCTTGCAACA GATTTCTTCT TTGGAGCAGA ATAAAAGATC TGGCCCATCA GTTCACACAG 480
GTCCAGCGGG ACATGTTTAC CCTGGAGGAC ACCTGCTTAG GCTACCTTGC TGATGACCTC 540
ACATGGTGTG GTGAATTTCA CACTTCCAAA ATAACTATC AATCTTGCCC AGACTGGAGA 600
AAGGACTGCA GCAACAACCC TGTTCAGTA TTCTGGAAAA CGGTTTCCCG CAGGTTTGCA 660
GAAGCTGCCT GTGATGTGGT CCATGTGATG CTCATGGGAT CCCGAGTAA AATCTTTGAC 720
AAAAACAGCA CTTTTGGGAG TGTGGAAGTC CATAATTTGC AACCCAGAGG GGTTCAGACA 780
CTAGAGGCTT GGGTGATACA TGGTGAAGA GAAGATTCCA GAGACTTATG CCAGGATCCC 840
ACCATAAAAG AGCTGGAATC GATTATAAGC AAAAGGAATA TTCAATTTTC CTGCAAGAAT 900
ATCTACAGAC CTGACAAGTT TCTTCAGTGT GTGAAAAATC CTGAGGATTC ATCTTGCAAC 960
TCTGAGATCT GAGCCAGTGC CTGTGTTTGT TTTAGCTCCT TGACTCCTTG TGGTTTATGT 1020
CATCATACAT GACTACGATC ACCTGCTGGT GCAGAGCTGA AGATTTTGA GGGTCTCTCA 1080
CAATAAGGTC AATGCCAGAG ACGGAAGCCT TTTTCCCAA AGTCTTAAA TAACTTATAT 1140
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Seq ID NO: C186 DNA Sequence
Nucleic Acid Accession #: XM_120513.2
Coding sequence: 1..2208

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AGGACCCCAA AGCCCGGTAA ACACCGCGCG ACCACCCGGG CCAAGATCTT CAAGAGGTTT 180
TTTTAGAGAG GATCGGAGAG CAATTCCCGA TTGGTAGAAG AACTTGCTGT AATACACAAG 240
TACTCTGACG ACCCCGCCCC AACGACTAGC CCTCTCTCTG TGCAACCCCG AGAGTTTGGG 300
GTCATGACAG GGGCGCCACG AGCTCGTTTC GGAAGCCGGA CCCCGCCCCG AGCCGACAGG 360
GCCCTGAGTC CATCTCTGGG CATTTGGGAG GCAGCCTGTC AATCAGGAGC TCGGGCGGCA 420
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Seq ID NO: C187 DNA Sequence

Nucleic Acid Accession #: AB037745.1

Coding sequence: 26..1744

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Seq ID NO: C188 DNA Sequence

Nucleic Acid Accession #: NM_014324.1

Coding sequence: 89..1237

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GTCCGGCCTG	GCCCCGGGCC	GTNTCTGTGC	TATGCTCTG	GCTGACTTCG	GGGCGGCTGT	180
GGTACGGCTG	GACCGGCCCG	GCTCCCGCTA	CGAAGTGAGC	CGCTTGGGCC	GGGGCAAGCG	240
CTGCTAGTGT	CTGCACTGA	AGCAGCCGCG	GGAGCCGCGT	GCTGCGGCGT	CTGTGCAAGC	300
GGTGGAGTGT	GCTGCTGGAG	CCCTTCGCC	GGGTGTCTAT	GGAGAACTC	CAGCTGGGCC	360
CAGAGATTCT	GCAGCGGGAA	AATCCAAGGC	TTATTTATGC	CAGGCTGAGT	GGATTGGGCC	420
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CACACGCTAT	GACAGGGGTC	AGGTCAATGA	TGCATATATG	GTGGAAGGAA	CAGCATATTT	660
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Seq ID NO: C189 DNA Sequence

Nucleic Acid Accession #: XM_091332.1

Coding sequence: 1..1401

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Seq ID NO: C190 DNA Sequence
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 Coding sequence: 26..2902

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 Nucleic Acid Accession #: NM_000793.2
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	TAAGCCTTTC	GTGTTTTTCC	ACAGGTGTTT	AAGCTTCTCT	GTACAGTTGA	AATAAACAGA	5580
	CAGCAAAATG	GTAAAAAATA	AAAAAATAA	A			5611

Seq ID NO: C193 DNA Sequence
Nucleic Acid Accession #: NM_018646
Coding sequence: 217..2394

60	1	11	21	31	41	51	
	GCTCTGCCAA	GTGTAACAAA	CTCACAGCCC	TCTCCAAACT	GGCTGGGGCT	GCTGGGAGAC	60
	TCCCAAGGAA	CTGCTCAGGA	AGGCAGGAGA	CAGGAGACGG	GACCTCTACA	GGGAGACGGT	120
	GGGCCGGCCC	TTGGGGGGGC	TGATGTGGCC	CCAAGGCTGA	GTCCCGTCAG	GGTCTGGGCT	180
	CGGCCTCAGC	CCCCCAAGGA	GCCGGCCCTA	CACCCCATGG	GTTTGTCACT	GCCCAAGGAG	240
65	AAAGGGCTAA	TTCTCTGCCCT	ATGGAGCAAG	TTCTGCAGAT	GGTTCCAGAG	ACGGGAGTCC	300
	TGGGCCCAAG	CCGAGATGTA	GCAGAACCTG	CTGCAGCAGA	AGAGGATCTG	GGAGTCTCCT	360
	CTCCTTCTAG	CTGCCAAAGA	TAATGATGTC	CAGGCCCTGA	ACAAGTTGCT	CAAGTATGAG	420
	GATTGCAAGG	TGCACCAGAG	AGGAGCCATG	GGGGAACAG	CGCTACACAT	AGCAGCCCTC	480
	TATGACAACC	TGGAGGCCGC	CATGGTCTG	ATGGAGGCTG	CCCGGAGCTG	GCTCTTTGAG	540
70	CCCATGACAT	CTGAGCTCTA	TGAGGGTCAG	ACTGCACATG	ACATCGCTGT	TGTGAACCCAG	600
	AACATGAACC	TGGTGGGAGC	CCTGCTTGCC	CGCAGGGCCA	GTGCTCTGTC	CAGAGCCACA	660
	GGCACTGGCT	TCCGCGGTAG	TCCCTGCAAC	CTCATCTACT	TTGGGGAGCA	CCCTTTGTCC	720
	TTTGTGCTCT	GTGTGAACAG	TGAGGAGATC	GTGCGGCTGC	TCATTGAGCA	TGGAGCTGAC	780
	ATCCGGGCC	AGGACTCCCT	GGGAAACACA	GTGTTACACA	TCTCTATCCT	CCAGCCCAAC	840
75	AAAACCTTTG	CCTGCCAGAT	GTACAACTG	TTGCTGTCTT	ACGACAGACA	TGGGGACCAC	900
	CTGCAGCCCC	TGGACCTCGT	GCCCAATCAC	CAGGGTCTCA	CCCTTTTCAA	GCTGGCTGGA	960
	GTGGAGGGTA	ACACTGTGAT	GTTTCAGCAC	CTGATGCAGA	AGCGGAAGCA	CACCCAGTGG	1020
	ACGTATGGAC	CACCTGACCT	GACTCTCTAT	GACCTCACAG	AGATCGACTC	CTCAGGGGAT	1080
80	GAGCATCTCC	TGCTGGAAC	TATCATCAAC	ACCAAGAAGC	GGGAGGCTCG	CCAGATCCTG	1140
	GACCAGAAGC	CGGTGAAGGA	GCTGGTGAGC	CTCAAGTGGG	AGCGGTACGG	GCGGCCGTAC	1200
	TTCTGTCATG	TGGGTGCCAT	ATATCTGCTG	TACATCATCT	GCTTCACCAT	GTGCTGCATC	1260
	TACCGGCCCC	TCAAGCCGAG	GACCAATAAC	CGCACGAGCC	CCCGGACCAA	CACCCCTTTA	1320
	CAGCAGAAGC	TACTTCAGGA	AGCCTACATG	ACCCCTAAGG	ACGATATCCG	GCTGGTCCGG	1380
	GAGCTGGTGA	CTGTCAITGG	GGCTATCATC	ATCCTGCTGG	TAGAGGTTCC	AGACATCTTC	1440
	AGAATGGGGG	TCACTCGCTT	CTTTGGACAG	ACCAATCTTG	GGGGCCCAT	CCATGCTCTC	1500

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GCCTGTTCCT GCACTCTGGA GCTGTTCTTT ACCATCATCG ATGGCCAGC CAACTACAAC 1860
GTGACCTGTC CCTTTCATGA CAGCATCACC TATGCTGCCT TTGCCATCAT CGCCACACTG 1920
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TTTTGGATC CCTGAAAAA AAAAAA 2918
  
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Seq ID NO: C194 DNA Sequence

Nucleic Acid Accession #: NM_021910.1

Coding sequence: 260..601

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ATTCTCCCG GAACCTCTGC TCAGCCTGGT GAACACACA GGCCGAGTT TCACCCAGTC 180
CCCACTCCAC GGTGCGAGCTG CGGCTTATCT CTCAGCCAG CGAGATGCCA GCCTTCTGT 240
CCCGGGCCAG CGCTCTGACA TGCAAGAGT GACCTGGGC CTGCTTGTGT TCCTGGCAGG 300
CTTCTCTGTC CTGGAAGCCA ATGACCTAGA AGATAAAAC AGTCCTTCT ACTATGACTG 360
GCACAGCCTC CAGGTTGGCG GGTCTCATCTG CGCTGGGTT CTGTGGCCA TGGGCATCAT 420
CATGCTCATG AGTGAAGTGA GGAGCTCGGG GGAGCAGGCG GGCCGGGGCT GGGGCTCCCC 480
TCCCTCGACC GGTCTGAGCT CTCCCAACAG TGCAAAATGC AAATGCAAGT TTGGCCAGAA 540
GTCCGGTCA CATTCCAGGG AGACTCCACC TCTCATCACC CCGGCTCAG CCCAAAGCTG 600
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GGCAGGGCTC CATCTACCT CTCGCAAGAG GGTCTCTTTG TTCAATTTT TTAACTCTAA 780
AATGATTGAG CTTCTGCCCC AGCAGCCTGG AGACTTCTTA TGTGTGCAAT GGGGTGGGGC 840
TTGGGGCTAG ATGAGAAGGT TGGGCTGCCC TGGAGGCTGA CACAGAGGCT GGCACTGAGC 900
CTGCTTGTG GGAAGAGGCC ACAGGCTGT TCCCTTGTGG CTGGGACAT GGCAAGGCC 960
CGCCCTCTGC CTCTCAGCC ATGGGACCTC ATATGCAATT TGGGATTTAC TAGTAGCCAA 1020
AAGGAATGAA AGAGAGCTCT AACAGATGG AACACTGGAA CATTCCAGTG GACCTTGGAC 1080
CATTCCAGCA AACTTGGGAC ATAGGATGCT CCGCTATGA TGGAAAGTGT CAGACAGTTT 1140
ATAATAGTAA GCCCTGTGA CCTCTCACT TACCCGAGA CCTCACTTA TTACAAGATC 1200
TTTCCAAATA CCCAATATC CTTGCAAGCC CGTTAAATAA TTCCCTATGC TACCCCTAAT 1260
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CTCAAAACAC CCAAAATAT CTCTCCAAT GTCTGAGAC ATGAACCCAA AAAGAGACCC 1440
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Seq ID NO: C195 DNA Sequence

Nucleic Acid Accession #: NM_005971.2

Coding sequence: 176..439

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ATTCTCCCG GAACCTCTGC TCAGCCTGGT GAACACACA GGCCGAGTT TCACCCAGTC 180
GAAGGTGACC CTGGGCTGCG TTGTGTTCTT GGCAGGCTTT CCGTCTCTG ACGCCAATGA 240
CCTAGAAGAT AAAAACATG CTTTCTACTA TGACTGGCAC AGCCTCCAGG TTGGCGGGCT 300
CATCTGCGCT GGGGTTCTGT GCGCCATGGG CATCATCATC GTCATGAGTG CAAAATGCAA 360
ATGCAAGTTT GGCAGAAAGT CCGGTCAACA TCCAGGGGAG ACTCCACCTC TCATCACCCC 420
AGGCTCAGCC CAAAGCTGAT GAGGACAGAC CAGCTGAAAT TGGGTGGAGG ACGTCTCTCT 480
GTCCCAAGGT CTTGTCTCTG CACAGAAAT TGAATCCAG GATGGAATTC TTCTCTCTCT 540
GCTTGGGATC CTTTGCATGG CAGGGGCTCA TCTCACTCT CGCAAGAGGG TCTCTTGTGT 600
CAATTTTTTT TAATCTAAAA TGATTGTGCC TCTGCCAAG CAGCTGGAG ACTTCTATG 660
TGTGATCTGG GGTGGGCTTT GGGGCACCAT GAGAAGTTG GCGTGCCTTG GAGGCTGACA 720
CAGAGGCTGG CATTAGGCTC GTTGTGTTGG AAAAGCCAC AGGCTGTGTC CCTTGTGGCT 780
TGGGACATGG CACAGGCCCG CCCTCTGCT CCTCAGGCT GGGACCTCAT ATGCAATTTG 840
GGATTTACTA GTAGCCAAAA GGAATGAAAG AGAGCTCTAA CCAGATGGA CACTGGAACA 900
TTCCAGTGA CCTGGAACA TTCCAGGAAA ACTGGGACAT AGGATGCTCC CGCTATGATG 960
GAAGTGTCA GACAGTTTAT AATAGTAAGC CCTGTGACC CTCTCACTTA CCCGAGAGCC 1020
TCACTTTATT ACAGATCTTT TCCAAATACC CAAATATCCC TGCAAGCCCG TTAATAAATT 1080
CCCTATGCTA CCCTTAATAA CATAAATGA CCACATAGTG TGAGAACTTC CAACAAGCCT 1140
CAAGTCCCT TGAGACTCCC CAATACCTAA TAAGGCATGC GAAATGTTCT CATGAACCTA 1200
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1304

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5 CCAAGTTGGAT TTTACAGGAG TGAGCAACAA AACTGAAATA ATCACAACCC CAGTTGGTGA 1020
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 25 CTGGCATTAT CCCTTTAGGA AGAGGGGGGG GCAGCAAGAG AGCCTATTG GGACAGCATT 2400
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 30 CCAGGGCACA CTGTGGGAGT TCTATCACTT GCTTGACCCC TGGACCCATA AACCACTCCA 2760
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 35 GTACAGATT TCTGTGGGAC TGTGGATCTC ACTGGAAGCT ATCCAAGAGC CCACTGTAC 3000
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 CCTGAGGTGC TCAGACTGCC CCAAGATCA AATCTCTCT GCGTGTAGTA ACCCAGTGA 3180
 ATGAATTTGG ACATGCCCA ATGCTTCTAT ATGCTAAGTG AAATCTGTGT CTGTAATTTG 3240
 40 TTGGGGGTGG GATAGGGTGG GGTCTCCATC TACTTTTTGT CACCATCATC TGAATGGGG 3300
 AAATATGTAA ATAAATATAT CAGCAAGG 3329

Seq ID NO: C198 DNA Sequence
 Nucleic Acid Accession #: NM_021987.1
 Coding sequence: 572..1657

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 TCAGACTGAA TCAAGAAGT AAGCCTCTTC CGGTGATGTT GTCTATGGCC CCCAGCCCCA 360
 55 GCCTCTGGA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG 420
 CAGAGTTGGC AAACCTCCAG AAGCCTCTCG CATCCTGAAC ACTATCCTGA GTAATTATGA 480
 CCACAACTG CGCCCTGGCA TTGGAGAGAA GCCCACTGTG GTCACTGTTG AGATCTCCGT 540
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 60 CCGCATCTAC AAGGATGGCA AGGTGTTGTA CACAATTAGG ATGACCATG ATGCCGATG 720
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 AATAATCACA ACCCCAGTTG GTGACTTCAT GGTCAATGAG ATTTTCTTCA ATGTGAGCAG 960
 65 GGGTTTGGC TATGTTGCC TTCAAACTA TGTCCCTTCT TCGTGACCA CGATGCTCTC 1020
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 CTCTGTTCTG ACCATGACCA GTTGGGCAC CTTTCTCTGT AAGAAATTCC CGGTGTCTC 1140
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20 Seq ID NO: C199 DNA Sequence
Nucleic Acid Accession #: NM_021990.1
Coding sequence: 1309..2490

1325

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TTCTCTTCTG TCACCTCTGC TGGCACACCA GTGGCAAGGC CCAGAAATGGC GACCTCTCTT 3840
TAGCTCAATT TCTGGGCGCT AGGTGCTCAG ACTGCCCCCA AGATCAAATC TCTCTGGGCT 3900
GTAGTAACCC AGTGAATGA ATTGACAT GCCCAATGC TTCTATATGC TAAGTGAAAT 3960
CTGTGTCTGT AATTTGTTGG GGGGTGGATA GGGTGGGCTC TCCATCTACT TTTTGTCAAC 4020
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Seq ID NO: C200 DNA Sequence
Nucleic Acid Accession #: NM_021819.1
Coding sequence: 39..1619

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CTCCTCTAGC CAGGTTTGAG TACAAGCTCA GCTTCAAAGG CCCAAGGCTG GCATTGCTCG 180
GGGCTGGAAT ACCCTTCTGG AGCCATCATG GAGACGCCAT CCTGGGCTG GAGGAAGTGC 240
GGCTGACGCC ATCCATGAGG AACCGGAGTG GCGCGGTGTG GAGCAGGGCC TCTGTCCCT 300
TCTCTGCCCT GGAAGTAGAG GTGCAATGA GGGTGAAGGC ACTGGGGCGC CGGGGAGCCC 360
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GAGCAGGGAT CACCTACTGG GGGCAGAGGC TGGCATGTTC CTGAAACAGT GGCCTCACTC 660
CCAGTGTACC AGGTGAGTTC TGTGTGGATG TGGGGCCCTT GCTTTTGGTC CTGGAGGTT 720
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A 1801
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Seq ID NO: C201 DNA Sequence
Nucleic Acid Accession #: XM_117036.1
Coding sequence: 25..495

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GGCCCGTGGG GGCTGTTCCG ACCACACAGG TGCCCGAGGG AGGCAGGGCA GGCCCGGGT 240
GGACCCAGCC CGAAAACGCA GGTGTGCGCC CAGTTTGCA GCGCGCTCG CGTGTGGGT 300
GATGAGCGGG AACCGGGGGG CGGCGCTAC GCAATGCAAG TTACGCGCGT GTGGAAGGGG 360
TGTCACCGCC ACAGCGGCGC CACCGTGGCT GGCTCTGTTT CTTGAAACG TCCAGAACAG 420
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TGCGGATGGG GCTGAGGTTT TTCTGAAGG ATGAATGCTC TGAAGCTGTG AATAGACACA 540
CGGAACCTGT CAGCTTCACT GGTGAACCGT GTGGGGAGTG AATCCATCTC AACAGAGCTG 600
TTACACAGTG AACAGAGCA CGANGGGTGG AGGCCNCTTG TCTGCTCTG CAGATCGAGC 660
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Seq ID NO: C202 DNA Sequence
Nucleic Acid Accession #: XM_167803.2
Coding sequence: 1162..1488

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GTGCGCCCACT ATGTCATCTT CCTCTTTGGC GGGCTGGGGA GCGGCCCCCA GCGGGGACGG 180
GAGGCGAGCG ACCCGAGGCG CTGCTGGAGC TGGGAGAGAG TGTGGTGGGA AGTCTTGAGC 240
GGAGGAGGGG ATCTGCCCTT CTCCACTCTT CTCTTGGATC CGCCTCGGTT TCCTGTCCCC 300
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Seq ID NO: C203 DNA Sequence
Nucleic Acid Accession #: NM_024780.1
Coding sequence: 31..1023

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Seq ID NO: C204 Protein Sequence
Protein Accession #: Eos sequence

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Seq ID NO: C205 DNA Sequence
Nucleic Acid Accession #: NM_002250.1
Coding sequence: 397..1680

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Nucleic Acid Accession #: NM_025257.1
Coding sequence: 1..2139

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Seq ID NO: C207 DNA Sequence
 Nucleic Acid Accession #: NM_016180.1
 Coding sequence: 26..1618

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Seq ID NO: C208 DNA Sequence
 Nucleic Acid Accession #: NM_003273.1
 Coding sequence: 255..2024

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GGGACATGGC CTGGGTGCCC TTCACCTACA GCCTGCAGGC CCAAGTTCCTG CTGCACCAAC 1500
CGCAGCCCTT GGGGTGTGCC ATGGCTCTGT TCATCTGCCT CATCAATGCT ACTGGTTACT 1560
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GGTGGGTATG GGTCCGCCAT CCCAACTATC TTGGAGACCT CATCATGCTT CTGGCTTGGT 1740
CCTTGGCCCTG CCGGGGTGTC CACCTGCTGC CCTACTCTTA CCTCTCTAC TTCACCGCGC 1800
TGCTGTGTGA CCGTGAGGCC CGGGATGAGC GGAGTGCCTG CAGAAGTACG GCCTGGGCTG 1860
GCAGGAGTAC TGCCGCGCTG TGCCCTTACC CATCATGCCC TACATCTACT GAAGCGGCTC 1920
CACCACCCCA GGTGGGCGAT GTGCCCACTC ATCCACCAGC ACACCCAGGA CCAGGAGCCT 1980
CGACACACTT GGGACTCAAG GGCCTGCACC CCACCCAGGC CTGAGGATGA ACAACCTCAG 2040
AGAAGAGGTT GTTTAGAGCA AGGAAAAAAA TGAAACCACT GACCAAAAAA AAAAAAAA 2100

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Seq ID NO: C209 DNA Sequence
Nucleic Acid Accession #: NM_015720.1
Coding sequence: 21..1838

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CTGATGAGCG TGGCCAGAGG GGCCTCACTT CCACCTCCCT GCTAGACCTC CTGCTGCCCA 180
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CACCACAGTA CTTCTGGGAA GAGGAGGAAG AGCTGAATGA CTCAGTCTG GACCTGGGAC 360
CCACTGCAGA TTATGTTTTT CCGTACTTAA CTGAGAAGGC AGGTTCCATT GAAGACACTA 420
GCCAGGCTCA AGAGCTGGCA AACCTCCCTT CTCCCTTGCC CAAGATGAAT CTGGTTGAGC 480
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CCCCAGGGGC CACCAAAAGG AGGCATGAAG ACTCCGGGGA CCAGGCCCTA TCAGGTGTGG 720
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ATTCTACGCA GGTGATCTGC AAGGACTGGA GCAATCTGGC TGGGAAAAAC TACATCATTC 1200
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CTTCTGTGCG CCGGGGACTC AATTAAACCC GCGCGGAGAC CACGCGGGCC CAGCGAAAAA 2160
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Seq ID NO: C210 DNA Sequence
Nucleic Acid Accession #: NM_001197.3
Coding sequence: 61..543

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5 CTCTGGAAC CCCGACCAT GGAGGTTCTT GGCATGACTG ACTCTGAAGA GGACCTGGAC 180
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 TTCCAGTTTT CGTTTTTTCT AAAAGATGAA TTCTATGGC TCTGCAATTG TCACCGGTTA 780
 ACTGTGGCCT GTGCCAGGA AGAGCCATTG ACTCTGCCC CTGCCACAC GGCAGGTAGC 840
 AGGGGGAGTG CTGCTCACAC CCTGTGTGA TATGTATGC CCTCGGCAA GAATCTACTG 900
 15 GAATAGATTG CGAGGAGCAG GAGTGCTCAA TAAATGTTG GTTTCAGCA AAAAAAAAAA 960
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Seq ID NO: C211 DNA Sequence
 Nucleic Acid Accession #: AF272357
 Coding sequence: 83..1060

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 25 GCGGCTGCTG CCGCTGCTGC TCTCCGGCCT CGTCTCGGCG GCGGCTGCTG GTGGAGCGCG 180
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 30 CAGACTGGAA GGTGTTTCT ACTTCTGGC CCAGGAGCTT GCGCGGAAGG AGTCTGGACA 420
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 CTCGGCACCG GGGCAGGGGC TGGAGCTGGG CCTCCCTTCC ACTCCAGGAA CCCCCACGCC 540
 CACGCCCCAC ACCTCCCTGG GCTCCCTGTG GTCATCCGAC CCGGTGCACA TGTGCGCCCT 600
 GGAGCCCGCG GGAGGGCAAG GCGACGGCCT CGCCCTGTGT CTGATCCTGG CGTCTGTGTG 660
 GCGCGGTGCA GCGGCGCTCT CGGTAGCCTC CTTCTGCTGG TGCAGGCTGC AGCGTGAGAT 720
 35 CCGCCTGACT CAGAAGGCGC ACTACGCCAC TCGGAAGGCC CCTGGCTCAC CTGCAGCTCC 780
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 CCAACCGCAA ACCTGCTGTG GCCTGGAGCG GCATAAAGAG CCACCAAGG AGCTGGACAC 900
 GGCTCTCTCG GATGAGGAGA ATGAGGACGG AGACTTCAGG GTGTACAGAT GCGCGGCGCT 960
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 40 GCGCCTGCGG GCGCCAGCT CACCGCTGCG ACTGCCATGA CCTGGAGGCA GACAGACGCC 1080
 CACCTGTCTC CCGACCTCGA GCGCCCGGGG GAGGGGCGAG GCGTGGAGCT TCCCACTAAA 1140
 AACATGTTTT GATGCTGTGT GCTTTTGGCT GGGCCTCGGG CTCACGGCCC TGGGAGCCCT 1200
 TGCCAGGGAG ACCCCCGAAC CTTTGTGCCA GGACACCTCC TGGTCCCTCG CACCTCTCCT 1260
 45 GTTCGGTTTA GACCCCGAAA CTGGAGGGGG CATGGAGAAC CGTAGAGCGC AGGAACGGGT 1320
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Seq ID NO: C212 DNA Sequence
 Nucleic Acid Accession #: NM_004445.1
 Coding sequence: 799..3819

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 55 GACCCGGGAC CCAGCTTGGC GACGGCGATT CTCGAGCGGG GCGCCACGGA TTCTCCCGGC 120
 GCGCCACCTC TGGAGCAGCC CCGCGCGCCA GCGTCAGGTC CACCCCGGAA TCCAGGGGAC 180
 TCTCGGCGCC GAACGAGACC GGGCGGGTGC AACGGGGTCC CCGGACTGGA GAAGAGCGGG 240
 GTGGCACCGT GCGAGCTCCA GGAGCCCGGG GTCCACTGCG AGGCGTCCGG GGGCGCAGAC 300
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 60 CTTCTGAGAC TCAGACAGA GGAGAGATAG AGAACCGCCA ATCTCTAGAT CAACAAGCAA 420
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 CCCTCTTCTT TGTGTGTGCC TCGAATGGCA GAAAAAGGGG TGGCTGTGAG AGGAAGGGAG 600
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 65 CTTAGCTGTA CACCTGAGT CTTGCAAAAG CTGCAGCCCC ACCCAGGAGC AGGGTGTGTG 720
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 GGGAAACAGG TGGCGGGCAT GGTGTGTAGC CTATGGGTGC TGCTCCTGGT GTCTTCAGTT 840
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 ACCTACCCAC CAGGGGGGTG GGACGAGGTG AGTGTCTGCG ACGACAGCG AGCGCTGACT 960
 70 CCGACCTTGG AGGCAATGTA TGTGGCAGGG GCGCCTCCAG GCACCGGGCA GGCACATTTG 1020
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 75 TCCTCTCTCT CTCTTCTCTC TGCAGCGTGG GCTGTGGGAC CCCACGGGGC TGGGCGAGCG 1320
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 GCTGGGGGGG CCTCCCTGGT GGCAGCTGTG GGCACCTGTG TGGCTCATGC AGAGCCAGAG 1560
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 GGAGACAAGG CTGCCCCAGC CTGCCCCAGG GGGCTCTATA AGTCTTCTGC TGGGAATGCT 1740
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 TGCTGGAGGG GCTTCTACCG GGCAGTTTCC GACCCACAGG AGGCCCCCTG CACTGGTCTC 1860
 CCACTCGGCTC CCCAGGAGCT TTGTTTGGAG GTGCAAGGCT CAGCACTCAT GCTACACTGG 1920

5	CGCCTGCCTC	GGGAGCTGGG	GGGTGAGGG	GACCTGCTCT	TCAATGTCGT	GTGCAAGGAG	1980
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	GAGGTCCACT	TCGACCCCTG	CCAGAGAGGC	CTGACTGAGA	GCCGAGTGT	AGTGGGGGA	2100
	CTCCGGGCAC	ACGTACCCCTA	CATCTTAGAG	GTGCAGGCTG	TTAATGGGGT	GTCTGAGCTC	2160
	AGCCCTGACC	CTCCTCAGGC	TGCAGCCATC	AATGTGAGCA	CCAGCCATGA	AGTGCCTCT	2220
	GCTGTCCCTG	TGGTGACCA	GGTGAGCCGG	GCATCCAACA	GCATCACGGT	GTCCTGGCCG	2280
	CAGCCCGACC	AGACCAATGG	GAACATCCTG	GACTATCAGC	TCCGCTACTA	TGACCAGGCA	2340
	GAAGACGAAT	CCCACTCCTT	CACCTTGACC	AGCGAGACCA	ACACTGCCAC	CGTGACACAG	2400
10	CTGAGCCCTG	GCCACATCTA	TGGTTTCCAG	GTGCGGGCCC	GGACTGCTGC	CGGCCACGGC	2460
	CCCTACGGGG	GCAAGATCTA	TTTCCAGACA	CTTCTCAAG	GGGAGCTGTC	TTCCAGCTT	2520
	CCGGAAGGAC	TCTCCTTGGT	GATCGGCTCC	ATCCTGGGGG	CTTTGGCCTT	CCTCCTGCTG	2580
	GCAGCCATCA	CCGTGCTGGC	GGTCTGTCTC	CAGCGGAAGC	GGCGTGGGAC	TGGCTACACG	2640
	GAGCAGCTGC	AGCAATACAG	CAGCCAGGGA	CTCGGGGTGA	AGTATTACAT	CGACCCCTCC	2700
15	ACCTACGAGG	ACCCCTGTCA	GGCCATCCGA	GAACCTGCCC	GGGAAGTCGA	TCCTGCTTAT	2760
	ATCAAGATTG	AGGAGTTCAT	TGGGACAGGC	TCTTTTGAG	AAGTGCGCCA	GGGCCGCTG	2820
	CAGCCACGGG	GACGAGAGGA	GCAGACTGTG	GCCATCCAGG	CCCTGTGGGC	CGGGGGCGCC	2880
	GAAAGCCTGC	AGATGACCTT	CCTGGGCGGG	GCCGAGTGC	TGGGTCAAGT	CCAGCACCCC	2940
	AACATCCTGC	GGCTGAGGGG	CGTGGTCACC	AAGAGCCGAC	CCCTCATGTT	GCTGACGGAG	3000
20	TTCATGGAGT	TGGCCCCCTC	GGACAGCTTC	CTCAGGCAGC	GGGAGGGCCA	GTTGAGCAGC	3060
	CTGCAGCTGG	TGGCATGCA	GCGGGGAGTG	GCTGCTGCCA	TGCAGTACCT	GTCCAGCTTT	3120
	GCCTTCGTCC	ATCGCTCGCT	GTCTGCCAC	AGCGTGTCTG	TGAATAGCCA	CTTGGTGTGC	3180
	AAGGTGGCCC	GTCTTGGCCA	CAGTCTCTAG	GGCCCAAGTT	GTTTGCTTCG	CTGGGCAGCC	3240
	CCAGAGGTCA	TTGCATGCG	AAGGCATACA	ACATCCAGTG	ATGTCTGGAG	CTTTGGGATA	3300
25	CTCATGTGGG	AACCTGATGAG	TTATGGAGAA	CGGCCTTACT	GGGACATGAG	TGAGCAGGAG	3360
	GTAATAATG	CAATAGAGCA	GGAGTTCGGG	CTGCCCCCGC	CTCCAGGCTG	TCCTCCTGGA	3420
	TTACATCTAC	TTATGTGGA	CACCTGGCAG	AAGGACCGTG	CCCGGGGGCC	TCATTTTGAC	3480
	CAGCTGGTGG	CTGCATTGGA	CAAGATGATC	CGCAAGCCAG	ATACCCCTGCA	GGCTGGGGGG	3540
	GACCCAGGGG	AAGGGCCTTC	CCAGGCCCTT	CTGACCCCTG	TGGCCCTGGA	CTTTCCTTGT	3600
30	CTGGACTCAC	CCAGGCCCTG	GCTTTCAGCC	ATTGGACTGG	AGTGTACCCA	GGACAACTTC	3660
	TCCAAGTTTG	GCCTCTGTAC	CTTCAGTGAT	GTGGCTCAGC	TCAGCCTAGA	AGACCTGCCT	3720
	GCCTGGGCA	TCACCTTGGC	TGGCCACAG	AAGAAGCTGC	TGCACCAT	CCAGCTCCTT	3780
	CAGAACACG	TGAGGCAGCA	GGGCTCAGTG	GAGGTCTGAG	AATGACGATA	CCCGTGACTC	3840
	AGCCCTGGAC	ACTGTCGGA	GAAGGGACAT	GTGGGAGCTG	AGCCGGGCTC	CAACAGCCTC	3900
35	TGTGAGAGAT	GCCCCACACC	AAACCCAAACC	CTCCGATGG	CTGCATTCCC	TGGTCTCCG	3960
	CCTCTCCACC	AGCCCCCTCC	TCATTAAAGG	GAAAGAAGGG	AATTTCGAAA		4010

Seq ID NO: C213 DNA Sequence
Nucleic Acid Accession #: XM_043340.4
Coding sequence: 195..1067

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45	GTGGCGAGTG	GCGAGTGTCA	GGGGGGGGGC	CGGCGGGGGC	GGGGCGGGCG	GAGGAGGCGT	120
	TGGCAGCGGG	CTGGAGCCCA	CGCGGCGCGG	CGGCGCGCGT	GGCCTGCAGC	GCTTCCACCC	180
	CGGCGGGCGG	CACGATGCCC	TTTGACTTCA	GGAGGTTTGA	CATCTACAGG	AAGGTGCCCA	240
	AGGACCTTAC	GACGCCAAAG	TACACGGGGG	CCATTATCTC	CATCTGCTGC	TGCTCTTCTA	300
	TCCTCTTCTT	CTTCTCTCTG	GAGCTCACCG	GATTTATAAC	GACAGAAGTT	GTGAACGAGC	360
50	TCTATGTCTG	TGACCCAGAC	AAGGACAGCG	GTGGCAAGAT	CGACGTCAGT	CTGAACATCA	420
	GTTTACCCTA	TCTGCACTGC	GAGTTGGTTG	GGCTTGACAT	TCAGGATGAG	ATGGGCAGGC	480
	ACGAAGTGGG	CCACATCGAC	AACTCCATGA	AGATCCCGCT	GAACAAATGG	GCAGGCTGCC	540
	GCTTCGAGGG	GCACTTCCAG	ATCAACAAGG	TCCCGGGCAA	CTTCCAAGTG	TCCACACACA	600
	GTGCCACAGC	CCAGCCACAG	AACCCAGACA	TGACGCATGT	CATCCACAAG	CTCTCTTTTG	660
55	GGGACACGCT	ACAGGTCAG	AACTCCACG	GAGCTTTCAA	TGCTCTCTGG	GGAGCAGACA	720
	GACTCACCTG	CGACGCTCAG	GCTTCCACG	ACTACATCCT	GAAGATTGTG	CCACGCTTTT	780
	ATGAGGACAA	GAGTGGCAAG	CAGCGGTACT	CCTACCACTA	CACGGTGCCG	AACAAAGGAA	840
	ACGTGCGCTA	CAGCCACACG	GGCCGATCA	TCCCTGCAAT	CTGGTTCCGC	TACGACCTCA	900
	GCCCCATCAC	GGTCAAGTAC	ACAGAGAGAC	GGCAGCGGCT	GTACAGATTG	ATCACCACGA	960
60	TCTGTGCCAT	CATTGGGGGG	ACCTTCCACG	TGCGCGGCAT	CCTGGACTCA	TGCATCTTCA	1020
	CAGCCTCTGA	GGCCTGGAAG	AAGATCCAGC	TGGGCAAGAT	GCATTGACGC	CACACCCAGC	1080
	CTAATGGCCG	AGGACCCCTG	GCATGCCAG	CCTTGCTCCG	AGTGCCCTGT	CTCCTTTGGC	1140
	CCTCAATCTG	GTCCCAATC	TGGCTGTGTC	CCAAAGGGTG	TGTGGGAAGT	GGGGGGAAAG	1200
	TAGAGGATGG	CTGATGTGTT	TGCAGTACC	TCTTTTCCCG	GTGTTTCTTT	TTAGACAAAT	1260
65	TACACTGCCT	GAAATTGCTG	TTCCCTTTTC	CCTGGGGAGC	CCCAAGAAC	GAGTCAGGCA	1320
	AGGGGTGGGG	AGTCCAGGGG	AACATCCAG	AATGCATATC	GATCAGCTCT	CAGCCAGGCT	1380
	TGACCAATCT	CGCAGCCCCC	ACTAGGTGGA	CACATTAATG	ATTGGTTCCT	TCCCTGGGCG	1440
	AGCCAACTGT	CCCCAGAGGC	ACCAGACCTG	GGCTTTTCAG	TTTGGGACCA	GGCTGCCCAA	1500
	AGGTACTCCT	TTATACACCC	GGCACCTTCC	AOGAAAGATG	GTACTTCCCA	AGCAAGCCCC	1560
70	TATGATTGTT	CACATAGAT	GGAATGTGTT	GGCATGCACA	TGAGTTGAAA	TTCTTTTATG	1620
	CATTTTTCTG	AAGAAAAAAA	AAAAAACAA	TCTGAGGACA	TAGGGGATGT	CAGTTTCTTA	1680
	TGGAAGAGAC	ACCTCTGACC	CGTTATTTCT	ATAATCAAAA	TCTGAAGGGA	AAAAAATGTT	1740
	TTAGTTCTTT	CCCCACTCGT	TGGGTTCAAC	TAGATTAAAA	GGCTGATTTT	CAG	1793

Seq ID NO: C214 DNA Sequence
Nucleic Acid Accession #: NM_002151.1
Coding sequence: 246..1499

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	TGCCACGGCC	TGAGACTGGA	CCCGACCCCG	GCATACCTTC	GAGGCTCCGC	CCCCACCTGC	180
	TGGACCCACG	GGTCCACACC	TGGCCACGGA	GGTCAGCCAG	GGAATCATTA	ACAAGAGGCA	240
	GTGACATGGC	GCAGAAGGAG	GGTGGCCGGA	CTGTGCCATG	CTGCTCCAGA	CCCAAGGTGG	300

5	CAGCTCTC	AC	TGCGGG	BACC	CTGCTACT	TC	TGACAG	CCAT	CGGGG	CGGCA	TCCTGG	GCCA	360
	TTGTGG	CTGT	TCTCCT	CAGG	AGTGACC	AGG	AGCCG	CTGT	CCAGT	GCAG	GTGAG	CTCTG	420
	CGGACG	CTCG	GCTCAT	GGTC	TTTGACA	AGA	CGGAAG	GGGAC	GTGGG	GGCTG	CTGTG	CTCT	480
	CGCGCT	CCAA	CGCCAG	GGTA	GCGGACT	CA	GCTGCG	AGGA	GATGG	GGCTT	CTCAG	GGCAC	540
	TGACCC	ACTC	CGAGCT	GGAC	GTGCGA	ACGG	CGGGG	CGCAA	TGGCAC	GGTCG	GGCTT	CTTCT	600
	GTGTGG	ACGA	GGGAGG	CTG	CCCCAC	CCCC	AGAGG	CTGCT	GGAGG	TCATC	TCGGT	GTGTG	660
	ATTGCC	CCAG	AGGCG	TTTC	TTGGCC	GCCA	TCGCGA	AGA	CTGTG	GGCCG	AGGAAG	CTGTC	720
	CCGTGG	ACCG	CATCGT	GGGA	GGCCGG	GACA	CCAGCT	GGG	CGGCT	GGCCG	TGGCA	AGTCA	780
	GCCTTG	CTA	TGATGG	AGCA	CACCTC	CTGTG	GGGGAT	CCCT	GCTCT	CCGGG	GACTGG	GGTGC	840
10	TGACAG	CCCG	CCACTG	CTTC	COGGAG	CGGA	AOCGG	GTCT	GTCCG	ATGG	CGAGT	GTGTTG	900
	CGGTG	CTCT	CGCCAG	GGCC	TCTCCCC	ACG	GTCTG	CAGCT	GGGGG	TGCAG	GCTGT	GGTCT	960
	ACCA	CGGGG	CTATCT	TTCC	TTTGGG	AGCC	CCAAC	AGCGA	GGAGAA	CAGC	AACGAT	ATTG	1020
	CCCTGG	TCCA	CCTCTC	CAGT	CCCTTG	CCCC	TCACAGA	ATA	CATCC	AGCCT	GTGTG	CCCTC	1080
15	CAGCTG	CCCG	CCAGG	CCCTG	GTGGAT	GGCA	AGATCT	GTIAC	CGTGAC	GGG	TGGGG	CAACA	1140
	CGCAGT	ACTA	TGGCCA	ACAG	GCCGGG	TAC	TCCAGG	AGGC	TCGAGT	CCCC	ATAAT	CAGCA	1200
	ATGATG	CTCT	CAATG	GGCT	GACTTCT	ATG	GAACCA	GAT	CAAGCC	CAAG	ATGTT	CTGTG	1260
	CTGGTA	CCCC	CGAGGG	TGGC	ATTGAT	GCCT	GCCAGG	CGA	CAGCGG	TGGT	CCCTT	TGTGT	1320
	GTGAGG	ACAG	CATCTC	TCGG	ACGCCA	CGTT	GGCGG	CTGTG	TGGCAT	TGTG	AGTTG	GGGGT	1380
20	CTGGCT	GTGC	CTGGCC	CCAG	AAGCC	AGGCG	TCTACA	CCAA	AGTCAG	TGAC	TTCCG	GGAGT	1440
	GGATCT	TCCA	GGCCAT	AAAG	ACTCACT	CCG	AAGCC	AGCGG	CATGTG	TACC	CAGCT	CTGAC	1500
	CGGTGG	CTTC	TCGCTG	CGCA	GCCTCC	AGGG	CCGAGG	TGA	TCCCGG	TGGT	GGGAT	CCACG	1560
	CTGGGG	CGAG	GATGGG	AGT	TTTTCT	TCTT	GGGCC	CGGTC	CACAGG	TCCA	AGGAC	ACCCT	1620
	CCCTCC	AGGG	TCCTCT	CTTC	CACAGT	GGCG	GGCCCA	CTCA	GGCCG	AGAGC	CACCC	AACCT	1680
25	CACCTC	CTGT	ACCCCA	TGT	AAATAT	TGTT	CTGCTG	CTG	GGACTC	CTGT	CTAGG	TGCC	1740
	CTGATG	ATGG	GATGCT	CTTT	AAATAA	TAAA	GATGGT	TTTG	ATT				1783

Seq ID NO: C215 DNA Sequence

Nucleic Acid Accession #: AB037745.1

Coding sequence: 26..1744

30	1	11	21	31	41	51	
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	GTACAGAGGGC	ATGACAGGCT	GGGAGGTGGC	TGGTGATCAC	ATTACACAG	CTGCTGGAGC	120
35	CTCAGACAAT	GACTTTCATGA	TTCTCACTCT	GGTTGTGCCA	GGATTAGAC	CTCCGACATC	180
	GGTGATGGCA	GACACAGAGA	ATAAAGAGGT	GGCCAGAATC	ACATTTGTCT	TTGAGACCTT	240
	CTGTTCTGTG	AACTGTGAGC	TCTACTATCT	GGTGGGTGTG	AATTTCTAGA	CCAACACTCC	300
	TGTGGGAGCG	TGGAAGAGTT	CCAAAGGCCA	ACAGTCCCTAT	ACCTACATCA	TTGAGGAGAA	360
	CAC	TACACG	AGCTTCACT	GGGCTTCCA	GAGGACCACT	TTTCATGAGG	420
40	GTACACCAAT	GAOGTTGCCA	AGATCTACTC	CATCAATGTC	ACCAATGTTA	TGAATGGGGT	480
	GGCCTCTCTAC	TGGCTGCTCCT	GTGCCCTAGA	AGCCTCTGAT	GTGGGCTCCT	CCTGCACCTC	540
	TTGTCCTGTG	GGTACTATA	TTGACCGAGA	TTACAGGAAC	TGCCACTCCT	GGCCCCCTAA	600
	CACAA	AGCCCAAC	AGCCTTATGG	TGTCCAGGCC	TGTGTGCCCT	GTGGTCCAGG	660
	GACCAAGAAG	AACAAGATCC	ACTCTCTGTG	CTACAATGAT	TGCACCTTCT	CACGCAACAC	720
45	TCCAACCAGG	ACTTTCAACT	ACAAC	TCTCTC	CGCTTTGGCA	AACACCGTCA	780
	AGGGCCAGC	TTCACTTCCA	AAGGGTTGAA	ATACTTCCAT	CAC	CTTTACCC	840
	TGGA	AAAC	CGAG	GGTAG	AA		900
	TAGG	GGT	TAG	TCAGG	TTCT		960
50	CCCCCCAGAG	GTGACAGCT	ACAAGGCCGG	GGTTTCTCA	CAGCCTGTCA	GCCTTGTCTGA	1020
	TGCACTTATT	GGGGTGACAA	CAGATATGAC	TCTGGATGGA	ATCACCTCCC	CAGCTGAACT	1080
	TTTCCACCTG	GAGTCTCTGG	GAATACCGGA	CGTGATCTTC	TTTTATAGTT	CCAATGATGT	1140
	GACCCAGTCC	TGCAGTCTCG	GGAGATCAAC	CACCATCCGC	GTCAAGTGA	GTCCAACAGT	1200
	AAC	TGCTCCT	GGAG	AGTTTGC	TGCTG	CCAGG	1260
	CAACTTCCAC	TTCTGTGGG	AGAGCGCGCG	TAAGTGCOCG	CTCTGCTCAG	TGGCTGACTA	1320
55	CCATGCTATC	GTACAGAGCT	GTGTGGCTGG	GATCCAGAAG	ACTACTTACG	TGTGGCGAGA	1380
	ACCCAGGCTA	TGCTCTGGTG	GCAATTTCTCT	GCCTGAGCAG	AGAGTCA	CTGCAAAAC	1440
	CATAGATTTT	TGGCTGAAAG	TGGGCATCTC	TGCAGGCACC	TGTACTG	CTCTGCTCAC	1500
	CGTCTTGACC	TGCTACTTTT	GGAAAAGAA	TCAAAAACTA	GAGTACAAGT	ACTCCAAGCT	1560
60	GGTGATGAAT	GCTACTCTCA	AGGACTGTGA	CTGCGCAGCA	GCTGACAGCT	GCGCCATCAT	1620
	GGAAGGGCAG	GATGTAGAGG	ACGACCTCAT	CTTTACCAGC	AAGAAGTCAC	TCTTTGGGAA	1680
	GATCAAAATCA	TTTACCTCCA	AGACGCCAGC	TCCTGTCA	ATCTCTCTT	CAGAGGACATC	1740
	CTGATGTGAT	TGACTCACTG	CGCTGAAGA	CATCCTCAGG	AGGCCAGAC	ATGAGCCTGT	1800
	GAGAGGCATC	GCCTGCTCTA	CTCTGCTCT	CACCTTG	AGCACTTTG	CAGAGCTGOG	1860
65	GCGATTTGGG	TGCCAGATC	CTGCAACACC	CACCTGTGGA	AATCTCTTCA	TTGTGGCCTT	1920
	ATCAGATGTT	TGAATTTTCA	ATCTTTTTTT	ATAGAGTACC	CAAA	CCCTCC	1980
	CCTCAAACT	GCCAAATATA	CCCACTAT	GTTTGTAAAT	TATGCCCTTG	CTTGTATCTT	2040
	GTTTCCCAA	ATGGCCATC	CGCCAGAGCT	ATAGCTTCTG	CTGCTATAA	TCTTATAGT	2100
	TTTGAATGA	AAATATTTCT	ATCTTCTTAA	GTATAGAAAC	TATTTCTCT	GTCTCTAAC	2160
70	TTAAGGCGAG	AAACAGCTGG	GAGTTTCTCT	CGCATGCCCT	CAGCTCATGA	TCTCTTCAGG	2220
	AGAGAGGCTG	GGTGAGGAGG	GTGTGCGGGT	TCCCTGGTGG	ATAATCTTCA	TAGCAGCCTG	2280
	GATCCATTC	CCCTGGATAA	CCAGCTCAAA	GGGAGTGA	ATGGTAGTCT	GAGGGGCAAGG	2340
	GGAGCAGAGC	TGGGTAA	AAAGCCTTGA	AAGCATAAA	AAGAGCGCGG	GCGCGCTGGC	2400
	TCACGCTGT	AATCCCGACA	CTTTGGGAGG	CCGAGGCGGG	CAGATCATGA	GCTGGGAGGA	2460
	TTGAGACCAT	CCTGGCTAAC	ACGGTGAAAGC	CCGCTCTCTA	CTGAAAATAC	AAAAAATTAG	2520
75	CGGGGCGTGG	TGGCGGGTGC	CTGTGTCTCC	AGCTACTCGG	GAGGCTGAGG	CGGGAGAAATA	2580
	GCGTGGGCTG	GGAAGGGGGA	GCTTGCACTG	AGCCGAGATC	GCGCCACTGC	ACTCCATCCA	2640
	GCTGGGTGA	CAGAGTGAGA	CTCTGCCCTA	AAAAA	AAAAA	AAGCA	2700
	AGAGGCAACA	AGGAATGTTT	TGTTT	TGTTGA	GACAGGCTCT	CACCTGTGCA	2760
80	AGTGCACTGG	CGTAATCACT	GTTCAGTGA	GCCTCAAGCT	CTTGGGCTCA	GGCTATCTCT	2820
	CATCTCTCAGC	CTCTCAAGTA	GCTGGGACTA	CGAGTGTGCA	CCACCAAGGCT	CAC	2880
	TGTGTTTTAT	GTAGACACGG	GGTTTCAACC	TGTTGCCAG	GCTGGTCTCC	AAC	2940
	CTCAAGTGTAT	CTGTCCGCT	CGGCTTCCA	AAGCTGTGG	ATTACAGCTCA	TAA	3000
	CAC	TAGCCT	TTTAT	TGTT	TTTAA	ACCA	3060
	ATAGATATTC	TCACTGAA	CAAGGAAATA	AGTTTCAAA	GAAAAATGCC	AAG	3120

5 TGGATACATC CTCCTATCT TTTTAAAA CCTTCCACTA TCACCTATG ACACTGAAAA 3180
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 TTTTAATGGG GCACCTTAGG GGATACAGCC CACAATGGCA TGGGCTGAG GTGGCCGTGA 3420
 TGCTCTGCTC TAAGCTTAAC GCATCTGCTC AGGCACAGAA TAAACGTCTA GGCTGGCCAA 3480
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 10 AATCCCAAGG CAGAATGGTG GCTTGAGCTC AGGAGTTCAA GACCAGCCTG GGCAACACAG 3660
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 15 TACCTAGAAT GGGTAAAAAC AGAGCAAGAC TTTAAATTAC CTCTCTCTT CTCTACTGG 3960
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 CCATGATTG TCCCTGTGCC CTTCTCCAG TGACCAATTG GTGACCAGAT GGTAGATATA 4080
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 20 GGCCATCAAC AGTGTGGTG ACGCCAGGGA GTCCCTTGG TTTAATAAAT CCAGTTTTC 4260
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 GTGCCAACAA AACTTTTTT TGTCTGACTA CATTAAAGAT AAGACTGACT ATATTATAC 5400
 40 AACAGAAATC TTTTATAGA TTTTTCAGC TTTGTGAAT CGAATTTT TTTATCAGG 5460
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Seq ID NO: C216 DNA Sequence

Nucleic Acid Accession #: NM_004864.1

Coding sequence: 26-952

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 GGCCGAGGCG AGCCGCGCAA GTTTCOCGGG ACCCTCAGAG TTGCACTCCG AAGACTCCAG 180
 ATTCCGAGAG TTGCGGAAC GCTACGAGGA CCTGCTAAC AGGCTGCGGG CCAACAGAG 240
 CTGGAAGATC TGAACACCG ACCTGTCTCC GGCCCTGCA GTCCGGATAC TCACGCCAGA 300
 55 AGTGGCGCTG GGATCCGCGC GCAACCTGCA CCTGCTATC TCTCGGGCCG CCTTCCCGA 360
 GGGGCTCCCC GAGGCTCCG GCCTTCACCG GGCTCTGTTT CGGCTGTCTC CGACGGGCTC 420
 AAGGTGTGGG GAGCTGACAC GACCGCTGCG GGTCTGAGCT AGCCTTGCAA GACCCCAAGC 480
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 60 CCGCAGAGCG CGTGGCGCA ACGGGGACGA CTGTCCGCTC GGGCCCGGGC GTTGCTGCCG 660
 TCTGCACACG GTCGGCGGCT CGCTGGAAGA CCTGGGCTGG GCGGATTTGG TGCTGTGGCC 720
 ACGGGAGGTG CAGATGACCA TGTGCATCGG CGGTGCCCC AGCCAGTTCC GGGCGGCAAA 780
 CATGCAAGCG CAGATCAAGA CGAGCCTGCA CGGCTGAAG CCGACACCG AGCCAGCGCC 840
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 65 GTCGCTCCAG ACCTATGATG ACTTGTAGC CAAAGACTGC CACTGCATAT GAGCAGTCT 960
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 GGGCTCAAGG TTCTGAGAT ACOCGATTCC TGCCCAACA GCTGTATTTA TATAAGTCTG 1080
 TTATTTATTA TTAATTTAT GGGGTGAAC TCTTGGGAC TCGGGGGCTG GTCTGATGGA 1140
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 70 AAAA 1204

Seq ID NO: C432 DNA Sequence

Nucleic Acid Accession #: NM_052858.1

Coding sequence: 54..1259

75 1 11 21 31 41 51
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 CCCACCCAGA CCAAGCGCGC ACCCAAGATC GACCGCGGGA CCGACCCGGG GACCCGCGCA 180
 80 GGAAGCGAAG CAGCGACGGG AACCGGCGAA GGGACGGGGA CCGGGAACCG AAGAGAGACC 240
 AGGAGAGGGA CGGGAACCGC GACCGGAACC GGGACCGGGA GAGGAGAGGA GAGAGGGAAA 300
 GAGACCGGGA CGGAGGCCCC CGCGGGGACA CACACAGGGA CGCGGGCCCT CGCGCAGGTG 360
 AACACGAGGT TTGGGAAAA CGCGGCCAAA GCGGAGCGG GAGCGGAGCC CGGGGACTGA 420
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5 CGCAGAGGAA GGGAGACCCC GGGGCGCGCA GACCCGAAAG TGAACCCCTT TOGGAGAGAT 540
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25 Seq ID NO: C434 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 261..2861

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 35 AGAGGGAGCA CACTGCCAGG ATGGGAGCTG TGGGAGGCA GGACTTCTCT TTCAAGSCCA 300
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 40 TCGAACCCTG GCACATCTTG ATTGACAAAG GAGGAGAGCT GCATGCTGGG AGTGCCTCT 600
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 ATGTGCACTT CAAGAAGTCA CTGTCAAGA AATAAAGAAT TGTCTTAAAT GTCATGATTG 4560
 GAGATGTCCT TTGCATTGCT TGGAAAGGGT GTACCTAGAG CCAAGGAAAT TGGCTCTGGT 4620
 TTGGAATAAT TTTGCTGTTA TTATAGTAAA CATACAAAGG ATGTCAAAAA AAAAAAATAA 4680
 25 AAAAAAATAA AAAAAAATAA AA 4702

Seq ID NO: C217 Protein Sequence
Protein Accession #: NP_005805.1

30 1 11 21 31 41 51
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 LLLTHTSERV IWPFSNKNYI HGELYKNRVS ISNNAEQSDA SITIDQLTMA DNGTYECSVS 120
 LMSDLEGNK SRVRLLVLP PSKPECIGIE ETIIIGNNIQL TCQSKEGSPT PQYSWKRYNI 180
 35 LNQEOPLAQP ASGGQVSLKN ISTDTSGYII CTSSNEEGTQ FCNITVAVR SPMNVALYVG 240
 IAVGVVAALI IIGIIYCC CCRGKDDNTED KEDARPNREA YEBPPEQLRE LSREREEDDD 300
 YRQEEQRSTG RESPDHLDQ 319

Seq ID NO: C218 Protein Sequence
Protein Accession #: Eos sequence

40 1 11 21 31 41 51
 MGSRTFESPL HAVQLRWGPR RRPPLPLLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60
 GFSVEFYRPG TDGVSVLVGA PKANTSQPOV LQGGAVYLCP WGAAPTQCTP IEFDSKGSRL 120
 45 LESSLSSEEP EEPFVYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPGVTCYLSL 180
 DNPTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFNO QGILSATQEQ 240
 IAESYYPEYL INLVQQLQT RQASSIYDSS YLGYSVAVGE FSGDDTDFV AGVPKGNLTY 300
 GYVTTILNGS IRSLYNFSGE QMASYFYGAV AATDVNGDGL DDLVVGAPLL MDRTPDGRPQ 360
 50 EVGRVYVYIQ HPAGIEPTPT LTLTGHDHFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420
 QQGVVFPFPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRLDNGNG YPDLIVGSFG 480
 VDKAVVYRGR PIVSASASLT IFFAMFNPEE RSCSLBGNFV ACINLSFCLN ASGKHVADSI 540
 GFTVELQLDW QKQKGGVRRR LPLASRQATL TOTLLIQNGA REDCREMKIY LRNESEFRDX 600
 55 LSPHIALINF SLDPQAPVDS HGLRPLALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660
 GEQNHVYLG D KNALNLTPEA QNVGEGGAYE AELRVTAPE AEYSGLVHRP GNFSSLSCDY 720
 FAVNQSRLLV COLGNPMKAG ASLWGLRFT VPHLRDTKKT IQPDFQLSK NLNNSQSDVV 780
 SPRLSVEAQA QVTLNGVSKP EAVLPFVSDV HPRDQPKKEE DLGPAVHVY ELINQGPSSI 840
 SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPGSLHH QOKREAPSR 900
 60 SASSGPQILK CPEABCFRLR CELGPLHQOE SQSLQLHFRV WAKTFLOREH QPFSIQCEAV 960
 YKALMFPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFGL LLLGLLIYIL 1020
 YKLGFFKRSL PYGTAMEKAQ LKPPATSDA 1049

Seq ID NO: C219 Protein Sequence
Protein Accession #: NP_002412.1

65 1 11 21 31 41 51
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGFV 60
 VEKLQMQEP FGLKVTGKPD AETLKVMKQP RCGVPDVAQP VLTEGNPRWE QTHLTYRIEN 120
 70 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAHAEL GHSGLSHST DIGALMYPST 240
 TFSGDVQLAQ DDIDGIAIY GRSONPVQPI GPQTPKACDS KLTPDAITTI RGEVMFPKDR 300
 FYMRTNPFYP EVELNFISVF WQPLPNGLA AYEPADRDEV RPFKGNKYWA VQGNVLEHY 360
 75 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FPFVANKYRWY DEYKRSDMPG YPKMIAHDFP 420
 GIGHKVDVAF MKDGFYFPFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN 469

Seq ID NO: C220 Protein Sequence
Protein Accession #: Eos sequence

80 1 11 21 31 41 51
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGFV 60
 VEKLQMQEP FGLKVTGKPD AETLKVMKQP RCGVPDVAQP VLTEGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAHAEL GHSGLSHST DIGALMYPST 240

TFSGDVQLAQ DDIDIGIAIY GRSONPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
 FYMRNTFFYP EVELNFISVF WPQLFNGLEA AYEFADRDEV RFFKGKNKYWA VQGGQNVLHG 360
 PKDIYSSFGF PRTVRHIDAA LSEENTGKTY FFVANKYWRV DEYKRSMDPG YPKMIAHDFP 420
 GIGHKVDVAV MKDGGFFYFFH GTRQYKFDPK TKRILTQKA NSWFNCRKN 469

Seq ID NO: C221 Protein Sequence
 Protein Accession #: NP_055146.1

1 11 21 31 41 51
 MVRKPVVSTI SKGGYLQGNV NGRLPSLGNK EPPGOEKVQL KRKVTLLRGV SIIIGTIIGA 60
 GIFISPKGVL QNTGSVGMSL TIWTVCGVLS LFGALSYAEL GTTIKKSGGH YTYILEVFGP 120
 LPAFVRVWVE LLIRPAATA VISLAFGRYI LEPFFIQCEI PELAIKLITA VGITVVMVLN 180
 SMSVSWASARI QIFLTPCKLT AILIIIVPGV MQLIKGQTQN FKDAFSGRDS SITRLPLAFY 240
 YGMAYAGWF YLNFVTEVEE NPEKTIPLAI CISMATITGV YVLTNVAYFT TINAEEELLS 300
 NAVAVTFSEK LIGNFSLAVP IFVALSCPGS MNGGVFAVSR LFYVASREGH LPEILSMIHV 360
 RKHTPLPAVI VLHPLTMIML FSGDLDSLNL FLSPARWLF GLAVAGLTYL RYKCPDMHRP 420
 FKVPLFIPAL FSPITCLFMA LSLYSDPPST GIGFVITLTG VPAYYLFIIW DKPKRWFPRM 480
 SEKITRTLQI ILEVVEEDK L 501

Seq ID NO: C222 Protein Sequence
 Protein Accession #: NP_003237.1

1 11 21 31 41 51
 MGLAWGLGVL FLMHVCGTNR IPESGGDNV FDIPELTGAA RKSGSRLRVK GPDSPSPAPR 60
 IEDANLIPPV PDKFQDLVD AVRAEKGFLL LASLRQMKKT RGTLLALBRK DHSQGVFSVV 120
 SNGKAGTDL DLSTVQKGQHV VSVEEALLAT GQWKSITLTV QEDRAQLYID CEKMEAEELD 180
 VPIQSVFTDR LAGLARLRIA KGGVNDNFQV VLQNVRFVFG TTPEDILRNK GCSSSTSVLL 240
 TLNNVNVNGS SPAIRTNVIG HKTIDQLAIC GISCELSM VLELRGLRTI VTTLDQDSIRK 300
 VTENKELAN ELRRPPLCYH NGVQYRNNEE WTVDSCTECH QNSVTICK VSCPIMPASN 360
 ATPDGECCP RCWPSDSADD GWSFSEWTS CSTSCNGIQ QRGRSCDSL NRCEGSSVQT 420
 RTCHIQECCK RFKQDGGWSH WSPSSSCSVT CGDGVITRIR LCNSPSPQMN GKPCBGEARE 480
 TRACKDACP INGGWGPWSP WDCSVTCGG GVQKRSRLCN NPAPQFGGKD CVGDVTENQI 540
 CNKQDCPIDG CLSNPCFAGV KCTSYPDGSW KCGACPPGYS GNGIQCTDVD ECKEVPDACP 600
 NNHGEHRCEN TDPGYNCLPC PPRFTGSQPF GQGVHEHATAN KQVCKPRNPC TDGTHDCNKN 660
 AKCNYLGHYS DPMYRCECKP GYAGNGIICG EDTDLGWPEN ENLVCVANAT YHCKKDCNCPN 720
 LPNSGGEDYD KQDGGDACDD DDDNDKIPDD RDNCFPHYNP AQDYDVRDDV GDRCDNCFYN 780
 HNPDQADTDN NGECDACAAD IDGDGILNER DNCQYVYVND QRDTDMGVG DQCDNCPLEH 840
 NPQQLDSDSD RIGDTCDNNQ DIDEHGHQNN LDNCPYVFNQ NQADHDKDGK GDACDHDDN 900
 DGIPDDKDCN RLVPNDQDQD SDGDDGRDAC KDDPDHDSVP DIDDICPENV DISETDFRRD 960
 QMIFLDFKGT SQNDPNWVVR HQGKELVQTV NCDPGLAVGY DEFNAVDFSG TPFINTERDD 1020
 DYAGFVFGYQ SSSRFVVMVM KQVTSQSWDT NPTRAQGYSG LSVKVVNSTT GPGEHLRNAL 1080
 WHTGNTPGQV RTLWHDPRHI GWKDFYAYRW RLSHRPKTGF IRVVMYEGKK IMADSGPIYD 1140
 KTYAGRLGL VVFSQEMVFP SDLYECPDRP 1170

Seq ID NO: C223 Protein Sequence
 Protein Accession #: NP_002183.1

1 11 21 31 41 51
 MPLLWLRGFL LASCWIIVR SPTPGSEHGS AAPDCPSAL AALPKDVFN S QPEMVEAVKK 60
 HILNMLBLKK RPDVTQPVPK AALLNAIRKL HVGKVGNGY VEIEDIGRR AEMNEMEQT 120
 SEIITPAESG TARKTLHFEI SKEGSDLSVV ERAEVWLFK VPKANRTRK VTIRLPQQK 180
 HPQSLDTGE EAEVGLKGE RSELLLSEKV VDARKSTWHV FVSSSIQRL LDQKSSLDV 240
 RIACEQCQES GASLVLLGKK KKKKEEGEGK KKGGEGBGAG ADEEKEQSHR PFLMLQARQS 300
 EDHPHRRRRR GLECDGKVIN CCKKQFFVSF KDIGWMDWII APSGYBANYC EGECPSHIAG 360
 TSGSSLSFHS TVINHYMRG HSPFANLKSC CVPTKLPRMS MLYYDDGQNI IKKDIQNMIV 420
 EECGCS 426

Seq ID NO: C224 Protein Sequence
 Protein Accession #: NP_000086.1

1 11 21 31 41 51
 MVPDTACVLL LTALALGASG QGQSPILGSDL GPQMLRELQR TNAALQDVND WLRQVREIT 60
 FLKNTVMBCD ACGMQSVRT GLPSVRPLH CAPGPCFPGV ACIQTESGGR CGPCPAGFTG 120
 NGSHCTDVNB CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
 INECETQGNH CVPNSVCINT RGSFQCGPCQ PGFVGDAQSG CQGAQRFCP DGSFSECHH 240
 ADCVLERDGS RSCVCRVWMA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSSQ 300
 EDVDRDGDG ACDPADGDG VFNKDNCPFL VRNPDQRNTD EDKWDACDN CRSQKNDQK 360
 DTDQDGRGDA CDDIDGDRI RNQADNCPRV FNSDQKDSGD DGIGDADNDC PQKSNPDQAD 420
 VDHDVGDGAC DSDQDQDGDG HQDSRDNCPV VPNSAQEDSD HDGQGDACDD DDDNDGVFDS 480
 RDNCRFLVNP GQEDADRQDV GDVCQDDFDA DKVVDKIDVC PENAETLTD FRAFQTVVLD 540
 PEGDAQIDFN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEPTFHVNT VTDDYAGFI 600
 FGYQDSSSFY VVMWKQMEQT YWQANPFRV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT 660
 ESQVRLWKD PRNVGWKDKK SYRWPLQHRP QVGYIRVRFY EGPELVADSN VVLDITMRGG 720
 RLGVFCFSQE NIINANLRYR CNDTIPEDYE THQLRQA 757

80 Seq ID NO: C225 Protein Sequence
 Protein Accession #: NP_612464

1 11 21 31 41 51

MRPQGPAASP QRLRGLLLLL LLQLPAPSSA SEIPKKGKQA QLRQREVVDL YNGMCLQGPA 60
 GVPGRDGSFG ANGIPTGTFGI PGRDGFKGK GECLRESFEE SWTPNYKQCS WSSLYNGIDL 120
 GKIAECTFTT MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECSGPL PIEAIYLDL 180
 GSPENNSTIN IHRSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240
 LPK 243

Seq ID NO: C226 Protein Sequence
 Protein Accession #: NP_003216.1

1 11 21 31 41 51
 MATMENKVIC ALVLVSMAL GTLABAQTET CTVAPRERQN CGFPFGVTPSQ CANKGCCFDD 60
 TVRGVPWCFY PNTIDVPPEE ECEF 84

Seq ID NO: C227 Protein Sequence
 Protein Accession #: NP_056234.1

1 11 21 31 41 51
 MPKRAHWGAL SUVLLILWGH PRVALACPHP CACYVPSEVH CTFRSLASVP AGIARHVERI 60
 NLGFNSIQAL SETSPAGITK LELLMHNGNE IPSIPDGLAL DLSSLQVFKF SYNKLKRVITG 120
 QTLQGLSNLM RLHIDHNKIE FIHPQAFNGL TSLRLHLLEG NLLHQLHPST FSTFTFLDYF 180
 RLSTIRHLYL AENMVRLTPA SMLRNMPLLE NLYLQGNPWT CDCEMRWFLE WDAKSRGILK 240
 CKDKKAYEFG QLCAMCFSPK KLYKHEIHKL KDMTCLKPSI ESPLRQNRER SIEEEQEQUE 300
 DGGSQLELEK FQLPQWSISL NMTDEHGNMV NLVCDIKKPM DVYKIHNLQT DPPDIDINAT 360
 VALDFECFMT RENYEKLWKL IAYYSEVPVK LHRELMLSKD PRVSQYVRQD ADEEALYTTG 420
 VRAQLAEPE WVMQPSIDIQ LNRRQSTAKK VLLSYTYQYS QTISTKDTRO ARGRSWVME 480
 PSGAVQRDQT VLEGQFQCLS CNVKASESPS IFWVLPDGS I LKAPMDPDFS KFSILSSGWL 540
 RIKSMEPSDS GLYQCIQAVR DEMDRMVYRV LVQSPSTQPA EKDTVTIGKN PGESVTLPQN 600
 ALAIEPAHLS WILPNRRIIN DLANTSHVYM LPNGTLSIPK VQVSDSGYYR CVAVNQGGAD 660
 HFTVGITVTK KSGSLPSKRG RRPKAKALSR VREDIVEDEG GSGMGDEBENT SRLLHFKDQ 720
 EVFLKTKDDA INQDKKAKKG RRLKILWKHS EKEPETNVAE GRRVFESRRR INMANKQINP 780
 ERWADILAKV RGINLFGKTE VPPLIKTTSF PSLSLEVTTP FPAVSPSPAS PVQTVTSAGE 840
 SSADVPLLGE EEHVLTGISS ASMGLEHNNH GVILVEPEVT STPLEEVVDD LSEKTEEITS 900
 TEGDLKGTAA PTLISEPYEP SPTLHTLDTV YEKPTHEETA TEGNSAADVG SSPEPTSSEY 960
 EPPLDAVSLA ESEPMQYFDP DLETKSQPDE DKMKEDTFAH LTPTPTIWNV DSSTSQLFED 1020
 STIGEPGVPG QSHLQGLTDN IHLVKSSLST QDTLLIKKGM KEMSQTLLQG NMLEGDPHVS 1080
 RSSESEGGES KSITLDPSTL GIMSSMSPVK KPAETTVGTL LDKDTTITVT TPRQKVPAS 1140
 TMSTHPSRRR PNGRRRLRPN KFRHRHKQTP PTTAPSETF STQPTQAPDI KISSQVESSL 1200
 VPTANVDNTV NTPKQLEMEK NAEPTSKGTP RRKHGKRPNK HRYTPSTVSS RASGSKPSPS 1260
 PENKRNIVT PSSETILLPR TVSLKTEGYP DSLDYMTTTR KIYSSYPKVQ ETLFVYTKPT 1320
 SDGKEIKDDV ATNVDKHKSD ILVTGESITN AIPTSRSLVS TMGEFKEESS PVGFGPTPTW 1380
 NPSRTAQPCR LQTDIVPVTG GENLTDPLL KELEDVDFTS EFLSSLTVST PFHQEAGSS 1440
 TTLSSIKVEV ASSQABTTTL DQDHELTVA ILLSETRPQN HTPTAARMKE PASSSPSTIL 1500
 MSLGQTTTK PALPSPRISQ ASRDSKENVF LNYVGNPTE ATPVNNBGTQ HMSGPNELST 1560
 PSSDDADAPNL STKLELEKQV FGSRLRPGF DSQRQDGRVH ASEQLTRVPA KPILPATVR 1620
 LPEMSQAS RYFVTSQSPR HWINKPEITT YPSGALPENK QFTTPRLST TIPLELHMSK 1680
 PSIPSKFTDR RTDQFNGYSK VFGNNNIPEA RNPVGKPPSP RIPHYSNGRL PFFTNKTLF 1740
 PQLGVTRRQ IPTSPAPVMR ERKVINGSYN RIHSHSTFHL DFGPPAPPLL HTPQTGSPS 1800
 TNLQNPVMS STQSSISFIT SSVQSSGSPH QSSSKFPAGG PPASKFWSLG EKPQLITKSP 1860
 QTVSVTAETD TVPFCBATGK PKPFVWTWKV STGALMTENT RIQRFELVN GTLVIRKQVQ 1920
 QDRGQMCCTA SNLHGLDRMV VLLSVTVQQP QILASEYQDV TVYLGDTIAM ECLAKGPAP 1980
 QISWIPFDRR VWQTVSPVES RITLHENRTL SIKEASPSDR GYKCVASNA AGADSLAIRL 2040
 HVAALPPVH QKLENIISLP PGLSIHICT AKAAPLPSVR WVLGDGTQIR PSQFLHGNLF 2100
 VFPNGTLYR NLAKPDSGRY ECVAANLVGS ARRTVQLNVQ RAAANARITG TSPRRTDVRY 2160
 GGTLLKDCSA SGGPWPRIW RLPKSRMIDA LFSFDSRIKV FANGTLVKS VTDKADAGYL 2220
 CVARNKQDST VYVLKVDVVM KPAKIEHKEE NDHKVFGGD LKVDCAVTLG PNEISWSLP 2280
 DGSLVNSFMQ SDDSGGRTRK YVVFNNGTLY FNEVGMREEG DYTCAENQV GKDEMRVRVK 2340
 VVTAPATIRN KTYLAVQVPY GDVVTVACEA KGEPMPKVTW LSPITNKVPT SSEKYQIYQD 2400
 GTLLIQKAQR SDSGNYTCLV RNSAGEDRKT VWIHVNVQPP KINGNPNPIT TVREIAAGSS 2460
 RKLIDCKAEG IPTPRVLWAF PEGVVLPAFY YGNRITVHGN GSILDIRSLRK SDSVLQVCMA 2520
 RNEGGEARLI VQLTVLEPME KPIPHDPISE KITAMAGHTI SLNCSAAGTP TPSLVWVLPN 2580
 GTDLQSGQQL QRFYHKADGM LHISGLSSVD AGAYRCVARN AAGHTERLVS LKVGKPEAN 2640
 KQYHNLSII NGETLKL PCT PPGAGQGRFS WTLFNGMHLE GPQTLGRVSL LDNGTLTVRE 2700
 ASVEDRGTYV CRMETEYGPS VTSIFVIVIA YPRITSEPT FYIYTRPGNT VKLNCMAMGI 2760
 PKADITWELP DKSHLKAGVQ ARLYGNRFLH PQGSLTIQHA TQRDAGFYKC MAKNILGSDS 2820
 KTTYIHVF 2828

Seq ID NO: C228 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MPQTKLIRTG APADYRVILK TSQEDLDVPP DDISVRVMSS QSVLVSWVDP VLEKQKKVVA 60
 SRQYTVKRYE KGELARWYK QIANRRVLIE NLIFDVTVEF AVRI SQGERD GKWSTSVFPQ 120
 TPESAPTTAP ENLNVWVNG KPTVVAASWD ALPETEGKVK VCLLDGTGLFS VSSFQPSAKS 180
 PQNTFFHTPR LSNHLEQSPS PILETLALLP WMVCSLGNAI FSKSGPQTGE AMDLTPKPSL 240
 SLCCQECSCST QKDFSCLAYL IDIQTKQVKN DPQLEGSVFG PCFLFYFLTF MLDIGGFSPI 300
 MCYEDFPVSS LTGNSLKSVA ASKADVQONT EDNGKPEKPE PSSSPSPAPA SSQHPSPVPS 360
 PQGRNAKDLL LDLLKNILAN GGAPRKPQLR AKKAEELDLQ STBITGEEEL GSREDSFMS 420
 SDTQDQKRTL RPPSRHGHV VAPGRATAVA RMPALPRREG VDKPGFSLAT QPRGAPPSA 480
 SASPAHAST QGTSRPSLP ASLNDNDLVD SDEDERAVGS LHPKGAFAPQ RPALSPSRQS 540
 PPSVLDRSS VHPGAKPAS ARRTPHSGAA EEDSSASAPP SRLSPPHGGS SLLLTQPHL 600
 SSPLSKGGKD GEDAPATNSN APSRSTMSSS VSSHLSSRTQ VSEGAESDG BSHGDTGRED 660

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GGRQAEATAQ TLRARPASGH PHLLRHKPPA ANGRSPSRFS IGRGPRLQPS SSPQSTVPSR 720
 AHPRVPSHSD SHPKLSSGIH GDEEDEKPLP ATVVNDHVPS SSRQPISRGW EDLRRSPQRG 780
 ASLHRKSPIP ENPKSTGADT HPQGYSSLA SKAQDVQOST DADTEGHSPK AQPGSTDRHA 840
 SPARPPAARS QQHPSPVPRM TPGRAPQQP PPPVATSQHH PGQSRDAGR SPQSPRLSLT 900
 AQGRFRPTSQ GRSHSSSDPY TASSRGMLEP ALQNDQDEDAQ GSYDDSDTEV EAQDVRAPAH 960
 AARAKEAAS LPKHQQVESP TGAGAGGDHR SQRGHAASPA RPSRPGGPQS RARVPSRAAP 1020
 GKSEPPSKRP LSSKSQSVS AEDEEEEDAG FFKGGKEDLL SSSVPKWPSS STPRGGKDAD 1080
 GSLAKEEREP AIALAPRGS LAPVKRPLPP PPGSSPRASH VPSRPPPSA ATVSPVAGTH 1140
 PWPRYTTRAP PGHFTTTPML SLRQRMHAR FRNPLSRQPA RPSYRQGYNG RPNVEGKVLV 1200
 GSNKGPNQOR IINGPQGTGW VVDLDRGLVL NABGRYLQDS HGNPLRIKLG GDGRTIVDLE 1260
 GTFVVSVDGL PLFGQGRHGT PLANAQDKPI LSLGGKPLVG LEVIKKTTHP PTTTMMQPTT 1320
 TTPLPTTTT RPTTATTMQP TTTTTPLPPT TPRPTTATTR RTTTRRPTT VRTTTRTTT 1380
 TTPKPTTIP TCPPGTLEH DDDGNLIMSS NGIPECYAEE DEFSGLETDT AVPTTEAYVI 1440
 YDEDEYFETS RPTTTEPST TATTPRVPE EGAISSFPBE EFDLAGRKRFP VAPYVTVLNK 1500
 DPSAPCSLTD ALDHQVDSL DEIIPNDLKK SDLPQGHAPR NITVVAVEGC HSFVIVDWDK 1560
 ATPGLVLTGY LVYSASYEDF IRNKFSTQAS SVTHLPIENL KPNTRYFFKV QAQNPHGYGP 1620
 ISPSVSFVTE SDNPLLVVRP PGELSGSHS LSNMIPATRT AMDGNM 1666

20 Seq ID NO: C229 Protein Sequence
 Protein Accession #: NP_003005.1

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1 11 21 31 41 51
 MFLSILVALC LMLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ 60
 YEELVDVNC AVLRFFFCAM YAPICTLEFL HDPIKPKCSV CQRARDDCEP LMKMYNHSWP 120
 ESLACDELFP YDRGVCISPE AIUTDLPEVD KWIDITPDM VQERPLDVC KRLSPDRCKC 180
 KKKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTVVDV KBIFKSSSP PRTOVPLITN 240
 SSCQCPHILP HQDVLIMCYE WRSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD 300
 KKKTAGRTSR SNPPKPKGPK PAPKPASPKK NIKTRSAQKR TNPKRV 346

35 Seq ID NO: C230 Protein Sequence
 Protein Accession #: NP_005931.1

40
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1 11 21 31 41 51
 MAPAAWLRS AARALLPPML LLLLPFPPLL ARALFPDVHH LHAERRGQP WHAALPSSPA 60
 PAPATQEAEP PASSLRPPRC GVPDPDSGLS ARNRQKRFVL SGRWEKTDL TYRIIRFPWQ 120
 LVQEQVRQTM AEALKVWSDV TPLTFTVEHE GRADIMIDFA RYWHGDDLPF DGPGLLAHA 180
 FFPKTRREGD VHPDYDETNT IGDDQGTDL QVAAREFGHV LGLQHTTAAK ALMSAFYTFR 240
 YPLSLSPDDC RGQVHLYGQP WPTVTSRTPA LGPQAGIDTN ETAPLEPDAP PDACEASFDA 300
 VSTIRGELEF PKAGFVWRLR GGQLQPGYPA LASREWQGLP SPVDAAFEDA QGHINFPQGA 360
 QYVWYDGEKP VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YPFRGRDYWR FHPSTRRVDS 420
 VPPRRATDRL GVPSEIDAAF QDADGYAYFL RGRLYWKFDP VKVKALEGFP RLVGPDFFGC 480
 AEPANTFL 488

50 Seq ID NO: C231 Protein Sequence
 Protein Accession #: NP_076927

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60

1 11 21 31 41 51
 MGENDPPAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKPPF IIVIGIALI 60
 LALAIGLGIH PDCSGKYRCR SSPKCIELIA RCDGVSDCKD GEDEYRCRV GQNAVQLQV 120
 TAASWTKMCS DDWNGHYANV ACAQLGFPSY VSSDNLVSS LEGQFREEFV SIDHLLPDDK 180
 VTALHHSVVV REGCASGHV TLQCTACGHR RGYSSRIVGG NMSLLSQWFW QASLQFQGYH 240
 LCGGSVITPL WIITAHCYV DLYLPSKWTI QVGLVSLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QVCLPNSSE NPPDGKVCWT SGWGATEDGG DASPLVNHA 360
 VPLISNKN CNHRDVGIGIIS PSMLCAGYLT GGVDSCQGDG GGPLVCQERR LKWLVGATSF 420
 GIGCAEVNKP GVTYRTVSFL DWIHEQMERD LKT 453

65 Seq ID NO: C232 Protein Sequence
 Protein Accession #: NP_003211

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75

1 11 21 31 41 51
 MLWKLTDNIK YEDCEDRHDG TSNGTARLPQ LGTVGQSPYT SAPPLSHTPN ADFQPPYFPP 60
 PYQPIYPQSQ DPYSHVNDPY SLNPLHAQPO PQHPGWPGQR QSQESGLLHT HRGLPHQLSG 120
 LDPRRDYRRH EDLLHGPHAL SSGLDLSIH SLFHAIEBP HVEDPGINIP DQTVIKKGPV 180
 SLKSNSNAV SAIPINKNL FGVVNPNEV FCSVPGRSL LSSTSKYKVT VAEVQRRLSP 240
 PECLNASLLG GVLRRASKN GGRSLREKLD KIGLNLPAQR RKAANVTLLT SLVEGEAVHL 300
 ARDFGYCET EPPAKAVAEF LNRQHSDPNE QVTRKNMLLA TKQICKBPTD LLAQDRSPLG 360
 NSRPNPILFP GIQSCLTIFN LISHGFGSPA VCAAVTALQN YLTEALKAMD KMYLSNNPNS 420
 HTDNNAKSSD KEEKRHK 437

80 Seq ID NO: C233 Protein Sequence
 Protein Accession #: NP_002979.1

1 11 21 31 41 51
 MKGLAALLV LVCTMALCSC AQVGTNKELC CLVYTSWQIP QKPIVDYSET SPQCPKPGVI 60
 LLTKRGRQIC ADFNKKWQK YISDLKANA 89

Seq ID NO: C234 Protein Sequence
 Protein Accession #: NP_004054.1

	1	11	21	31	41	51	
5	MILQAHLSL	CLMLYLATG	YGQEGKFSGP	LKPMTFISIYE	GQEPSQIIFQ	FKANPPAVTF	60
	ELTGETONIF	VIERBQLLYY	NRALDRETRS	THNLQVAALD	ANGIIVEGVPV	PITIEVKDIN	120
	DNRPTFLQSK	YEGSVQRNSR	PGKPFLLVNA	TDLDDPATPN	GQLVYQIVIQ	LFMINNVMYF	180
	QINNKTGAIS	LTREGSQELN	PAKNPSYNLV	ISVDMGGQS	ENSFSDTTSV	DIIVTENIWK	240
	APKPVEMVEN	STDPHPKIT	QVRWNDPGAQ	YSLVDKEKLP	RFPFSIDQEG	DIYVTQPLDR	300
10	EKKDAYVPYA	VAKDEYGGKL	SYPLEIHVKV	KDINDNPFTC	PSPVTVFVEQ	ENERLQNSIG	360
	TLTAHDRDEE	NTANSFLNVR	IVEQTPKLFM	DGLFLIQTYA	GMLQLAKQSL	KKQDTPQYNL	420
	TIEVSDKDFK	TLCFQVINVI	DINDQIPIFE	KSDYGNLTLA	EDTNIGSTIL	TIQATDADEP	480
	FTGSSKILYH	IIKGDSEGR	GVDTPHTNT	GYVIIKKPLD	FETAAVSNIV	FKAENPEPLV	540
	FGVKYNASSF	AKFTLIVTDV	NEAPQFSQHV	FQAKVSESDA	IGTKVGNVTA	KDPEGLDISY	600
15	SLRGDTRGWL	KIDHVTGEIF	SVAPLDREAG	SPYRVQVVAT	EVGGSSLSV	SEPHLILMDV	660
	NDNPPRLAKD	YTGLPFCHPL	SAPGSLIFEA	TDDDQHLFRG	PHFTFSLGSG	SLQNDWEVSK	720
	INGTHARLST	RHTEFEERYE	VVLIRINDGG	RPPLEGIVSL	PVTFPCSCVEG	SCFRPAGHQT	780
	GIFTVGMVAG	ILLTLLLVIG	IILAVVFIRI	KKDKGKDNVE	SAQASEVKPL	RS	832

Seq ID NO: C235 Protein Sequence

Protein Accession #: NP_004434.1

	1	11	21	31	41	51	
25	MARARPPPPP	SPPPGLLPLL	PPLLLLPLLL	LPAGCRALER	TLMDTKWVTS	ELAWTSHPEB	60
	GWEVSGYDE	AMNPRTYQV	CNVRESSQNN	WLRGFIWRR	DVQRVYVELK	FTVRDCNSIP	120
	NIPGSCKETP	NLFYVADSD	VASASSPFWM	ENPYVKVDTI	AFDESFSRLD	AGRVTNKRVS	180
	FGPLSKAGFY	LAFODQGACM	SLISVRAFYK	KCASTTAGFA	LPETLTGAE	PTSLVIAPGT	240
	CIPNAVEVS	PLKLYCNGDG	EMWVPVGACT	CATGHEPAAK	ESQCRPCPPG	SYKAKQGEGP	300
30	CLPCPFNSRT	TSPAASICTC	HNNFYRADSD	SADSACTTVP	SPPRGVISNV	NETSLILEMS	360
	EPRLGGRDD	LLYNVICKKC	HGAGGASACS	RCDNVEFVP	RQLGLTERRV	HISHLAHR	420
	YTPEVQAVNG	VSGKSPLPFR	YAAVNITNQ	AAPSEVPTLR	LHSSGSSSLT	LSWAPPERPN	480
	GVILDYEMKY	FEKSEGIAT	VTSQMSVQL	DGLRFDARYV	VQVRARTVAG	YQGYRPAEF	540
	ETTSESGSGA	QQLQEQLPLI	VGSATAGLVE	VVAVVIAIV	CLRKQRHOSD	SEYTEKLQYQ	600
	IAPGMKVYID	PFTYEDPNEA	VREFAKEIDV	SCVKIEEVIG	AGEFGEVCRG	RLKQPGRRV	660
35	FVAIKTLKVG	YTERQRDPL	SEASIMGQPD	HPNIIIRLEGV	VTKSRPVMIL	TEFMENCALD	720
	SFLRLNDGGF	TVIQLVGLMR	GIAAGMKYLS	EMNVVHRDLA	ARNILVNSNL	VCKVSDPGLS	780
	RFLEDDPSDP	TYTSSLGGKI	PIRNTAPEAI	AYRKFTSASD	VMSYGIWMWE	VMSYGERPYW	840
	DMSNQDVINA	VEQDYRLPPP	MDCPALHQL	MLDCHVRDRN	LRPKFSQIVN	TLDKLIIRNAA	900
40	SLKVIASAGS	GMSQPLDRT	VPDYTTFTTV	GMWLDAIKMG	RYKESFVSAG	FASFDLVAQM	960
	TAEDLLRIGV	TLAGHQKIL	SSIQDMRLQM	NQTLFPVQV			998

Seq ID NO: C236 Protein Sequence

Protein Accession #: NP_001795.1

	1	11	21	31	41	51	
45	MYVGVLDKD	SPVYGPAPAR	ASLGLGPANY	GPPAPPPAPP	QYPDFSSYSH	VEPAPAPPTA	60
	WGAPFPAPKD	DWAAAYGPGP	AAPAAASPASL	APGPPPDFSP	VPAPPGPGPG	LLAQPLGGPG	120
50	TPSSPGAQRP	TPYEMRRSV	AAGGGGSGK	TRTKDKYRVV	YTDHQRLELE	KEPHYSTRYT	180
	IRKSELAAN	LGLTERQVKI	WFQNRRAKER	KVNKKKQQQQ	QPPQPPMAHD	ITATPAGPSL	240
	GGLCPSNTSL	LATSSPMPVK	EEFLP				265

Seq ID NO: C237 Protein Sequence

Protein Accession #: NP_068813.1

	1	11	21	31	41	51	
60	MGSDRARKGG	GGPKDFGAGL	KYNSRHEKVN	GLEEGVEFLP	VNNVKKVEKH	GPGRWVVLAA	60
	VLIQGLLVLL	GIGFLVWHLQ	YRDVRVQKVF	NGYMRITNEN	FVDAYENSNS	TEFVSLASKV	120
	KDALKLYSG	VPFLGPHYKE	SAVTAFSBGS	VIAYYNSBFS	IPQHLVEEAE	RVMAEERVVM	180
	LPPRARSLKS	FVVTSVVAFP	TDSKTVQRTQ	DNSSCSGLHA	RGVELMRFTT	PGFPDSPYPA	240
	HARQWALRG	DADSVLSLTF	RSFDLASDCE	RGSDLVTVYN	TLSPMEPHAL	VQLCGTYPSP	300
	YNLTFFSSQN	VLLITLITNT	ERRHPGFEBT	FFQLPRMSSC	GGRLRKAQGT	FNSFYYPGHY	360
65	PNIDICTWNI	EVPMNQHVKV	RKFIFYLLEP	GVPACTCPKD	YVEINGEKYC	GERSQFVVT	420
	NSNKITVRFH	SDQSYTDGTF	LAELYSDSS	DPCPGQFTCR	TGRCIRKBLR	CDGWADCTDH	480
	SDELNCSDA	GHQFTCKNKF	CKPLFWVCD	VNDGDNDSDE	QGCSCPAQTF	RCSNGKCLSK	540
	SQQCNGKDDC	GDGSDASCP	KVNVTCTKH	TYRCLNGLCL	SKGNPCDCK	EDCSGDSDEK	600
	DCDCGLRSFT	RQARVVGTD	ADEGEWFWQV	SLHALGQGH	CGASLISPNN	LVSAAHCYID	660
70	DRGFRYSDF	QWTAFLGLHD	QSQRAPGVQ	ERRLKRIISH	PPFNDPTFDY	DIALLELEKP	720
	AEYSSMVRPI	CLPDASHVFP	AGKAIWVTGW	GHTQYGGTGA	LILQKGEIRV	INQTTCEML	780
	PQITPRMCM	VGFLSGGVDS	CQGDSSGGLS	SVEADGRIFQ	AGVVSNGDGC	AQRNKGVTY	840
	RLPLFRDNWK	ENTGV					855

Seq ID NO: C238 Protein Sequence

Protein Accession #: Bos sequence

	1	11	21	31	41	51	
80	MPPFLLEAV	CVPLFSRVFP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMPLLDGSN	60
	SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAFQFSSTPH	LEFPDLSPT	QQEVKARIKR	120
	MVFKGGRTET	BLALKYLLHR	GLPGGRNASV	PQILIVTDG	KSQGDVALPS	QQLKERGVTV	180
	FAVGVRFRPM	BEIHALASEP	RGQHVLLABQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCZERTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCFFYSWK	RVFLTHPATC	YRTTCCPGCD	300
	SQPCQNGGTC	VPEGLDGYQC	LCPLAFGGEA	NCAKLSLEEC	RVDLLFLDLS	SAGTTLDGFL	360

5 RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVFVGEY QDVPDLVWSL DGIPFRGGPT 420
 LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480
 EAVRAELEEI TGSFKHVMVY SDPQDLFNQI PELQGLKCSR QRPGRCTQAL DLVFMMLDTSA 540
 SVGPENFAQM QSFVRSCALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVLT GGRGAEDAAV PAQKLRNNGI 660
 SVLVVGVGPV LSEGLRLLAG PRDSLHVAA YADLRYHQDV LIEWLCEGAK RPNVNLCKPSP 720
 CMNEGSCVLQ NGSYRCKCRD GWGPHCENR FLRRP 755

10 Seq ID NO: C239 Protein Sequence
 Protein Accession #: Eos sequence

15 1 11 21 31 41 51
 | | | | | |
 MPFFLLLEAV CVPLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLDGSN 60
 SVGKGSFERS KHFATVCDG LDISPERVRV GAFQFSSTPH LEFFLDSPST QQEVKARIKR 120
 MVFKGRTET ELALIKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKRGVTV 180
 FAVGVRFPRW EELHALASEP RQOHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLMV RRFAGNAPCN RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCPGPCD 300
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDS SAGTTLDGFL 360
 20 RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVFVGEY QDVPDLVWSL DGIPFRGGPT 420
 LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480
 EAVRAELEEI TGSFKHVMVY SDPQDLFNQI PELQGLKCSR QRPGRCTQAL DLVFMMLDTSA 540
 SVGPENFAQM QSFVRSCALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 25 APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVLT GGRGAEDAAV PAQKLRNNGI 660
 SVLVVGVGPV LSEGLRLLAG PRDSLHVAA YADLRYHQDV LIEWLCEGAK QPNVNLCKPSP 720
 CMNEGSCVLQ NGSYRCKCRD GWGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
 RTPPSNYREG LGTEMVPTFM NVCAAPG 807

30 Seq ID NO: C240 Protein Sequence
 Protein Accession #: XP_097386.1

35 1 11 21 31 41 51
 | | | | | |
 MPKSEPLGCL SPASRAPGSA AATGAWLPAA SGGPGPLGPP CTCPPRSLGR GRAGSRAGSS 60
 PSGCVCSGI LRVVSVGDPA SRRWVDLSN SEDLSLLTP MIVGTGGVGG GWARGWVPAQ 120
 EKEVAEGSGH AGRGNRRRLQ RVYGARSWIL GRKPCQLRLL PASGGPVQPP PCPSPATACR 180
 WGFKFGVAFW GAAQHPLPCR LGGGRVPSA TRTLDGF 217

40 Seq ID NO: C241 Protein Sequence
 Protein Accession #: CAC03433

45 1 11 21 31 41 51
 | | | | | |
 MLSTDTFTA SWELVVRVDH PNEEQQKDV LRVSGDLHVG GVMLKIVEQI NISQDWSDEA 60
 LWWEQKHCWL LKTHWTLDKY GVQADAKLLF TPQHKMLRLR LPNLKMWRLR VSPSAVVFKA 120
 VSDICKILNI RRSEELSLK PSQDYFKKK KDKNNKEPI IEDILNLESS PTASGSSVSP 180
 GLYSKIMTPI YDPINGTPAS STMTWFSDSF LTEQNCSILA PSQPPQSPEA LADMYQPRSL 240
 VDKAKINAGW LDSSRSLMEQ GIOEDEQLLL RFKYYSFFDL NPKYDAVRIN QLYEQARWAI 300
 50 LLEBIDCTE EMLIPAAQY HISKLSLSAE TQDPAGESEV DEIBAALSNL EVTLEGGKAD 360
 SLLEDITDIP KLADNLKLFY PKLLPKAFK QYWIFIKDTS IAYFNKLELE QGEPLKLNIL 420
 RGCEVVPDYN VAGRKFGIKL LIPVADGMNE MYLRCDHENQ YAQWMAACML ASKGMTMADS 480
 SYQPEVLNLL SFLEMKNRNS ASQVASSLEN MDMNPECFVS PRCAKHKHSK QLAARILEAH 540
 QNVAQNPLVE AKLRFIQAMQ SLPEFGLTYY LVRPKGSKKD DILGVSYNRL IKIDAATGIP 600
 55 VTTWRFTNIK QMNVNWTETQ VVIEFDQNVF TAFTCLSDAC KIVHEYIGGY IFLSTRSKDQ 660
 NETLDEDLFH KLTGGQD 677

60 Seq ID NO: C242 DNA Sequence
 Nucleic Acid Accession #: NM_005170
 Coding sequence: 337..918

65 1 11 21 31 41 51
 | | | | | |
 GGGCGTGAGA AAGGOGACGG CGGCGGCGCG GAGGAGGGTT ATCTATACAT TTA AAAACCA 60
 GCGGCTCTGC CCGGCGCTGC GGAGACCTGG GAGAGTCGG CCGCACGCGC GGGACACGAG 120
 CGTCCACGCG TCCCTGGCGC GTACGGCGCT CCACCACTAG GCTCTCTATC CCGGGCTCTC 180
 AGACGACCTA GGAGCGCTGC CTTGGGGAGT TGCTTGGCGG CGCGGTGCCA GAAGCCCTCT 240
 TGGGGCGCCA CAGTTTTCCT CGTCGCTCTC GGTTCCTCTG CTGCACTCTT CTGCGGCGCG 300
 GCGGGGAACT GGAGCGGGCG GGTGGATGCA GCGCGATGG ACGGCGGAC ACTGCCGAGG 360
 70 TCCGCGCCCC CTGCGCCCCC CGTCCCTGTC GGCTGCGCTG CCGGCGGAG ACCCGCGTCC 420
 CCGGAACCTG TGCGCTGCGC CCGGCGGCGG CGACCGGCCA CCGCAGAGAC CGGAGGCGGC 480
 GCAGCGGCGG TAGCGCGGCG CAATGAGGCG GAGCGCAACC GCGTGAAGCT GGTGAACCTG 540
 GGCTTCAGG CGCTGCGGCA GCACTGCGG CACGCGGCGG CCAGCAAGAA GCTGAGCAAG 600
 GTGAGAGCGG TGCGCTCAGC CGTGAGATAC ATCGCGCGCG TGCGAGCGCT GCTGGCGGAG 660
 75 CACGAGCGCG TGCGCAAGCG GCTGGCGGGA GGGCTGAGGC CGCAGGCGGT GCGGCGGTCT 720
 GCGGCGGCGG GCGGCGGAGG GACCAACCGG GTGCGCGCT CGCCCTCCCG CGCTTCTCTG 780
 TCCCGGGGCC GCGGGGGCAG CTCGGAGGCC GGCTCCCGCG GTTCCGCTCA CTGCTGGAGC 840
 GACAGCGGCT GCGAAGGCGG GCTGAGTCT CCGGAGCGCG AGCTACTCGA CTCTCCAGC 900
 80 TGGTTAGGGG GCTACTGAGC GCCCTCGACC TA 932

Seq ID NO: C243 Protein Sequence
 Protein Accession #: NP_060233.1

1 11 21 31 41 51

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MSGGHQLQLA	ALWFWLLMAT	LQAGFGRTGL	VLAADVESER	SAEQKAVIRV	IPLKMDPTGK	60
LMLTLEGVFA	GVAEITPAEG	KLMQSHPLYL	CNASDDNLE	PGFISIVKLE	SPRRAPRPL	120
SLASKARMAG	ERGAVALFD	ITEDRAAAEQ	LQQLGLTWP	VVLIWGNAB	KLMEFYVKNQ	180
KAHVRIELKE	PPAWPDYDVM	ILMTVVGTIF	VIIILASVLR	RCRPRHSRP	PLQORTAWAI	240
SQLATRRYQA	SCRQARGSWP	DSGSSCSSAP	VCAICLEEF	EGQELRVISC	LHEFHRNCVD	300
PWLHQHRTCP	LCVFNITBGD	SFSQSLGPSR	SYQEPGRRLH	LIRQHPGHAH	YHLPAAYLLG	360
PSRSAVARPP	RPGFPLPSQE	PGMGPRHHRF	PRAAHPRAPG	EQQLLAGAQH	PYAQGWGMSH	420
LQSTSQHFAA	CPVPLRRARP	FDSSGSGESY	CTERSGYLAD	GPASDSSSGP	CHGSSSDSVV	480
NCTDISLQGV	HGSSSTFCSS	LSSDFPLVY	CSPKGDPRV	DMQPSVTSRP	RSLSDSVVFTG	540
ETQVSSHVHY	HRHRHHYKK	RFQWHGRKPG	PETGVQSRP	PIPRTPQPE	PPSPDQQVTG	600
SNSAAPSGRL	SNPQCPRALP	EPAPGPVDAS	SICPSTSSLF	NLQKSSLSAR	HPQRKRRGGP	660
SEPTPGSRPQ	DATVHPACQI	FPHYTPSVAY	PWSPEAHPLI	CGPPGLDKRL	LPETPGPCYS	720
NSQPFVWLCLT	PRQPLEPHFP	GEGPSEWSSD	TAEGRPCYP	HCQVLSAQPG	SEEELEELCE	780
QAV						783

Seq ID NO: C244 DNA Sequence
 Nucleic Acid Accession #: NM_004289
 Coding sequence: 493..1695

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1	11	21	31	41	51	
GCCGCGGCT	CGTCCACCG	AGGAGCGGC	GCCAGCGTG	ACGGCGGCG	CCAGGCTGTG	60
CAGGGGGGCG	GCGGGGACCC	CGAGCGGCT	CGGAGTGGCC	CCTTGGACGC	CGGGGAAGAG	120
GAGAAGGCAC	CGCGGAACC	GACGCTCAG	GTGCGGACG	CTGGCGGATG	TGCGAGCGAG	180
GAGAAATGGG	TACTAAGAGA	AAAGCACGAA	GCTGTGGATC	ATAGTTCCCA	GCATGAGGAA	240
AATGAAGAAA	GGGTGTCAGC	CCAGAAGGAG	AACTCACTTC	AGCAGAATGA	TGATGATGAA	300
AACAATAATG	CAGAGAAACC	TGACTGGGAG	GCAGAAAGA	CCACTGAATC	TAGAAATGAG	360
AGACATCTGA	ATGGGACAGA	TACTTCTTTC	TCTCTGGAAG	ACTTATTCCT	GTTGCTTTCA	420
TCACAGCCTG	AAAATTCACT	GGAGGGCATC	TCATTGGGAG	ATATTCTCTT	TCCAGGSCAGT	480
ATCAGTGATG	GCATGAATTC	TTCAGCACAT	TATCATGTAA	ACCTTCAGCCA	GGCTATAAGT	540
CAGGATGTGA	ATCTCTCATG	GGCCATCTTG	CTTTGTCCCA	ACAATACATT	TAGAAGAGAT	600
CCACAGCAAA	GGACTTCACA	GTCACAAGAA	CCATTTCATC	AGTTAAATTC	TCATACCAACC	660
AATCCTGAGC	AAACCCCTCC	TGGAACCTAAT	TTGACAGGAT	TTCTTTCACC	GGTTGACAAT	720
CATATGAGGA	ATCTAACCAAG	CCAAGACCTA	CTGTATGACC	TTGACATAAA	TATATTGTAT	780
GAGATAAACT	TAATGTCACT	GGCCACAGAA	GACAACTTTG	ATCCAATCGA	TGTTTCTCAG	840
CTTTTGTATG	AACAGAGATC	TGATTCTGGC	CTTTCTTTAG	ATTCAAGTCA	CAATAATACC	900
TCTGTATCA	AGTCTAATTC	CTCTCACTCT	GTGTGTGATG	AAGGTGCTAT	AGGTTATTGC	960
ACTGACCATG	AATCTAGTTC	CCATCATGAC	TTAGAAGGTG	CTGTAGGTGG	CTACTACCCA	1020
GAACCCAGTA	AGCTTTGTCA	CTTGGATCAA	AGTGATTCTG	ATTTCCATGG	AGATCTTACA	1080
TTTCAACAGC	TATTTATATA	CCCACTTAC	CACCTACAGC	CAACTGCACC	AGAATCTACT	1140
TCTGAAGTCT	TTCGTTGGCC	TGGGAAGTCA	CAGAAGATAA	GGAGTAGATA	CTTGAAGAGC	1200
ACAGATAGAA	ACTTGAGCCG	TGATGAACAG	CGTGCTAAAG	CTTTGCATAT	CCCTTTTCTT	1260
GTAGATGAAA	TTGTGGCAT	GCCTGTTGAT	TCTTTCAATA	GCATGTTAAG	TAGATATTAT	1320
CTGACAGACC	TACAAGTCTC	ACTTATCCGT	GACATCAGAC	GAAGAGGGAA	AAATAAAGTT	1380
GCTGCGCAGA	ACTGTGTGTA	ACGCAAAATG	GACATAATTT	TGAATTTAGA	AGATGATGTA	1440
TGTAACCTTC	AAGCAAGAAA	GGAAACTCTT	AAGAGAGAGC	AAGCACAATG	TACAAAGCTT	1500
ATTAACATAA	TGAAACAGAA	ACTGCATGAC	CTTTATCATG	ATATTTTATG	TAGATTAGAA	1560
GATGACCAAG	GTAGGCCAGT	CAATCCCAAC	CACATATGTC	TCCAGTGTAC	CCATGATGGA	1620
AGTATCTTGA	TAGTACCCAA	AGAACTGGTG	GCCTCAGGCC	ACAAAAGGAA	AACCCAAAGT	1680
GGAAAGAGAA	AGTGAGAGAA	AACTGAAGAT	GGACTCTATT	ATGTGAAGTA	GTAATGTTCA	1740
GAAACTGATT	ATTTGGATCA	GAAACCATTG	AAACTGCTTC	AAGAATTGTA	TCITTAAGTA	1800
CTGCTACTTG	AATAACTCAG	TTAAGCGTGT	TTTGAAGCTT	ACATGGACAA	ATGTTTAGGA	1860
CTTCAAGATG	ACACTTGTGG	GCAATCTGGG	GGAGCCACAA	CTTTTCATGA	AGTGCATTGT	1920
ATACAAAATT	CATAGTTATG	TCCAAAGAAT	AGGTTAACAT	GAAAAACCCG	TAAAGACTTTC	1980
CATCTTGCCA	GCCATCTCTT	TTAAGAGTAA	GTTGGTTACT	TCAAAAAGAG	CAAACTACTG	2040
GGATCAAATT	ATTTTAAGAG	GTAATTCAGT	TTTAAATGCA	AAATAGCCTT	ATTTTCATT	2100
AGTTTGTATG	CATATAGTGT	AGCTTTTCAA	ACACTATTTT	AATCTTTATA	TTTAACCTAT	2160
AAATTTTGCT	TTCT					2174

Seq ID NO: C245 Protein Sequence
 Protein Accession #: NP_004433

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1	11	21	31	41	51	
MALRRIGAAL	LLPLLAAVE	ETLMDSTTAT	AELGWMVHPF	SGWEEVSGVD	ENMNTIRTYQ	60
VGNVFESSQN	NWLRTKPIRR	RGAHRIHVEM	KFSVRDCSSI	PSVPGSCKET	FNLYYYEADF	120
DSATKTFPNW	MENPVVKVDT	IAADESPSQV	DLGGRVMKIN	TEVRSFPGVS	RSGFYLAQD	180
YGGCMSLLAV	RVFYRKCPRI	IQNGAIFQET	LSGAESTSLV	AARGSCIANA	EEVDVPIKLY	240
CNGDGEMLVP	IGRCMKKAGF	EAVENGTVCR	GCPSTGTFKAN	QGDEACTHCP	INSRTTSEGA	300
TNCVCRNGYY	RADLDPLDMP	CTTIPSAPQA	VISSVNETSL	MLEWTPPRDS	GGREDLVYNI	360
ICKSGSGSRG	ACTRCGDNVQ	YAPRQLGLTE	PRYIISDLIA	HTQYTFEIQ	VNGVTQDSPP	420
SPQFASVNIT	TNQAPSAVS	IMHQVSRVTD	SITLSWSQPD	QPNQVILDYE	LQYYEKELSE	480
YNATAIKSPT	NTVTYQGLKA	GAIVVFQVRA	RTVAGYGRYS	GKMYFQMTAE	AEYQTSIQEK	540
LPLIIGSSAA	GLVFLIAVVV	IAIVCNRRRG	PERADSEYTD	KLQHYTSGHM	TPGMKIYIDP	600
PTYEDPNEAV	REFAKEIDIS	CVKIEQVIGA	GEFGEVCSGH	LKLPKREIF	VAIKTLKSGY	660
TEKQRDRFLS	EASIMGQFDH	PNVIHLEGVV	TKSTFVMIIT	BFMENGSLDS	FLRQNDGQPT	720
VIQLVGMMLRG	IAAGMKYLDL	MNYVHRDLAA	RNILVNSNLV	CKVSDFLSLR	FLEDDTSDPT	780
YTSALGKXIP	IRWTAPEAIQ	YRKFTSASDV	WSYGIVMWEV	MSYGERPYWD	MTNQDVINAI	840
EQDYRLPPFM	DCPSALHQLM	LDCWQKDRNH	RPKFGQIVNT	LDMIRNPNFS	LKAMAPLSSG	900
INPLLDRTI	PDYTSFNTVD	EWLEAIKMGQ	YKESPANAGF	TSFDDVVSQMM	MEDILRVGLT	960
LAGHQKILIN	SIQVMRAQNN	QIQSVFV				987

Seq ID NO: C246 Protein Sequence

Protein Accession #: NP_114148.1

1 11 21 31 41 51
 5 MDARRVPQKD LRVKKNLKKF RYVKLISMET SSSDDSDSDS PASDNFANTR LQSVREGCRT 60
 RSQCRHSGPL RVAMKFPARS TRGATNKKAE SRQPSSENSVT DSNDSDEDES GMPLEKRAL 120
 NIKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRRPR RRTFPGVASR RNPERRARPL 180
 TRSRSRILGS LDALPMEEEE EEDKYMLVRK RKTVDGYMNE DDLPRSSRRS SSVTLPHIIR 240
 10 PVEEITEGGV SERLQQPSKR RYITVHWALL VINAVRLLI PKQTAETQTA GAPEASSVAP 300
 AFETVMVKRS GMLCWIRTGI ARLVEESATA VSAGSEMDGV RLGLSLCI 347

Seq ID NO: C247 Protein Sequence
Protein Accession #: NP_036577.1

1 11 21 31 41 51
 15 MENPSPAAL GKALCALLLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAFPKQY 60
 PLFRPPAQWS SLGAHAHSSD YSMWRKNQYV SNGLRDPFAER GEAWALMKEI EAAGEALQSV 120
 HAVFSAVAVP SGTGQTSAEL EVQRHSLVS FVVRIVPSPD WFGVDSLDL CDGDRWREQA 180
 20 ALDLYPYDAG TDSQGTFFSSP NFATIPQDTV TEITSSSPSH PANSFYYPRL KALPPIARVT 240
 LVRLRQSPRA FIPFAPVLPs RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GRCGLGTSKS 300
 RTRYVRVQPA NNGSPCELE EEAECVPDNC V 331

Seq ID NO: C248 Protein Sequence
Protein Accession #: NP_063947.1

1 11 21 31 41 51
 30 MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIVV VLIKVILDKY 60
 YFLOGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSPFEPG AVAVRLSKOR STLQVLOSAT 120
 GWNFSGACPDN FTALAEATAC RQMGYSKSPK FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
 GPCLSGSLVS LHLCLAGKSL KTRPVVGGEE ASVDSWPWQV SIQYDKQHVC GGSILDPHWV 240
 LTAHCFRKH TDVFNKVKRA GSKLGSFSP LAVAKIIIE FNPMPKND IALMLQFPL 300
 35 TFSQTVRPIK LPFFDEELTP ATPLWIIGWG PTKQNGGKMS DILLQASQV IDSTRNADD 360
 AYQGEVTEGM MCAGIPEGGV DTCQGDSDGG LMYQSDQHWV VGIWSWGYGC GGPSTPGVYT 420
 KVSAYLNWLY NVWKAL 437

Seq ID NO: C249 Protein Sequence
Protein Accession #: NP_003036.1

1 11 21 31 41 51
 40 MGCKVLINIG QQLRRKVVVD CSREBTRLSR CLNTFDLVAL GVGSTLGAGV YVLGAVARE 60
 NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTGELWA FITGNLILS 120
 45 YIIGTSSVAR AWSATFDEL GRPIGEFSRT HMTLNAPGVL AENPDIPAVI IILILTGLLT 180
 LGVKESAMVN KIFTCINLV LGFIMVSGVF KGSVKNQLT EEDFGNTSGR LCLNNDTKEG 240
 KPGVGGLFMP GFSGLVSGAA TCFYAFVGF CIATTGEEVK NPQKAI PVGI VASLLICFIA 300
 YFGVSAALIT MPMYFCLDNN SPLPDAFKHV GWGAKYAVA VGSLCALSAS LLGSMFMPMR 360
 50 VIYAAEDGL LFKFLANVND RTKTPIIATL ASGAVAAVMA FLFDLKDLDV LMSIGTLAY 420
 SLVAACVLVL RYQPEQNLV YQMASTSDLE DPADQNELAS TNDSQLGLFLP EAEMFSLKTI 480
 LSPKNMEPSK ISGLIVNIST SLIAVLIIT CIVTVLGRE A LTKGALWAVF LLAGSALLCA 540
 VVTGVIWRQP ESKTKLSFKV PFLPVLPILS IFNVVYLMMQ LDQGTWRVPA VWMLIGFTIY 600
 FGYGLWHESE ASLDADQART PDGNLDQCK 629

Seq ID NO: C250 Protein Sequence
Protein Accession #: NP_002767.1

1 11 21 31 41 51
 60 MRAPHLHLISA ASGARALAKL LPLLMAQLWA AEAALLPOND TRLDPEAYGA PCARGSQPWQ 60
 VSLFNGLSFH CAGVLVDQSW VLTAAHCCNK PLWARVGDH LLLLQGEQLR RTRRSVVHFK 120
 YHQSGSPILP RRTDEHDLML LKLARPVVPG PRVRAQLQPY RCAQPGDQCQ VAGWGTTAAR 180
 RVKYNKGLTC SSITILSPKE CEVFPYGVVT NNMICAGLDR GQDPQSDSG GPLVCDDELQ 240
 65 GILSWGVYPC GSAQHPAVYT QICKYMSWIN KVRISN 276

Seq ID NO: C251 Protein Sequence
Protein Accession #: XP_095088.3

1 11 21 31 41 51
 70 MTRAAATBEP RVSPASPARS TAGLPRAFLO SLRTLLDILD DWQRGCVHLR EIQLNVEAR 60
 ELPSGVLEGL SQRRGPQPGA AVSRRRGGAV PRGARAVPER CAGTETRGR RCSGLQRLGG 120
 GFRGCPADPC ARGEHRRHTI TSGVDCGLLK QMKELEQKE VLLQGLEMA QGRDWYQQQL 180
 75 QQVQERQRL GQSRASADFG AVGSPRPLGR LLPKVQEVAR WLGLLAEAC AGRALPTSSS 240
 GPCCSALTST SSPGWQQII LMLKEQNRL TQEVTEKSER ITQLEQKSAL IKQLFEARAL 300
 SQDGLGLSPA PHIEPLTRP RLPVLTWAGA LLSPHSPQLL LPLSADSGGP LHLPDTWFF 360
 AVLAVVPSPG KRTAHARLHF HQRPAEGAWQ LGCGAEAAPE TCGTLPHFES HKTCCEPDSL 420
 GGPCPQEGDR SWSHLGAADF VAPAVAKVTF NREDAAGSRH GDICPLCPKG LLTFRDIAIE 480
 80 FSLAEWQCLD HQQNLVYRDV MLENYRNLF S LGMTVSKPDL IACLEQNKEP QNKRNEMAA 540
 KHPVTCSEFN QDLQPEBSIK DSIQKVIPRT YGKCGHENLQ LKCKCKRVDE CEVHKGGYND 600
 LNQCLSNTQN KIFQTHKCVK VFSKPSNSNR HNARYTGKHK LKCKKYGKSF CMPSHLNQHQ 660
 IHTKEKSYK CEECGKSPNH SSGTTHKRI LTGEKPYRCE EOGKAPRWPS NLTRHKRIHT 720
 GEKPYACEEC GQAFRRSSTL TNHRIHTGE RPYKCECGK AFSVSSALIY HKRIHTGEKP 780
 YTCECGKAP NCSSTLTKTHK IHTGEKPYT CEEGRTFNC SSTVKAHKRI HTGEKPYKCE 840

5
10
ECDAKFWKHS SLAKHKIHT GEKPYKCSDS KALAKSSEVQ KVSXGDEGNG IRVHKKKETO 900
GWLVRNKNEN RTGLFQIRAA VRPNRDPSPG QOEGSLDPI QRKEEPDLQN HYDHQNALED 960
QNTGVGGLL TFRDVIIEFS LEEMQCLDHA QONLYRDVML ENYRNLVSLG IAVSKPDLIT 1020
CLEQNKEPWN IKRNMVTKH PDLPPELGIK DSLQKVIPRR YKSGHDNLQ VKTCKSMGEC 1080
EVQKGGCNEV NQCLSTTQNK IFQTHKCVKV FGKFSNSNRH KTRHTGKKHF KCKCYGKSFC 1140
MVSQHLQHQI IHTRENSYQC EBCGKPFNCB STLSKHKRIH TGEKPYRCEE CGKAPTWSST 1200
LTKHRRHTG EKPYTCBECG QAFSRSSSTA NHKRIHTGEK PYTCBECGKA PSLSSSLTYH 1260
KRIHTGEKPY TCCECGKAFN CSSTLKHKHI IHTGEKPYKC KECGKAFAPS STLNTHKRIH 1320
TGEFPYKCEE CDKAFKWSSS LANHKSMTGT EKPYKCE 1357

Seq ID NO: C252 Protein Sequence
Protein Accession #: NP_114433.1

15
1 11 21 31 41 51
MASRSMRLLL LLSCIAKTGV LGDIIMRPSC APGWPHYKSN CYGYFRKLRLN WSDAELECOQS 60
YNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLYRSWSG 120
KSMGDNKHC AEMSSNNFLT WSSNECNKRQ HFLCKYRP 158

20
Seq ID NO: C253 Protein Sequence
Protein Accession #: XP_051860.2

25
30
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40
1 11 21 31 41 51
MDGVNLSTEV VYKKGQDYRF ACYDRGRACR SYRVRFLCGK PVRPKLTVTI DTNNVSTILN 60
LEDNVQSWKP GDTLVIATSD YSMYQAEFQ VLPSCRSCAPN QVKVAGKPMY LHIGSEIDGV 120
DMRAEVLGLS RNIIVMGEME DKCYPYRNHI CNFFDFDTFG GHIFPALGPK AHALEGTELK 180
HMQQQLVGQY PIHFHLAGDV DERGGYDPPY YIRDLSTHHT FSRCTVTHGS NGLLIKDVG 240
YNSLGHCFPT EDGPERNTP DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300
DCNAVSTFW ANPNMNLINC AAGSEETGF WPIFHHVPTG PSVGMYSFGY SEHIPGLGKY 360
NNRAHNSYRA GMIDNGVKT TEASAKDKRP FLSTISARYS PHQDADPLKP REPAIRHFI 420
AYKNQDHGAW LRGGDWLDS CRFADNGIGL TLASGGTFPY DDGSKQELIK SLFVGESGNV 480
GTEMMDNRIW GPGLDHSGR TLPICQNFPI RGIQLYDGPI NIQCTFRKP VALEGRHTSA 540
LAFRLNNAW SCPHNVTGI AFEDVPITSR VFFGEPGFWP NQLDMDGDKT SVFHDVDSV 600
SEYPGSYLTN NDNLVVRHPD CINVPDWRGA ICSGCYQMY IQAYKTSNLR MKIINKDFPS 660
HPLYLBSALT RSTHYQQYQP VVTLQKGYTI HWDQTAPAEI AIWLINFNKG DWIRVGLCYP 720
RGTTFSILSD VHNRLKQTS KTGVPVRLTQ MDKVEQSYPG RSHYYWDEDS GLLFLKLQAQ 780
NEREKPAFCS MKGCERIKIK ALIPKNAGVS DCTATAYPKF TERAVVDVPM PKKLPGSQLK 840
TKDHFLEVM ESKQHFFHL WNDPAYIEVD GKYPSSSEDG IQVVVIDGNQ GRVVSHTSFR 900
NSILQGIPIW LFNYVATIPD NSIVLMASKG RYVSRGPWTR VLEKLADARG LKLKEQMAFV 960
GFKGSFRPIW VTLDTEHKA KIFQVVPFV VKKKKL 996

Seq ID NO: C254 Protein Sequence
Protein Accession #: NP_055188.1

45
50
1 11 21 31 41 51
MTALSSENC SFOYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLGMRRKNT CQNFMEYFCI 60
SLAFVDDLLL VNISILYFR DFLVLSIRFT KYHICLPTQI ISFTYGFLEY PVFLTACIDY 120
CLNFSKTKTL SFKQKLFYF FTVILLIWSV LAYVLGDPAL YQSLKAQNAV SRHCPFYVSI 180
QSYWLSFFMV MILKVAITC WEEVTLVQA IRTSYMNET ILYFPFSSHS SYTVRSKKIF 240
LSKLIVCFLS TWLPFVLQV IIVLLKVQIP AYIEMNIPWL YFVNSFLIAT VYWFNCHKLN 300
LKDGLFLDP FVNNKCFPI LTIPNLEQIE KPISIMIC 338

55
Seq ID NO: C255 Protein Sequence
Protein Accession #: Eos sequence

60
65
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75
1 11 21 31 41 51
MALVLGSLLL LGLCGNSFSG QPSSSTDAPK AMNYELPATN YETQDSHKAG PIGILFELVH 60
IFLYVVQPRD FPEDTLRKPL QKAYESKIDY DKIVYYEAGI ILCCVLGLLF IILMPLVGYF 120
FCMCRCCNKC GGEMHQKQKE NGPFLRKCPA ISLLVICIII SIGIFYGFVA NHQVTRIKR 180
SRKLADSNFK DLRTLLNETP EKIYILAQY NTKDKAPTQ LNSINSVLGG GILDRLRPNI 240
IPVLDEIKSM ATAIKETKEA LENMNSTLKS LHQOSTQLSS SLTSVKTSLR SSLNDPLCLV 300
HPSSETCNSI RLSSLQNLNS PELRQLPPVD AELDNVNVVL RTDLGLVQV GYQSLNDIPD 360
RVQRQTTTV AGIKRVLNSI GSDIDNVTR LPIQDILSAF SVYVNTESY IHRNLPTLEE 420
YDSYWLGLL VICSLTLTIV IFYLLGLLGG VCGYDRHATP TTRGCVSNTG GVPLMVGVGL 480
SFLFCWILMI IIVLTFVFGA NVEKLICEPY TSKEFLRVLD TPYLLNEDWE YYLSGKLPNK 540
SKMKLTPEQV YSDCKKNRGT YGTLHLQNSF NISEHLNINE HTGSISSELE SLKVNLAIFL 600
LGAAGRKNLQ DFAACGIDRM NYDSYLAQTG KSPAGVNLSS PAYDLKAXN SLPPGNLRNS 660
LKRDAQTKT IHQQRVLPIE QSLSTLYQSV KILQRTGNGL LERVTRILAS LDFAQNPITN 720
NTSSVIEET KYGRTIIGY FEHYLQWIEF SISEKVASC PVATALDTAV DVFLCSYIID 780
PLNLPWFGLG KATVFLPAL IFAVKLAKY RRMDSQDVYD DVETIPMKMN ENGNNGYHKO 840
HVGIGHNPMV TSPSQH 856

Seq ID NO: C256 Protein Sequence
Protein Accession #: NP_149038.1

80
1 11 21 31 41 51
MKAIHLTL LALLSVNTATN QGNSADAVTT TETATSGPTV AAADTTETNF PETASTTANT 60
PSFPTATSPA PPIIETHSSS TIPTAPPII STHSSSTIPI PTAADSESTI NVNLSATSDI 120
ITASSPDQL ITMVPSETQS NNEMSPTEED NQSSGPPTGT ALLETSTLNS TGPSNCPQDD 180
PCADNSLCVK LHNTSFLCL EGYYSNSTC KKGKVPFGKI SVTVSETFDP EEKHSMAQQD 240

5
 LHSEITSLPK DVFGTSVYQ TVILTVSTSL SPRSEMRADD KFNVTIVITI LAETTSDBNEK 300
 TVTEKINKAI RSSSSNPLNY DLTLRCDYYG CNQTADDCLN GLACDCKSDL QRPNPQSPFC 360
 VASSLKCPDA CNAQHKQCLI KKSOGAPECA CVPGYQEDAN GNCQKCAFYG SGLDCKDKFQ 420
 LILITIVGTIA GIVILSMIIA LIVTARSNNK TKHIEENLI DEDFQNLKLR STGFTNLGAE 480
 GSVFPKVRIT ASRDSQMNP YSRHSSMPRP DY 512

Seq ID NO: C257 Protein Sequence
 Protein Accession #: NP_001423.1

10
 1 11 21 31 41 51
 | | | | |
 MTAGRRMEL CAGRVPALLL CLGPHLLQAV LSTTVIPSCI PGESSDNCTA LVQTEDNPRV 60
 AQVSIKCSS DMNGYCLRGQ CIYLVDMSON YCRCEVGYTG VRCEHFFLTV HQPLSKEYVA 120
 15 LTVILILFL ITVVGSTYYP CRWYRNKRSK EPKKEYERVT SGDPFLPQV 169

Seq ID NO: C258 Protein Sequence
 Protein Accession #: AAC63902.1

20
 1 11 21 31 41 51
 | | | | |
 MDRSKENCIS GPVKATAPVG GPKRVLVLTQQ IPCQNPLPVN SGOAQRVLCF SNSSQVRVPLQ 60
 AQKLVSSHKP VQNKQKQQLQ ATSVHPVSR PLNNTQKSKQ PLPSAPENNP EBELASKQKN 120
 ESKRKQWAL EDFEIGRPLG KGKFGNVILA REKQSKFILA LKVLFAQLE KAGVEHQLRR 180
 25 EVEIQSHLRH PNILRLYGYF HDATRVYLIL EYAPLGTVYR ELQRLSKFDE QRTATYITEL 240
 ANALSYCHSK RVIHREDIKPE NLLLSAGEL KIADFGWSVH APSRRRTTLC GTLDYLPPEM 300
 IEGRMHDEKV DLWSLGLVLCY EPLVGKPPFE ANTYQETYKR ISRVEPTFD FVTEGARDLI 360
 SRLLKHNPSQ RPLMLREVLEH PWITANSKPK SNOQNKESAS KQS 403

30
 Seq ID NO: C259 Protein Sequence
 Protein Accession #: NP_037504.1

35
 1 11 21 31 41 51
 | | | | |
 MSRTAYTVGA LLLLLGTLLP AAEKKKKSQ GAIPPPDKAQ HNDSEQTQSP QPGSRNRGR 60
 GQGRGTAMPG EEVLESSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFCYG 120
 QCNSEYIPRH IRKEBGSFQS CSFCKPKKFT TMMVTINLCE LQPPTKKKRV TRVKQCRCIS 180
 IDLD 184

40
 Seq ID NO: C260 Protein Sequence
 Protein Accession #: Eos sequence

45
 1 11 21 31 41 51
 | | | | |
 MKVGVWLWIS FFTFDGHGG FLGKNDGIKT KKEILVNKKK HLGPEEYQL LLQVTYRDSK 60
 EKRDLRNLK LLKPPLWNSH GLIRIIRAKA TTDCLNLGV LQCTCEDSYT WFPSPCLDPQ 120
 NCYLHTAGAL PSCECHLNL SQSVNFCERT KIWGTFKINE RPTNDLLNS SAIYSKYANG 180
 IEIQLKAYE RIQGFESVQV TQFRNGSIVA GYEVVGSSSA SELLSAIEHV AEKAKTALHK 240
 LPFLLEDGSR VFGKAQNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV 300
 50 LSLLEELNKN FSMIVGNATE AAVSSFVQNL SVIIRQNPST TVGNLASVVS ILSNISLSL 360
 ASHFRVSNST MEDVISIADN ILSASVTNW TVLLREEKVA SSRLLSTLEN ISTLVPP TAL 420
 PLNPSRKFID WKGIPVNSQ LKRGYSYQIK MCPQNTSIFI RGRVLIGSDQ FQRLPETII 480
 SMASLTIGNI LPSKNGNAQ VNGPVISTVI QNYSINEVFL FFSKIESNLS QPHCVFWDPS 540
 HLQWNDAGCH LVNETQDIPT CQCTHLTSFS ILMSPFVPST IFPVVKNTY VGLGISIGSL 600
 55 ILCLIEALF WKQIKKSQTS HTRRIQMVNI ALSLLIADVM FTVGATVDT VNPSCVCTAA 660
 VFFTHFYLS LFFWMLMGI LLAYRIILVF HHMAQHLMA VGFCLGYGCP LIISVITIAV 720
 TQPSNTYKRR DVCWLNWSNG SKPLAFVVP ALAIVAVNFV VVLLVLTKLW RPTVGERLSR 780
 DDKATIIIRVG KSLILITPLL GLTWGFGIGT IVDSQNLAWH VIFALLNAFQ GFFILCFGIL 840
 LDSKLRLQLF NKLSALSSWK QTEKQSSDL SAKPKFSKFP NPLQNKGHYA PSHTGDSSDN 900
 60 IMLTQFVNSE 910

Seq ID NO: C261 Protein Sequence
 Protein Accession #: NP_000575.1

65
 1 11 21 31 41 51
 | | | | |
 MTSKLAVALL AAFILISAALC EGAVLFRSAK ELRCQCIKTY SKPFHPKFIK ELRVIESGPH 60
 CANTEIIVKL SDGRELCIDP KENWVQRVVE KFLKRAENS 99

70
 Seq ID NO: C262 Protein Sequence
 Protein Accession #: NP_005594.1

75
 1 11 21 31 41 51
 | | | | |
 MSTERDSETT FDEDSQPNDE VVPYSDDETE DELDDQGS AV EPQNRVNRE AEENREPFRR 60
 ECTWQVKAND RKYHEQPHFM NTKFLCIKES KYANNAIKTY KYNAFTPIPM NLPEQPKRAA 120
 NLYPLALLIL QAVPQISTLA WYTTLVPLLV VLGVTAKDL VDDVARHMD KEINNRTCEV 180
 IKDGRFKVAK WKEIQGVQVI RLKKNDFVFA DILLSSSEP NSLCYVETAE LDGETNLKFK 240
 MSLEITDQYL QREDTILATFD GFIECEPMN RLDKFTGTLF WRNTSFPLDA DKILLRGCVI 300
 80 RNTDFCHGLV IFAGADTRIM KNSGKTRFKR TKIDYLMNYM VYTIFFVVLIL LSAGLAIGHA 360
 YNEAQVGNSS WLYLDGEDT PSYRGFLIFW GYIIVLNTMV PISLYVSVEV IRLGQSHFIN 420
 WDLQMYAEK DTPAKARTTT LNEQLGQIHF IPSDKTGLT QNIMTFKKCC INQIYGDHR 480
 DASQHNHMK EQVDFSWNTY ADGKLAFVDH YLIEQIQSGK EPEVRQFFFL LAVCHTVMD 540
 RTDQQLNYQA ASPDEGALVN AARNFGFAFL ARTQNTITIS ELGTERTYV LAILDPMNDR 600
 KRMSIIVRTP EGNIKLYCKG ADTVIYERLH RMNPTKQETO DALDIPANET LRTLCLCYKE 660

5 IEEKEFTSMN KKFMAASVAS TNRDEALDKV YEEIEKDLIL LGATAIEDKL QDGVPEITISK 720
 LAKADIKIWI LTGDKKETAE NIGFACELLT EDTTICYGED INSLHARME NORNRGGVYA 780
 KFAPVQESP FPPGKNRALI ITGSMWLEIL LEKKTTRNKI LKLFPRTEE ERRMRTQSKR 840
 RLEAKKEQRQ KNFVDLACEC SAVICCRVTP KQKAMVVDLV KRYKKAITLA IGDGANDVRM 900
 IKTAHIGVGI SQEGMQAVM SSDYSFAQFR YLQRLLLVHG RWSYIRMCKF LRYFFYKNPA 960
 FTLVHFWYSF FNGYSAQTAY EDWFITLYNV LYTSPLVLLM GLLDQDVSDK LSLRFPGLYI 1020
 VQORDLLFNY KRFFVSLHGH VLTSMLPFI PLGAYLQTVG QDGEAPSDVQ SFAVTIASAL 1080
 VITVNFQIGL DTSYWTFFNA FSIFGSIALY FGIMFDFHSA GIHVLFPSPAF QFTGTASNAL 1140
 10 RQPYIWLIII LTVAVCLLPV VAIRFLSMTI WPSEDKIQK HRKRLKAEQ WQRRQQVFRR 1200
 GVSTRRSAYA FSHQRGYADL ISSGRSIRKK RSLDAIVAD GTAERYRTGD S 1251

Seq ID NO: C263 Protein Sequence
 Protein Accession #: XM_044533

15 1 11 21 31 41 51
 MLRTAMGLRS WLAAPWALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60
 RFEAEHISNY TALLSRDGR TLYVGAREAL FALSSNLSPL PGGEYQELLW GADAEKKQQC 120
 20 SPKGDQPRD CQNYIKILLP LSGSHLFTCG TAAFSPMCTY INMENFTLAR DEKGNVLLED 180
 GKGRCPFPFN FSKTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SLNWLQDPAF 240
 VASAVIPESL GSIQQDDDKI YFFPSETGQE FEFENTIVS RIARICKGDE GGERVLQQRW 300
 TSFLKAQLLC SRPDGFPFN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV 360
 FTKMDVQVVF SGLYKEVNR TQMYTIVTTP VTPRPGACI TNSARERKIN SSLQLPDRVL 420
 25 NFKDHFIMD QVRSRMLLL QPQARYQVVA VHRVPLGHT YDVLFLGTGD GRLHKAVSVG 480
 PRVHIIIEELQ IFSSGQPVQN LLLDTHRGLL YAAHSGVVQ VPMANCSLYR SCGDCLLARD 540
 PYCAWSSSC KHVSLYQPOL ATRPWIQDIE GASAKDLCSA SSVVSPSFVP TGEKPCQVQ 600
 FQNTVNTLA CPILSNLATR LWLNRGAPVN ASASCHVLT GDLLVLGTQD LGFQPCWSLE 660
 EGGQQLVASY CPVVEDGVA DQTDGGGSPV VIISTSRVSA PAGGKASWA DRSYNKEFLV 720
 30 MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST 780
 PLDHRYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS BIRDSVV 837

Seq ID NO: C264 Protein Sequence
 Protein Accession #: NP_008950.1

35 1 11 21 31 41 51
 MASQNRDPA TSVAAARKGA EPSGGAARGP VGKRLQQLM TLMMSGDKGI SAFFESDNLF 60
 KVVGTIHGAA GTVYEDLRYK LSLEFPSPGY YNAPTVMKLT PCYHFNVDQ GNICLDILKE 120
 40 KWSALYDVRT ILLSIQSLLG BPNIDSPLNT HAAELWKNPT AFKKYLQETY SKQVTSQEP 179

Seq ID NO: C265 Protein Sequence
 Protein Accession #: NP_055399.1

45 1 11 21 31 41 51
 MGRGWGFLFG LLGAVLLSS GHGEEQPPET AAQRCFCQVS GYLLDDCTCDV ETIDRFNNYR 60
 LFPRLQKLE SDYFRYKYVN LKRPCPFWMD ISQCGRRDCA VKPCQSDVFP DGKKSASYKY 120
 SEEANLIEE CEQAERLGA DESLSEBTQK AVLQNTKIDD SSDNFCADD IQSPBAEYVD 180
 50 LLLNPERYTG YKGPDAWKI NVIYEENCFK PQTIKRPLNP LASGQGTSEE NTFYSWLEGL 240
 CVERAFYRL ISGLHASINV HLSARYLLQE TWLEKKWGHN ITEPQQRFDG ILTEGEGPRR 300
 LKNLYFLYLI ELRALSKVLP FFERPDPQLF TGNKIQDEEN KMLLEILHE IKSFPPLHFE 360
 NSFFAGDKKE AHKLKEDFRL HFRNISRIMD CVGCFKRLW GKLTQGLGT ALKILFSEKL 420
 IANMPESGPS YEFILTRQEI VSLFNAFGRI STSVKELENF RNLLQNIH 468

55 Seq ID NO: C266 Protein Sequence
 Protein Accession #: NP_002879.1

60 1 11 21 31 41 51
 MQPRRQLPA FWSGPRGPRP TAPLLALLL LAPVAAPAGS GGPDDFGQPQ DAGVPRRLQ 60
 QKARAALHFF NFRSGSPSAL RVLAEOBGR AWINPKEGCK VHVVFSTERY NPESLLQEGE 120
 GRLGKCSARV FFKNQKPRPT INVTCTRIE KKKRQQEDYL LYKQMKQLXN PLEIVSIPDN 180
 HGHIDPSLRL IWDLAFGLSS YVMWEMTTQV SHYLAQLTS VRQWVRKT 228

65 Seq ID NO: C267 Protein Sequence
 Protein Accession #: NP_005400.1

70 1 11 21 31 41 51
 MSVKGMAIAL AVILCATVVQ GFPMFKRGRC LCIGPGVKAV KVADIEKASI MYPNNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF 94

75 Seq ID NO: C268 Protein Sequence
 Protein Accession #: FGENESH predicted

80 1 11 21 31 41 51
 MLRQVLRRLG QSFCHRLGLC VSRHPVFFLT VPAVLITITFG LSALNRFQPE GDLERLVAPS 60
 HSLAKIERSL ASSLFPLDQS KSQLYSDLHT PGRYGRVILL SPTGDNILLQ AEGILQTHRA 120
 VLEMKVNHKG YNYTFSHLCV LRNQDKKCVL DDIISVLEDL RQAAVSNKTT ARVQVRYFNT 180
 KLVKCSFCML LPIKEAALHP LP 202

Seq ID NO: C269 Protein Sequence
 Protein Accession #: NP_002429.1

	1	11	21	31	41	51	
5	MRLPLLLVFA	SVIPGAVLLL	DTRQFLIYNE	DHKRCVDAVS	PSAVQTAACN	QDAESQKFRW	60
	VSESQIMSV	FKLCLGVPSK	TDWVAITLYA	CDSKSEFQKW	ECKNDTLLGI	KGEDLFFNYG	120
	NRQEKINIMLY	KSGGLWSRWK	IYGTDDNLCS	RGYEAMYTLL	GNANGATCAF	PFKFENKMYA	180
	DCTSAGRSDG	WLNCGTTTDDY	DTDRLPGYCP	LKFESESLSW	NKDPLTSVSY	QINSKSALTW	240
	HQARKSCQQQ	NABELLSITEI	HEQTYLTGLT	SSLTSGLWIG	LNSLSFNNGW	QWSDRSPFRY	300
10	LNLWPGSPSA	EPGKSCVSLN	PGKNKAWENL	ECVQRLGYIC	KKGNTTLNSF	VIPSESDVPT	360
	HCPSQMWPYA	GHCYKIHRE	KKIQRDALTT	CRKEGGDLTS	IHTIEELDFI	ISQLGYEPND	420
	ELWIGLANDIK	IQMYFWSG	TPVTFTKWL	GEPSHENNRQ	EDCVVMKGD	GYWADRGCEW	480
	PLGYICKMKS	RSQGPPIVEV	EKGCRCGWK	HHFYCYMIGH	TLSTFAEANQ	TCNNENAYLT	540
	TIEDRYEAP	LTSFVGLRPE	KYFWTGLSDI	QTKGTFTQTI	EDEVFTWNN	SDMPGRKPGC	600
	VAMRTGIAGG	LWDVLKCEK	AKFVCKHWA	GVTHPPKPTT	TEPKCPEDW	GASSRTSLCF	660
15	KLVAKGHEK	KTFWESRDFC	RALGGDLASI	NNKBEQQTIN	RLITASGSYH	KLFWLGLTYG	720
	SPSEGFTWSD	GSPVSYENWA	YGEFNYYQNV	EYCGELKGD	TMSWMDINCE	HLNNWICQIQ	780
	KGQTPKPEPT	PAPQDNPPPT	EDGWVIYKDY	QYFYSKEKET	MDNARAFCKR	NFGDLVSIQS	840
	ESEKFLKFWY	VNRNDQAQAY	FIGLLISLKD	KFAMMDGSKV	DYVSWATGEP	NFANEDENCV	900
20	TMYSNGSGFW	DINCGYPNAF	ICQRENSGIN	ATTVMPTMS	VPSGCKEGWN	FYSNCKCFKIF	960
	GFMEBERKMW	QBARAKACIGF	GGNLVSIQNE	KEQAFITYHM	KDSTFSAWGT	LNDVNSEHTF	1020
	LWTDGRGVHY	TNWGKGYPGG	RRSSLSYEDA	DCVVIIGGAS	NEAGKWMDDT	CDSKRGYICQ	1080
	TRSDPSLTNP	PATIQDGFV	KYKSSYSLSM	RQKQWHEAE	TYCKLHNSLI	ASILDOPYSNA	1140
	FAWLQMETSN	ERVWIALNSN	LTDNQYTWD	KWRVRYTNWA	ADEPKLSKAC	VYLDLDGYWK	1200
	TAHCNESFFY	LCKRSDIPA	TEPPQLPGR	PSDHTANIP	FHGHYCYIES	SYTRNMGQAS	1260
25	LECLRMGSSL	VSIESAAESS	FLSYRVEFLK	SKTNEWIGLP	RNVQGTWLN	NNSPVSPVNW	1320
	NTGDPGGERN	DCVALHASSG	FWSNIHCSSY	KGYICKRPKI	IDAKPHELL	TTKADTRKMD	1380
	PSKPSSNVAG	VVIIVILLIL	TGAGLAAYFF	YKKRRVHLQ	EGAFENTLYP	NSQSSPGTSD	1440
	MKDLVGNIEQ	NEHSVI					1456

Seq ID NO: C270 Protein Sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
35	MVLLHWCLLW	LLFPLSSRTQ	KLPTRDEELF	QMQIRDKAPP	HDSSVIPDGA	EISSYLFRDT	60
	PKRYFPVVEE	DNTPLSVTVT	PCDAPLEWKL	SLQELPEDRS	GBGSGDLEPL	EQKQOIINE	120
	EGTELFSYKG	NDVEYFISSS	SPSGLYQLDL	LSTKEDTHFK	VYATTPESD	QPYPELPYDP	180
	RVDVTSLGRT	TVTLAWKPS	TASLLKQPIQ	YCVVINKEHN	FKSLCAVEAK	LSADDAFMA	240
	KPKGLDFSPF	DFAHFGPPSD	NSGKERSFQA	KPSPKLRHV	YSRPKVDIQK	ICIGNKNIFT	300
40	VSDLKPDQY	YFDVFNIN	SNMSTAYVGT	FARTKEERAK	KTVELKDGKI	TDVFKRKA	360
	KFLRPAFVSS	HQKVTFFIHS	CLDAVQIQVR	RDGKLLLSQN	VEGIQQFQLR	GKPKAKYLVR	420
	LKGNKKGASM	LKILATTRPT	KQSPFSLPED	TRIKAFDKLR	TCSSATVAWL	GTQERNKFCI	480
	YKKEVDNWN	EDQKKREQNG	CLGPDIRKKS	EKVLCKYFHS	QNLQKAVTTE	TIKGLQPGKS	540
45	YLLDVVYIGH	GGHSVKYQSK	VVKTRKFC				568

Seq ID NO: C271 Protein Sequence
Protein Accession #: AAH34229.1

	1	11	21	31	41	51	
50	MEKVQLEFEN	QEMKQLQEF	RSTRNKEKED	RESSEYWKKS	GKVGKLVNQS	YMSQNKGNV	60
	VKPSAGKVKL	KLLKEQIQEP	VKPTVNYKMA	NSSECEKPKI	NGKVCQCCEN	KAALLVLEC	120
	GEDYCSGCPA	NVHQKALKL	HRTTLQARS	QILFNVLDA	HQPIKDVNPD	EPKEENNSTK	180
	ETSKIQHKPK	SVLLQSSSE	VEITTMKRAQ	RTKPRKSLLC	EGSFDEEASA	QSPQEVLSQW	240
55	RTGNHDDNKK	QNLHAAVKDS	LEECEVQTNL	KIWRBEFLNIE	LKEDILSYME	KLWLKIGHRT	300
	PQEQQLFCYQ	IRSHIEMKPL	VMSVLRMKT	MKIVMVRPK	YNTQLFYCQ		349

Seq ID NO: C272 Protein Sequence
Protein Accession #: NP_078963.1

	1	11	21	31	41	51	
60	MEKMLWKHHR	RTPQEQLFKM	LSDTFFHPHE	TTGDAQCSQN	ENDESDGEE	TKVQHTALLL	60
	PVETLNIERP	EPSLKIVELD	DTYEEEFERA	ENIVPYKVKL	ADADSQRSCA	FHDQCKNSFP	120
65	YENGHQHVF	FDKGRDFLN	LCLRNSSTY	KDNSKGETSN	TDFDNIVDPD	VYSSDIEKIE	180
	ESTSEERNLK	EKNIGLESNQ	KSDDSVSLSE	SKOTLLGRDL	EKAPIEEKLS	QDIKESLELS	240
	NLYKRPSFEE	SKTTKSSLLL	QBIACRSKPI	TKQYQGLERF	PIFDTNERLN	LLPSHRLN	300
	NSSTRITLAE	DREWIPDHS	SEYADNAIVL	GVLQGAQSPS	SSRKQQRMG	KSRPSTANF	360
	PLNSVKESS	SCLSSSHPRS	RSAAAQSSSR	AASEISEIEY	IDITDQNELS	LDQTTDQHTL	420
70	DNLEKELQVL	RSLADTSEKL	YSLTSEEFDP	FSSQSLNISQ	ISTDFLKTSH	VRGPGVEEL	480
	SCSGRDTKIQ	SLLSLSESST	DEEEDFLNK	QHVITLFWSK	ST		522

Seq ID NO: C273 Protein Sequence
Protein Accession #: NP_005399.1

	1	11	21	31	41	51	
75	MKVSALLLCL	LIMTAAPNPQ	GLAQPDALNV	PSTOCFTFSS	KKISLQRLKS	YVITTSRCPC	60
80	KAVIFRTKLG	KETCADPKKE	WVQNYMRHLG	RKARTLKT			98

Seq ID NO: C274 Protein Sequence
Protein Accession #: BAC05158.1

	1	11	21	31	41	51
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MFLLTGGVSL	KSAEKNPDPT	WLQDKSWEEI	CRASEFPAPR	GLRQHPCEHI	YEWREIYDSK	60
EPHNAKFPAP	MDKNLNELOK	IIILRCLRPD	KITPAITNYV	TDKLGKKFVE	PPPDFLTKSY	120
LDSNCTIPLI	FVLSPGADPM	ASLLKFANDK	SMSGNKFAQI	SLGQGGQPIA	AKMIKAAIEE	180
GTWVCLQNCB	LAVSWMPMLE	KICEDFTSET	CNSSFRLWLT	SYPSKFPVPT	ILQNGVMTN	240
EPPTGLRLNL	LQSYLTDPVS	DPEFFKGCRC	KELLFINEYD	TIPFEAISYL	TGECNYGGRV	300
TDDWDRRELL	TMLADFYNLY	IVENPHYKFS	PSGNYFAPPK	GTVEDYIERFI	KKLPFTQHPE	360
IPGLHENVDI	SKDLQQTCTL	FESLLLTQGG	SKQTGASGST	DQILLEITKD	ILNKLPSDFD	420
IEMALRKYPV	RYEESMNTVL	VQEMERFNNL	IITIRNTLRD	LEKAIKGVV	MDSALEALSS	480
SLLVGKVPFI	NAKRSYPSLK	PLGSYITDFL	ARLNFLQDWY	NSGKPCVFWL	SGFFFTQAPL	540
TGAMQNYARK	YTFPIDLLGY	BFEVIPSOTS	DTSPEDGVYI	HGLYLDGARN	DRESGLLAEQ	600
YPKLLFDLMP	IIWIKPTQKS	RIIKSDAYVC	PLYKTSERKG	TLSTTGHSTN	FVIAMLLKTD	660
QPTRHWIKRG	VALLCQLDD					679

Seq ID NO: C275 Protein Sequence
Protein Accession #: AAA60212.1

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MAESHLQLWL	LLLLPTLCGP	GTAAWTSSL	ACAQGPEFWC	QSLQALQCR	ALGHCLQEVN	60
GHVADDLCQ	ECEDIVHILN	KMAKEAIFQD	TMRKPLEQEC	NVLPLKLIMP	QCNQVLDLDP	120
PLVIDYFQNG	TDSNGICMHL	GLCKSRQPEP	EQEPGMSDPL	PKPLRDPLPD	PLLDKLVLPV	180
LPGALQARPG	PHTQDLSEQQ	FPIPLPYCWL	CRALIKRIQA	MIPKALAVA	VAQVCRVVL	240
VAGGICQCLA	ERYSVILLDT	LLGRMLPQLV	CRLVLRCSMD	DSAGFRSPTG	EWLPRDSECH	300
LCMSVTQAG	NSSEQAIPQA	MLQACVGSWL	DREKCKQFVE	QHTPQLLTIV	PRGWDARTTC	360
QALGVCGTMS	SPLQCIHSPD	L				381

Seq ID NO: C276 Protein Sequence
Protein Accession #: NP_631911.1

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MLGCGIPALG	LLLLLQGSAD	GNGIQGFYFP	WCEGDIDWR	ESCGQAAID	SPNLCLRLRC	60
CYRNGVCVHQ	RPDENVRKHK	MWALVWTCSS	LLLLSCSICL	PWWAKRRDVL	HMPGFLAGPC	120
DMSKSVSLLS	KHRGTKKTPS	TGSVPVALSK	ESRDVEGGTE	GEGTEEGEET	EGEREED	177

Seq ID NO: C277 Protein Sequence
Protein Accession #: NP_473364.1

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MKLVITIFLLV	TISLCSYSAT	AFLINKVPLP	VDKLAPLPLD	NILPFMDPLK	LLLKTLGISV	60
EHLVEGLRRC	VNELGPEASE	AVKKLLEALS	HLV			93

Seq ID NO: C278 Protein Sequence
Protein Accession #: FGENSESH predicted

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MPLSYAYKNA	ETLAGRHTSS	WMSRGAYQRR	NTRAAGRPEE	CTDRNWEAGR	TRGINLGQLE	60
ERCSDVFGVS	FFWVVRGLAG	SGAKLQTFTP	AQEGAPTQOR	QAEALLKCRQ	SGRPGRGGA	120
SERARDASML	SPLSAAMRNY	PTSSTIPERR	SYSPTETIAHK	SYSCLPDMK	ISMAESGPSL	180
DSLDDILEDE	SGSPFLVTHL	YFLGVVTTGM	EQDLFETGPN	IFDLQIYVKD	EVGVTDLQVL	240
TVQVTDVNEP	PQPGQNLAE	HLRADQPHFN	AHSHTYVRV	ATALARHLRL	SSIGSPFLGT	300
FCVVVMQYF	LISPPKSRFM	SANGTLFSTT	ELDFEAGHRS	PHLIVEVRDS	GGLKASTELQ	360
VNIWNLNDEV	PRFTSPTRVY	TVLEELSPGT	IVANITAEADP	DDEGFPSHLL	YSITTVSKYF	420
MINQLTGTIQ	VAQRIDRDAG	ELRQNPTISL	EVLVKDRPYG	GQENRIQITF	IVEDVNDNPA	480
TCQKFTFRSS	LHPALCSKTL	TWMDTVLDCF	HAADKDIPVT	GRFTKERGLI	GLTVPHGNGS	540
LTIMABEKKE	QVTSYMDGSR	QRDRACVGKL	LLIKPSDLMR	LSHYHNNNSG	KTCPHDSISS	600
YQVEPTTCRN	SRIQATNNED	TSSVTVTVNI	LEENDEKPIK	TPNSYFLALP	VDLKVGTNIQ	660
NFKLTCTDLD	SSPRSPRYSI	GPGNVNNHPT	FSPNAGSNVT	RLLLTSRFDY	AGGFDPKINDY	720
KLIVYVTDNN	LMSDRKAEAA	LVETGTVTLS	IKVIPHTPTI	ITTTTPRPVT	YQVLRKNVYS	780
PSAWYVFFVI	TLGSILLGLL	LVYLVVLLAK	AIHRHCPCCKT	GKNKEPLTKK	GETKTAERDV	840
VVETIQMTFI	PDGEAIDPEP	EQASLELYAL	LPSCCDPSPV	TLRKVQVCGE	SEETGQCSGH	900
ITLPGKIPVD	DPRKQETGLQ	GDPEVNTLCP	AVKVVVGSPO	AERCIRLALS	LKKYSSD	957

Seq ID NO: C279 Protein Sequence
Protein Accession #: XP_168571.1

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MINQLTGTIQ	VAQRIDRDAG	ELRQNPTISL	EVLVKDRPYG	GQENRIQITF	IVEDVNDNPA	60
TCQKFTPSIM	VPERTAKGTL	LLDLNKPCCD	DDSEAFNNRP	NFTMPSGVGS	GSRLQDPAG	120
SGKIVLIGDL	DYENFSNLAA	GNKYTVIIQV	QDVAPPYKYN	NVYVYILTSP	ENEFPLIFDR	180
PSYVFDVSR	RPAQHLGGP	EEKRLLSICH	VRAVCHFGPL	HIASGSPRPV	GRPIGQSHPO	240
TLPLQDWEQ	GTSDKERRNE	DCRERRRGNN	YPDEHYL			277

Seq ID NO: C280 Protein Sequence
Protein Accession #: NP_005257.2

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MGDWSFLGNF	LEEVEHKKSTV	VGKVVLTVLV	IFRMLVLGTA	AESSWGDQEA	DFRCDTIQPG	60
CQNVCYDQAF	PISHIRYVWL	QIIFVSTPSL	VYMGHAMHTV	RMQEKRLRE	ABRAKEVRGS	120

5
 GSYEYPVAEK AELSCWEEGN GRIALQGTLL NTYVCSILIR TIMEVGFIIVG QYFIYGIFLT 180
 TLHVCRRSPC PHPVNCVVS R PTEKNVFIVF MLAVAALSLL LSLAELYHLG WKKIRQRVFK 240
 PRQHMMAKQQL SGPSVGIVQS CTPPPDFNQC LENGPGGKFF NPFSNNMASQ QNTDNLVTEQ 300
 VRGQEQTPGE GFIQVRVYQK PEVPNGVSPG HRLPHGYHSD KRRLSKASSK ARSDDLVS 358

Seq ID NO: C281 Protein Sequence
 Protein Accession #: NP_055274.2

10
 1 11 21 31 41 51
 | | | | |
 MYLSICCCFL LWAPALT LKN LNYSVPEEQG AGTVIGNIGR DARLQPLP AERGGGGRSK 60
 SSGSYRVLENS APHLLDVAD SGLLYTKQRI DRESLCRHA KCQLSLEVPA NDKBICMIKV 120
 EIQDINDNAP SFSSDQIEMD ISENAAPGTR FPLTSAHDFD AGENGLRXYL LTRDDHGLFG 180
 LDVKSRRDGT KFPELVIQKA LDREQQNHHT LVLTAIDGGE PPRSATVQIN VKVIDSNDNS 240
 15 PVFEAPSYLV ELPEANPLGT VVIDLNATDA DEGFNGEVLY SFSSYVPRV RELFSIDPKT 300
 GLIRVKGNDL YEENGMLRID VQARDLGPNP IPAHCKVTVK LIDRNDNAPS IGFVSVRQGA 360
 LSEAAPPPTV IALVRVTDRD SGKNGQLQCR VLGGGGTGGG GGLGGPGGSV PFKLEENYDN 420
 FTVTVTRPL DRETQDEYNV TIVARDGGSP PLNSTKSPAI KILDENDNPP RPTKGLYVLQ 480
 VHENNIPGEY LGSVLAQDFD LGQNGTVSYS ILPSHIGDVS IYTVSVNPT NGAIYALRSF 540
 20 NFEQTKAFEF KVLAKDSGAP AHLESNATVR VTVLDVNDNA PVIVLPTLQN DTAEVLQVRN 600
 AGLGLYVSTV RALDSDFGES GRITYEIVDG NDDHLFEIDP SSGEIRTLHP FWEDVTPVVE 660
 LVVKVTDGK PTLSAVALKI IRSVSGSLPE GVPRVNGEQH HWDMSLELIV TLSTISIILL 720
 AAMITIAVKC KRENKEIRTY NCRIAEYSHP QLGGGKGKIK KINKNDIMLV QSEVERNAM 780
 NVMNVSSPS LATSPMYFDY QTRLPLSSPR SEVMYLPAS NMLTVPQHA GCHTSFTGQG 840
 25 TNASETPATR MSIIQTDNFP AEPNMGSRQ QFVQSISVAP RLRTQKEPA 889

Seq ID NO: C282 Protein Sequence
 Protein Accession #: NP_005592.1

30
 1 11 21 31 41 51
 | | | | |
 MELCRSLALL GSGGLMFLC IALSTDFWFE AVGPTHSAHS GLWPTGHGDI ISGYIHVTQT 60
 FSIMAVLWAL VSVSFTVLSC PPSLFPFGHG PLVSTTAAPA AAISMVYAMA VYTSERWDQP 120
 35 PHPQIQTFPS WSPYLGWVSA ILLCTGALS LGAHCGGPRP GYETL 165

Seq ID NO: C283 Protein Sequence
 Protein Accession #: NP_006424.2

40
 1 11 21 31 41 51
 | | | | |
 MATWALLLLA AMLLGNPGLV FSRLSPEYVD LARAHLRDEE KSCPCLAQEG PQGDLLTKTQ 60
 ELGRDVRTCL TIVQKLMKV DKPTORSVSN AATRVCRTR SRWRDVCNRP MRRYQSRVTQ 120
 GLVAGETAQQ ICEDLRLCIP STGPL 145

45
 Seq ID NO: C284 Protein Sequence
 Protein Accession #: NP_005594.1

50
 1 11 21 31 41 51
 | | | | |
 MKVSAALAV ILIATALCAP ASASPYSSDT TPCCPAYIAR PLPRAHIKEY FYTSGKCSNP 60
 AVVFVTRKRN QVCANPEKKV VREYINSLEM S 91

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 Seq ID NO: C285 Protein Sequence
 Protein Accession #: NP_071437.1

60
 1 11 21 31 41 51
 | | | | |
 MAPGRAVAGL LLLAAAGLGG VAEGPGLAFS EDVLSVFGAN LSLSAAQLQH LLEQMGAASR 60
 VGVPEPGQLH FNOCLTAESI FSLHGFSNAT QITSSKFSVI CPAVLQQLNF HPCEDRPKHK 120
 TRPSHSEVWG YGFLSVTIIN LASLLGLILT FLIKKSYFFK ILTFVGLAI GTLFSNAIFQ 180
 LIPEAFGPDV KVDYSVEKAV AVFGGFYLLF FFERMLKMLL KTYGQNGHHT FGNDNFPGQE 240
 KTHQPKALPA INGVTCYANP AVTEANGHIH FDNVSVVSLQ DGKKEPSSCT CLKGPKLSEI 300
 65 GTIAWMITLC DALHNFDLGL AIGASCTLSL LQGLSTSLAI LCEEPFHELQ DFPVILLNAGM 360
 STRQALLFNF LSACSCYVGL AFGILVGNMF APNIIPALAG GMFLYISLAD MPPEMNDMLR 420
 EKVTRGRKTD TFFMIQNAQM LTGFTAILLI TLYAGEIELE 460

70
 Seq ID NO: C286 Protein Sequence
 Protein Accession #: NP_004175.1

75
 1 11 21 31 41 51
 | | | | |
 MPNSEPASLL ELFNISATQG ELVRSKAGN ASKDEIDSAV KMLVSLKMSY KAAAGEDYKA 60
 DCPGPNPAPT SNHGPDTEA EEDFVDPWTV QTSSAKGIDY DKLIVRFGSS KIDKELINRI 120
 ERATGQRFPH FLRRGIFFSH RDMNQVLDAY ENKKPFYLYT GRGFSSEAMH VGHLPFIPT 180
 KWLQDVFNVP LVIQMTDDEK YLWKDLTLQD AYGDVENAK DIIACGFDIN KTFIPSDLDY 240
 MGMTSGPYKN VVKIQKHVTF NQVKGIFGFT DSDCIGKISF PAIQAAFPSS NSFPQIFRDR 300
 80 TDIQCLIPCA IDQDPYFRMT RDVAPRIGYP KPALLHSTFF PALQGAQTKM SASDPNSSIF 360
 LTDATKQIKT KVNKHAFFSG RDTIEHRQF GGNCDVDVSF MYLTFPLEDD DKLEQIRKDY 420
 TSGAMLTGEL KALIEVLQP LIAEHQARRK EVTDEIVKEF MTPRKLSPDF Q 471

Seq ID NO: C287 Protein Sequence

Protein Accession #: NP_004929.1

	1	11	21	31	41	51	
5	MTVFRQENV	DYYDTGEEIG	SGQFAVVKKC	REKSTGLQYA	AKFIKKRRTK	SSRRGVSRED	60
	IEREVSILKE	IQHPNVITLH	EVYENKTDVI	LILELVAGGE	LFDFLAEKES	LTEEEATEFL	120
	KQILNGVYYL	HSLQIAHFDL	KPENIMLLDR	NVPKPRIKII	DFGLAHRKIDF	GNEFKNIFGT	180
	PEFVAPEIVN	YEPGLGEADM	WSIGVITYIL	LSGASPFPLGD	TQKETLANVS	AVNYEFEDFY	240
10	PSNTSALAKD	FIRRLLVKDP	KKRMTIQDSL	QHPWIKPKDT	QQALSRKASA	VNMEKPKKFA	300
	ARKKWKQSVR	LISLCQRLSR	SFLSRSNMSV	ARSDDTLDEE	DSFVVKAIH	AINDDNVPLG	360
	QHLLGSLSNY	DVNGPKNHGT	PPLLIAAGCG	NIQILQLLIK	RGSRIDVDQK	GGSNVYVWAA	420
	RHGHVDTLKF	LSNENKCPDLV	KDKSGEMALH	VAARYGHADV	AQVTCASAAQ	IPISRTKEEE	480
	TPLHCAAMHG	YYSVAKALCE	AGCNVNIKNR	EGETPPLLTA	ARGYHDIVEC	LAHAGADLNA	540
	CDKDGIALH	LAVRRQMEV	IKTLLSQGCF	VDYQDRHGNT	PLHVACKDGN	MPIVVALCEA	600
15	NCNLDISNKY	GRTPLHLAAN	NGILDVVRYL	CLMGASVEAL	TTDGKTAEDL	ARSEQHEHVA	660
	GLLARLRKDT	HRGFTIQQLR	PTQNLQPRIK	LKLFHSGSGS	KTTLVESLKC	GLRSFFRRR	720
	RPRLSSTNSS	RPPSPPLASK	PTVSVSINN	YPGCENSVR	SRSMMFEPGL	TKGMLVFPVA	780
	PTHHPHCSAD	DQSTKADIDQ	NAYLNGVDF	SVNEFSGNFV	YFCQYDPA	NDPTSIVHVV	840
20	FSLEEPYBQ	LNPVIFWLSF	LKSLVPVEEP	IAFGSKLQNP	LQVVLVATHA	DIMNVPRPAG	900
	GEFGYDKDTS	LLKEIRNRFG	NDLHISNKL	VLDAGASGSK	DMKVLNRHLQ	EIRSQIVSVC	960
	PPMTHLCEKI	ISTLPSWRKL	NGPNQLMSLQ	QFVYDVQDQL	NPLASEEDLR	RIAQQLHSTG	1020
	EEINIMQSETV	QDVLLLDPRW	LCTNVLGKLL	SVETPRALHH	YRGRTYVEDI	QRLVPDSDVE	1080
	ELLQILDAMD	ICARDLSSGT	MVDVPAIKT	DNLHRSWADE	EDEVVMVGGV	RIVPVEHLTP	1140
	FPGGIFHAKD	VNLCRWIHQ	STEGDADIRL	WVNGCKLANR	GAELLVLVNV	HGGGIEQVVR	1200
25	GLBTEKIKCC	LLLDVSVCTI	ENVMATLPG	LLTVKHVLS	QQLREHPEPV	MIYQPRDFPR	1260
	AQTLKETSLT	NIMGGYKESP	SSIMCFGCHD	VYSQASLGMD	IHASDLNLLT	RRKLSRLDLP	1320
	PDLPGKDWCL	LAMNLGLPDL	VAKYNTNNGA	PKDFLPSPLH	ALLREWTYP	ESTVGTLMSE	1380
	LRELGRDDAA	DLLLKASSVF	KINLDGNGQE	AYASSCNSGT	SYNSISSVVS	R	1431

Seq ID NO: C288 Protein Sequence
Protein Accession #: NP_002072.1

	1	11	21	31	41	51	
35	MELRARGWWL	LCAAAALVAC	ARGDPASKSR	SCGEVRQIYG	AKGFSLSDVP	QAEISGEHLR	60
	ICPGGYTCCT	SEMEENLANR	SHAELETALR	DSSRVQLAML	ATQLRSFDDH	FQHLNDSE	120
	TLQATFPFAG	GELYTQNRAR	FRDLYSELRL	YVRGANLHLE	ETLAEPFARL	LERLFQKLHP	180
	QLLLPDDYLD	CLGKQAEALR	PFGAPRELRL	LRATRAFVAA	RSEVQGLGVA	SDVVRKVAQV	240
40	PLGPECSRAV	MKLVCARHCL	GVPGARPCPD	YCRNVLKGCL	ANQADLDAEW	RNLLDSMVL	300
	TDKFWGTSRG	ESVIGSVHTW	LAEAINALQD	NRDTLTAKVI	QCGGNPKVNP	QGPPEEKRR	360
	RGKLAPRERP	PSGTLEKLVS	EAKAQLRDVQ	DFWISLPGTL	CSEKMAALSTA	SDRCRWNGMA	420
	RGRYLPVEMQ	DGLANQINNP	EVEVDITKPD	MTIRQQIMQL	KIMTNRLRSA	YNGNDVDFQD	480
	ASDDGSGSGS						490

Seq ID NO: C289 Protein Sequence
Protein Accession #: AAH30205.1

	1	11	21	31	41	51	
50	MIILIYFLLL	LWEDTQGWGF	KDGIFHNSIW	LERAAGVYHR	EARSQKYKLT	YAEAKAVCEP	60
	EGGHLATYKP	LEAARKIGFH	VCAAGWMAKG	RVGYPIVKPG	PNCGFGKTGI	IDYGIRLNRS	120
	ERWDAYCNP	HAKCEGCVFT	DPKQIFKSPG	FPNEYEDNQI	CYWHIRLKYG	QRIHLSFLDF	180
	DLEDDPGCLA	DYVEIYDSYD	DVHGPFVGRYC	GDELPPDDIIS	TGNVMTLKFL	SDASVTAGGF	240
55	QIKYVAMDPV	SKSSQGRNTS	TTSTGKNKFL	AGRPSEHL			277

Seq ID NO: C290 Protein Sequence
Protein Accession #: NP_001973.1

	1	11	21	31	41	51	
60	MRANDALQVL	GLLFSLARGS	EVGNSQAVCP	GTLNGLSVTG	DAENQYQTLY	KLYERCEVVM	60
	GNLEIVLTGH	NADLSFLQWI	REVTGYVLVA	MNEFSTLPLP	NLRVVRGTQV	YDGKFAIFVM	120
	LNYNNTSSHA	LRQLRLTQLT	BIILSGGVYIE	KNDKLCHMDT	IDWRDIVRDR	DAEIVVVKDNG	180
65	RSCPPCHEVC	KGRCWGPGE	DCQTLTKTIC	APQCNHCFPG	PNNPQCCHDE	CAGGCSGPQD	240
	TDCFACRHFN	DSGACVPRCP	QPLVYNKLTIF	QLEPNPHTKY	QYGGVCVASC	PNNFVVDQTS	300
	CVRACPPDKM	EVDKNGLKMC	EPCGGLCPKA	CEGTGSGSRF	QTVDSNIDG	FVNCTKILGN	360
	LDPLITGLNG	DPWHKIPALD	PEKLNVRFTV	REITGYLANIQ	SWPPHMNFVS	VFSNLTITIG	420
	RSLYNRGVSF	LIMKLNVTFS	LGFRSLKEIS	AGRIYISANR	QLCYHSLNAN	TKVLRGPTEE	480
70	RDLIKHNRPR	RDCVAGKVC	DPLCSSGGCW	GGPGQCLSC	RNYSRGGVCV	THCNFLNGEP	540
	REFAEAECEF	SCHEPCQPMG	GTATCNGSGS	DTCAQCAHFR	DGPHCVSSCP	HGVLAGKGP	600
	YKYPDVQNEC	RPCHENCCTG	CKGPELQDCL	GQTLVLIGKT	HLTMALTVIA	GLVVFMMILG	660
	GTFLYWRGRR	IQNKRAMRRY	LERGESIEPL	DPSEKANKVL	ARIKPELRL	KLKVLGSGVF	720
	GTVHKGVVIF	EGESIKIPVC	IKVIEDKSGR	QSFAVTDHM	LAIGSLDHAH	IVRLGLGCPG	780
75	SSLQLVTOYL	PLGSLLDHVR	QHRGALGPQL	LLNWGVQIAK	GMYYLEEHGM	VERNLAAENV	840
	LLKSPSQVQV	ADFGVADLLP	PDDKQLLYSE	AKTPIKMMAL	ESIHFQKYTH	QSDVWSYGV	900
	VVELMTFGAE	PYAGLRLEAV	PDLLEKGERL	AQPQICTIDV	YVMVVKCMMI	DENIRPTPKE	960
	LANEPTRMAR	DPPRYLVIKR	ESGPGIAPGP	EPHGLTNKKL	EEVELEPELD	LDLLEAEED	1020
80	LNATTLTGSF	LSLFPVGTNR	PRGSGSLLSP	SSGYMPHMQG	NLGGSCQESA	VSGSSERCPR	1080
	PVSLHPMPRG	CLASESSEGH	VTGSEALQE	KVSMCRSRSR	SRSRPRGDS	AYHSQRHSL	1140
	TPVTPLSPPG	LESEEDVNGV	MPDTHLKGTP	SSREGLTSSV	QLSSVLGTZE	EDEDEYEYEM	1200
	NRNRHSPHF	PPRPSLEEL	GYEYMDVSGD	LSASLGSTQS	CPLHFPVIMP	TAGTTDPEDY	1260
	EYMNRRQDGG	GGPGDYAAMG	ACPAEQGYE	EMRAFQGGH	QAPHVHYARL	KTLSLEATD	1320
	SAFDNFDYWH	SRLFPKANAQ	RT				1342

Seq ID NO: C291 Protein Sequence
Protein Accession #: NP_001207.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MAPLCPSFWL PLLIPAPAPG LTVQLLLSL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL 60
GEEDLPSEED SPRKEEDPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG 120
DPQEPQNNAH RDKEGDDQSH WRYGGDPPNP RVSPACAGRF QSPVDIRPQL AAFCPALRPL 180
ELLGFLPPL PELRLRNNGH SVQLTLPPGL EMALGFGREY RALQLHLHWG AAGRPGSEHT 240
10    VEGHRFPPEI HVVHLSTAFR RVDEALGRPG GLAVLAAPLE EGPEENSAYE QLLSRLEEIA 300
EEGSETQVPG LDISALLPSD PSRYFYEGGS LTTTPCAQGV IWTVFNQVTM LSAKQLHTLS 360
DTLWPGGDSR LQLNFRATQP LNRGVIEASF PAGVDSPPRA AEPVQLNSCL AAGDILALVF 420
GLLPAVTSVA FLVQMRQRHR RGTGKGVSYR PAEVAETGA 459

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15 Seq ID NO: C292 Protein Sequence
Protein Accession #: NP_004198.1

```

20      1      11      21      31      41      51
      |      |      |      |      |      |
MGGAVVDEGP TGVKAPDGGW GMAVLPGCFV ITGFSYAPFK AVSVFFKELI QEFGIGYSOT 60
AMISSILLAM LVGTGPLCSV CVNRFGCRFV MLVGGLPASL GMVAASFPRS IIQVYLTTGV 120
ITGLGLALNF QPSLMLNRY FSKRRPMANG LAAAGSPVFL CALSPLOQLL QDRYGRGGF 180
LLLGGLLNC CVCAALMRPL VVTAQPGSGP PRPSRRLDL SVFDRGFVL YAVAASVMVL 240
GLFVPPVFPV SVAKDLGVPD TKAAFLTLTIL GFIDIFARPA AGFVAGLGKV RPYSVYLFSP 300
25    SMFFNGLADL AGSTAGDYGG LVVFCIFFGI SYGMVGALQF EVLMAIVGTH KFSASIGLVL 360
LMEAVAVLVG PPSGGKLLDA THVMYVPFIL AGAEVLTSSL ILLLGNFFCI RKKPKPEQPE 420
VAAASEEKHL KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETSV 465

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30 Seq ID NO: C293 Protein Sequence
Protein Accession #: NP_000349.1

```

35      1      11      21      31      41      51
      |      |      |      |      |      |
MALFVRLAL ALALALGPAA TLGAPAKSPY QLVLQHSRLR GRQHGPNVCA VQKVIGTNRK 60
YFTNCKQYQ RKICCKSTVI SYECCPGYEK VPGKGCPCAA LPLSNLYETL GVGSTTTQL 120
YTDRTKLRP EMEGPGSPFI FAPSNEAWAS LPAEVLDSLV SNVNIELNA LRYHMVGRRV 180
LTDELKGMT LTMQYQNSNI QIRHYPNGIV TVNCARLLKA DHATNGVVH LIDKVITIT 240
NNIQIIEIE DTFETLRAAV AASGLNMLE GNGQYTLAP TNEAFEKIPS ETLNRILGDP 300
EALRDLNHN ILKSAMCAEA IVAGLSVETL EGTTLVEGCS GDMLTINGKA IISNKDILAT 360
NGVIHYDEL LIPDSAKTLF ELAAESDVST AIDLFRQAGL GNLSSGSRLL TLLAPLNSVF 420
KDGTPPIDAH TRNLLNHHI KDQLASKYLY HGQTLETGG KKLRFVYVRN SLCIENS CIA 480
AHDKRGRYGT LFTMDRVLTP PMGTVMVLK GDNRFSLVA AIQSAGLTET LNRGVYTVF 540
APTNEAFRAL PPRERSRLG DAKELANILK YHIGDEILVS GGIGALVRLK SLQGDKLEVS 600
LKNVSVSNK EPPAEFDIMA TNGVVHVTN VLQPPANRPQ ERGDELADSA LEIFKQASAF 660
45    SRASQSVRL APVYQKLLER MKH 683

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Seq ID NO: C294 Protein Sequence
Protein Accession #: NP_006527.1

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50      1      11      21      31      41      51
      |      |      |      |      |      |
MTQRSIAGPI CNLKFVTLIV ALSSELPLG AGVQLQDNGY NGLLIAINPQ VPENQNLSN 60
IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKAMNSK IKQESYEKAN VIVTDWYGAH 120
GDDPYTLQYR GCGKEGKYIH FTFNPLNDN LTAGYGSRRG VPVHEWAHLR WGVFDEYNND 180
55    KPPYINGNQ IKVTRCSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQATASI 240
MFMQSLSSVV EFCNASTHNQ EAPNLQNMCM SLRSAMDVIT DSADPHHSFP MNGTELPPPP 300
TPSLVQAGDK VVCLVLDVSS KMAEADRLQ LQQAAPFLM QIVEIHTFVG IASFDKSGEI 360
RAQLHQNIN DDKRLVSVYL PTTVSAKTDI SICSLKKGK EVVEKLNGKA YGSVMILVTS 420
GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLSELSRLT GGLKFFVFDI SNSNSMIDAF 480
60    SRISSTGCDI PQHQIQLEST GENVKPHQL KNTVTVDNTV GNDTFLVTW QASGPEIIL 540
FDPDGRKYIT NNFTITNLTPR TASLWIPGTA KPGHWYITLN NTHSLQALK VTVTSRASNS 600
AVPPATVEAF VERDSLHPPH PVMYIANVKQ GFYPILNATV TATVEPETGD PVTLLRLDDG 660
AGADVIKNDG IYSRYFPSPA ANGRYSKLVH VNHSPSISTP AHSIPGSHAM YVPGYTANGN 720
IQMNAPEKSV GRNEEERKMG PSRVSSGGSF SVLGVPAGPH PDVFPCKII DLEAVKVEE 780
65    LTLSTAPGE DFDQGQATSY EIRMSKSLQN IQDDFNAIL VNTSKRNQQ AGIREIFTFS 840
PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFI PP NSDPVPARDY 900
LILEGLVTAM GLIGIICLII VVTHETLSRK KRADKKENG T KLL 943

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70 Seq ID NO: C295 Protein Sequence
Protein Accession #: Eos sequence

```

75      1      11      21      31      41      51
      |      |      |      |      |      |
MKFLILLILQ ATASGALPLN SSTSLKKNV LFGERYLEKF YGLEINKLEF TKMKYSGNLM 60
KEKIQEMQHP LGLKVTQLD TSTLEMMAP RCGVPDVHHP REMPGGVPWR KHYITRINN 120
YTPMNRREDV DYAIRKAFQV WSNVTPKFS KINTGMADIL VVFARGAHGD PHAFDGKGGI 180
LAHAFPGPSG IGGDAHFDEP EFWTHHSGT NLELTAVHEI GHSILGLHSS DPEAVMPPY 240
KYVDINTFRL SADDIRGIQS LYGDQKENR LPNPDNSEPA LCDPNLSFDA VTTVGKIFF 300
80    FKDRFFWLKV SERPKTSVNL ISSLMPTLPS GIEAAYEIEA RNQVPLFKDD KYWLIENLRP 360
BENYPSKIDS FGFPNFVKKI DAAVFNPRFY RYFFVNDQY WRDERRQNM DPGYPKLITK 420
NEQIGIPKID AVFYSKNKYY YFFQGSNQFE YDFLLQRITK TLKSNWFGC 470

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Seq ID NO: C296 Protein Sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
 5 MKFLILLLLQ ATASGALPLN SSTSEKNNV LFGERYLEKF YGLEINKLPV TOMKYSGNLM 60
 KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHHP REMPGGPVWR KHYITYRINN 120
 YTPDMAREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAHD FHAFDGKGGI 180
 LAHAFGPGSG IGGDAHFDDE EFWTTHSGGT NLFLTAVHAI GHSLGLGHSS DPKAVMFPTY 240
 KYVDINTPRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF 300
 FKDRPFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLPKDD KYWLISNLRP 360
 10 EPNYPKSIHS FGFPNFVKKI DAAVFNRPFY RTYFFVDNQY WRVDERRQMM DPGYPKLITK 420
 NFQGIQPKID AVFYISNKYKY YFFQGSNQPE YDFLLQRTK TLKSNVWFGC 470

Seq ID NO: C297 Protein Sequence
 Protein Accession #: NP_008883.1

1 11 21 31 41 51
 15 MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYFLLEAT DNDDIYGAAW 60
 IGIFVGLCLF CLSVLGIQVI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL 120
 20 FLKQMLERYQ NNSPFPNDQD WKNNGVTWTK DRLMLQDNCC GVNQPSDNQK YTSAFRTENN 180
 DADYPWPRQC CVMNMLKEPL NLEACKLGVP GFYHNGQCYE LISGPMNRHA WGVAVFGFAI 240
 LCWTFWVLLG TMFYWSRIEY 260

Seq ID NO: C298 Protein Sequence
 Protein Accession #: NP_001784.2

1 11 21 31 41 51
 25 MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
 QEPALPSTDN DDFTVRNGET VQERRSLKER NPLKIPPSKR ILRRHKRDWV VAPISVPENG 120
 30 KGPPFORLQK LKSNKDRDTK IFYSITGPGA DSGPEGVFAV EKETGWLLEN KPLDREEIAK 180
 YELEGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAYITYN GUVAYSLSHQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 35 TMDXGDSST TAVAVVEILD ANDNAPMFDQ QKYEAVHPEN AVGHEVQRLT VTDLDAPNSP 360
 AWRATYLING GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEFVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLAMPD DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGLLLTLID 540
 VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPTSPFPQ AQLTDDSDIY WTAEVNEEGD 600
 40 TVVLSLKKFL KQDQYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660
 GAVLALLFL LVLALLVRKK RKIKPPLLLP EDDTRDNVFP YGEEGGGEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTIIIP TMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGEEDD 829

Seq ID NO: C299 Protein Sequence
 Protein Accession #: NP_005620.1

1 11 21 31 41 51
 45 MAKSAENGI YSVSGDEKKG FLIAPGPDGA PAKGDGPVGL GTPGGR LAVP PRETWTRQMD 60
 FIMSCVGFAY GLGNVWREFY LCYKNGGGVF LIPYVLIALV GGIPIFFLEI SLGQPMKAGS 120
 50 INVWNICPLF KGLGVASMI VPYCNTYYIM VLAWFYLYL KSFTTLTPWA TCGHTWNTPD 180
 CVEIFRHEDC ANASIANLTC DQLADRRSPV IEFWENKVL RSGGLEVPGA LNWVETLCCL 240
 ACWVLVYFCV WKGKSTGKI VYFTATFPYV VLVLVLRGV LPLGALDGI YLKPDPWSKL 300
 55 GSPQVWDAG TQIFFSYAIG LGALTALGSY NFNNNCYKD AILALINS GTSFFAGFVVF 360
 SILGFWMAEQ GHVHSKVAES GPGLAPIAYP RAVTLMVPAP LWAALFFFM LLLGLDSQFV 420
 GVEGFIPTGL DLLPASYIFR FQREISVALC CALCFVIDLS MVTGGMYVVF QLFDYYSAGS 480
 TYLLWQAFWE CVVAVNYGA DRFMDDIACM IGYRCPWPK WCNWFFTPLV CMGIFIFNVV 540
 60 YPEPLVYNT YVYPWGEAM GWAFALSSML CVPLHLGLCL LRAKGTMAER WQHLTQPIWG 600
 LHHLEYRAQD ADVRLTTLT FVSESSKVVV VESVM 635

Seq ID NO: C300 Protein Sequence
 Protein Accession #: NP_006507.1

1 11 21 31 41 51
 65 MEPSKKLTG RLMLAVGGAV LGSLLQPGYNT GVINAPQKVI BEFYNQTVWH RYGESILPTT 60
 LTLNLSLVA IPSVGGMIGS FSVGLFVNRF GRNNSMLMN LLAFAVSAVL GPSKLGKSPF 120
 70 MLILGRFIIG VYCGLTTFPV PMYVGEVSPT APRGALGTLH QLGIVVGILI AQVFGLDSIM 180
 GNKDLWPLL SIIFIPALLQ CIVLPFCPS PRELLINRNE ENRAKSVLKK LRGTADVTHD 240
 LQEMKEESRQ MREKKVITIL ELFRSPAYRQ PILIAVVLQ SQQLSGINAV FYYSTSIFPK 300
 AGVQPPVAT IGSGLVNTAF TVVSLFVVER AGRRTLHLIG LAGMAGCAIL MTIALALLEQ 360
 75 LPWMSYLSIV AIFGVAFPE VGGPIPWFI VAEFLSQGPR PAIAVAGFS NWTNPNFVGM 420
 CFQYVEQLCG PYVPIIFTVL LVLEFFITFY KVPETKGRTF DEIASGFRQG GASQSDKTPE 480
 ELPHPLGADS QV 492

Seq ID NO: C301 Protein Sequence
 Protein Accession #: XP_035292.2

1 11 21 31 41 51
 80 MAGAGPKRA LAAPAAEKEE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLINGVAITV 60
 GTIIGSGIFV TPTGVLKEAG SPGLALVWVA ACGVFSIVGA LCYAEIGTTI SKSGGDYAYM 120
 LEVYGSLEPAF LKMIELLII RPSSQYIVAL VFATYLLKPL PPTCFVPREA AKLVACLCLV 180
 LLTAVNCYSV KAATRVQDAF AAARKLLAL ILLGFPVQIG KGDVSNLDPN PSFEGTKLDV 240

5 GNVILALYSG LPAYGGWNYL NFWTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
 STEQMLSSSEA VAVDFGNVHL GVMNIIIPVF VGLSCPGSVN GSLPTSSRLF FVGSREGHLP 360
 SILSMIHPQL LTPVPVSLVFT CVMTLIYAFS KDIFSVINFP SFFNWLCLVAL AIIGMIWLRH 420
 RKPELERPIK VNIALPVFFFI LACFLIYAVS FWKTPVVECGI GFTIILSGLP VYPPGVWVWKN 480
 KPKWLLQGIF STTVLCQKLM QVVPQET 507

Seq ID NO: C302 Protein Sequence
 Protein Accession #: NP_005259.1

10 1 11 21 31 41 51
 MNWSIFEGLL SGVNYKSTAP GRIWLSLVFI FRVLVYLVT A ERVWSDDHKD FDCNTRQPGC 60
 SNVCDFEFPF VSHVRLMALQ LILVTCPSLL VVMHVAYREV QEKHREANG ENSGRLYLNP 120
 GKRRGGLWMT YVCSLVFKAS VDIAPLYVFH SFYPKYLPP VVKCHADPCP NIVDCFIISKP 180
 15 SEKNIFTLFM VATAAICILL NLVELIYLV S KRCHCLAA R KAQAMCTGHH PHGTTSSCKQ 240
 DDLSSGDLIF LGSDSHPPLL PDRPRDHVKK TIL 273

Seq ID NO: C303 Protein Sequence
 Protein Accession #: NP_005121.1

20 1 11 21 31 41 51
 MKICSLTLLS FILLAAQVLL VEGKKKVKNG LHSKVSEQK DTLGNTQIKQ KSRPGNKGKF 60
 VTKDQANCRW AATFQSEGIS LKVECTQLDH EFSCVFAGNP TSCLKLKDER VYWKQVARNL 120
 25 RSQKIDICRY S KTAVKTRVCR KDFPESSLKL VSSTLFGNTK PRKEKTEMSP REHIKGETT 180
 PSSLAVTQTM ATKAPECVED PDMANQRKTA LEFCGETWSS LCTFFLSIVQ DTSC 234

Seq ID NO: C304 Protein Sequence
 Protein Accession #: AAH22542

30 1 11 21 31 41 51
 MCSEIILRQE VLKDGFRDL LIKVKFGESI EDLHTRLLI KQDIPAGLYV DFYELASLRE 60
 RNITEAVMVS AATFIEAPNY LKSESEVLIY ARDSQCIDC FQAFLPVHCR YHRPHSEGE 120
 35 ASIVVNNPDL LMFCDQAGSR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180
 WNKMKKYSY KNVILQVVG LTVHTSLVCS VTLLITILCS KKKKK 225

Seq ID NO: C305 Protein Sequence
 Protein Accession #: NP_004985.1

40 1 11 21 31 41 51
 MSLWQPLVLV LLVLGCCFAA PRQRQSTLVL FPGDLRTNLT DRQLAEVLY RYGYTRVAEM 60
 45 RGEKSLGPA LLLLQKQLSL PETGELDSAT LKAMRTPRCG VPDIGRFQTF EGDLLKWHHN 120
 ITYWIQNYSE DLPRAVIDDA PARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP 180
 FDGKDGLLAH AFPPGPIQG DAHFDDEDLW SLGKGVVVT RFGNADGAAC HFPFIFEGRS 240
 YSACTTDRS DGLFWCSTTA NYDTDDRFGF CPSERLYTRD GNADGKPCQF PFIFQGSYS 300
 ACTTIDGRSDG YRNCATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST 360
 CTSEGRGDGR LWCATTNFD SKDKWGFCD QGYSLFLVAA HFGHALGLD HSSVPEALMY 420
 50 PMYRFTGEP LKCDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSER 480
 PTAGTGPFS AGPTGPFTAG PSTATTVPLS FVDDACVNI FDAIAEIGNQ LYLEKDGKYW 540
 RFSEGRGSRP QCFPLIADKV PALPRKLDV FEEPLSKLFP FFSGRQVWVY TGASVLGPRR 600
 LDKLGLGADV AQTGALRSR RGMILLFSGR RLWRFDVKAQ MVDPRSAVEV DRMPFGVPLD 660
 55 THDVFQYREK AYFCQDRFYW RVSSRSSELNQ VDQVGYVTYD ILQCPED 707

Seq ID NO: C306 Protein Sequence
 Protein Accession #: NP_000204

60 1 11 21 31 41 51
 MAGPRPSEFA RLLLAALISV SLSGTLANRC KKAPVKSCTE CVRVDRKDAY CTDEMFRDRR 60
 CNTQABELLA GQQRRESIVM ESSQITEET QIDTTLRRSQ MSPQGLRVRL RPGEERHFEL 120
 EVFEPLESPV DLYILMDFSN SMSDDLNLK KMGQNLARVL SOLTSDYITG PGKFVDKVS 180
 65 PQTDMRPEKL KEFWNSDPP SFSEKVISLT EDVDEFNKL QGERISGNLD APEGGFDAI 240
 QTAUCTRDIG WRPDSTHLLV FSTESAFHYE ADGANVLGI MSRNDERCHL DTTGTVTQYR 300
 TDQYPSVPTL VRLAKHNI PIPAVTINYSY SYEKLHYTF PVSSIGVLQE DSSNIVELLE 360
 BAFNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGVGVYQV QLRALREVDG 420
 THVCQLPEDQ KGNHILKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480
 70 CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHVCVYGEGR YEGQFCEYDN 540
 PQCPRTSGFL CNDRGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR 600
 CHCHQQLSYT DTICEINYS A IHPGLCEDLR SCVQCQAWGT GEKKGRTCEE CNFKVKMVE 660
 LKRAEEVVVR CSFRDEDDDC TYSYTMEDG APGFNSTVLV HKKDCPPGS FWMLIPLLL 720
 75 LPLALLLLL LCKYCACCK ACLALLPCN RGHMVGFKEH HYMLRENLMA SDHLDTPMLR 780
 SGNLKGDDV RNKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTRC 840
 AQLRQEVEEN LNEVYRQISG VHKLQQTFR QPNAGKKQD HTIVDTVIMA PRSAKPAK 900
 LTKGVQGR FHDLVAPGY YTLTADQAR GMVEFQEGVE LVDVRVPLFI RPEDDDEKQL 960
 LVEADIVPAG TATLGRLLVN ITIIEKQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG 1020
 KSGSYRTQD GTAQGNRDYI FVEGELLFQF GEAWKELQVK LLELQEVDSL LGROQVRRFH 1080
 80 VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPHGDLGAP QNPNKAAGS 1140
 RKIHFNWLPF SGKPMGYRVK YWIQGDSSE AHLDSKVPS VELTNLYPYC DYEMKVCAYG 1200
 AQGEGPYSSL VSCRTHQEV SEPGRAPNV VSTVTQLSW AEPATNGBI TAYEVCYGLV 1260
 NDDNRPFGPM KVLVDNPKN RMLLIENLRE SQPYRYTVKA RAGAGWGP RAIINLATQP 1320
 KRPMISPIIP DIPVIDAQSG EDYDSFLMYS DDVLRSPSGS QRPVSVDGTG CGWKFEPPLG 1380
 EELDRLRRVTW RLPELIPRL SASSGRSSDA BAPTAPRTTA ARAGRAAVP RSATGPPPG 1440

5
 HLVNGRMDFA FPGSTNSLHR MTTTSAAYG THLSPHVPHR VLSTSTLTLR DYNLSLTRSEH 1500
 SHSTTLPRDY STLTSSVSSH SRITAGVPDT PTRLVFSALG PTLRLVSNQSE PRCEPFLQGY 1560
 SVEYQLLNGG ELHRLNIPNP AQTSSVVVEDL LPNHSYVFRV RAQSQEGWGR EREGVITIES 1620
 QVHPQSPLCP LFQSAFTLST PSAPGLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCEM 1680
 AQGGGPATAP RVDGDSPESE LTVFGLSENV PYKFKVQART TEGFPGPEREG IITIESQDGG 1740
 PFPQLGSRAG LFQHPQLQSEY SSITTTHTSA TEPFLVDGLT LGAQHLEAGG SLTRHVTQEP 1800
 VSRTLTSTGT LSTHMDQQFF QT 1822

10
 Seq ID NO: C307 Protein Sequence
 Protein Accession #: NP_076404.1

15
 1 11 21 31 41 51
 MGFNLTAKL PNNELHGQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILIN 60
 GLAVWIFPH RNKTSPIFYI KNIVVADLIM TLTFPPRIHV DAGFGPWYFK FILCRYTSVL 120
 FYANMYTSIV FLGLISIDRY LKVVKPFQGS RMYSTPTKV LSVCVWVINA VLSLPIILT 180
 NGQPTEDNIH DCSKLKSPLG VKWHTAVTVV NSCLFVAVLV ILIGCYAIS RYHKSSRQF 240
 ISQSSRKRRH NQSIKRVVAV PFTCFPLPYL CRIPFTFSLH DRLLDESAQK ILYYCKEITL 300
 FLSACNVCLD PIITYFFMCRS FSRRLFKKSN IRTSRSESIRS LQSVRRSEVR IYYDYTDV 358

20
 Seq ID NO: C308 Protein Sequence
 Protein Accession #: NP_065840.1

25
 1 11 21 31 41 51
 MVWCLGLAVL SLVISQDAGD RGKPEVVSUV GRAEESVVLG CDLLPPAGRP FLHVIEWLRF 60
 GFLLPIFIQF GLYSFRIDPD YVGRVRLQKG ASLQIEGLRV EDQGWYECRV FFLDQHIPPED 120
 DFANGSVVHL TVNSPPQFQE TPPAVLEVQE LEPVTLRCVA RGSPLFPHVT KLRGKDLQGG 180
 QGQVQVNGT LRIRRVBRGS SGVYTCQASS TEGSATHATQ LVLGLPFIIV VPKNSTVNA 240
 SQDVSLACHA EAYPANLTVS WFQDNINVEH ISRLQPRVOI LVDGSLRLLA TQDDAGCYT 300
 CVPNSGLLHP PSASAYLTVL CMFQVIRCFV RANPPLLVS WTKDGKALQL DKFPQWSQGT 360
 EGSLLIALGN EDALGEYSCT PYNSLGTAGP SPVTRVLLKA PPAPIERPKE EYFQEVGREL 420
 LIPCSAQGDP PFVSVWTKVG RGLQQAQVD SNSSLILRPL TKEAHGHEWC SASNAVARVA 480
 TSTNVVYVLT SHVVTVNVSV VALPKGANVS WEPFGDGGYL QRFVWYTPPL AKRPFDMHHD 540
 WWSLAVPVGA AHLLVPGLQP HTQYQFSVLA QNKLGSPPFS EIVLSAPEGL PTTAAPGLP 600
 PTEIPPLSP PRGLVAVRTP RGVLLHWDPP ELVPKRLDGY VLEGRQGSQG WEVLDPVAVG 660
 TETELLVPGL IKDVLVEFRL VAPAGSFVSD PSNTANVSTS GLEVYPSRTQ LPGLLPQPV 720
 AGVVGVCFL GVAVLVSILA GCLLNRRRAA RRRRKRLRQD PPLIFSPTEG SAAPSALGSG 780
 SPDSVAKLKL QSPVPSLRQ SLLWGDPAQT PSFHPDPPSS RGLPLEPIC RGPDGRFVVG 840
 PTVAAPQERS GREQAERTP AQRLARSFDC SSSSPSGAPQ PLCIEDISPV APPPAAPPSP 900
 LFGPGFLQY LSLPFFREMN VDGDNWPLEE PSPAAPPDYM DTRRCPTSSF LRSPTETPVS 960
 PRESLPGAVV GAGATAEPY TALADWTLRE RLPLGLLPAA PRGSLTSQSS GRGSASFLEP 1020
 PSTAPSAGGS YLSPAPGDT SWSAGFERWP RREHVTVSK RRTSVSDENY EWDSEFPQDM 1080
 ELLETLLHGL ASSRLRPEAE TELGVKTPPE GCLLNTAEVT GPEARCAALR BEPLAFRRER 1140
 DATRARLPAY RQVFPHPEQA TLL 1163

50
 Seq ID NO: C309 Protein Sequence
 Protein Accession #:

55
 1 11 21 31 41 51
 MLTKPLQGP APPGTPTPPP GKKDREAFEA EYRLGPLLK GPGFTVFAGH RLTDRLQVAI 60
 KVIPNRVLG WSPFLSDSVTC PLEVALLWKV GAGGGHPGVI RLIDWFETQE GFMLVLERPL 120
 PAQDLFDYIT EKGPLGBGFS RCFPGQVAA IQCHSRGVV HRDIKIDENIL IDLRRCARL 180
 IDFGSGALLH DEPYTDFTGT RVYSPFEWIS RHQYHALPAT VWSLGLLYD MCGDIPFER 240
 DQEILEAEHL FFAHVSPPDC ALIRRLAPK PSSRPSLEEI LLDPMWQTPA EDVTPQPLQR 300
 RCPFGVLVLA TISLAWPLA PNGKSHFMA MSQG 334

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 Seq ID NO: C310 Protein Sequence
 Protein Accession #: NP_002501.1

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 1 11 21 31 41 51
 MECLYYFLGF LLLAARLPLD AAKRFHDVLG NERPSAYMRE HNQLNGWSSD ENDWNEKLYP 60
 VKRGDMRWK NSWKGGRVQA VLTSDSPALV GSNITFAVNL IFFRCQKEDA NGNIVYEKNC 120
 RNEAGLSADP YVYNWTAWSE DSDGENGTOG SHNVFPDGG PFPHPGWRW WNPFIYVFETL 180
 GQYFQKLGRG SVRVSVNTAN VTLGPQLMEV TVYRRHGRAY VPIAQVKDYY VVTDQIPFV 240
 TMFQKNDRNS SDTEFLKDLF IMPDVLIDP SHFLNYSTIN YKNSFGDNTG LRVSTNHTVN 300
 HTYVINGTFS LNLTVKAAAP GPCPPPPPPP RPSKPTPSLG PAGDNPLELS RIPDENCQIN 360
 RYGHFQATIT IVEGILEVNI IQMTDVLMEV PWPESLIDF VVTCQGSIFT EVCTIISDPT 420
 CEITQNTVCS FVDVDEMCLL TVRRTFNGSG TYCVNLTLGD DTSALATSTL ISVDFDRDPAS 480
 PLRMANSALE SVGCIAIFVT VISLLVYKXH KEYNPIENSP GNVVRSKGLS VFLNRAKAVF 540
 FPGNQEKDPL LRNQEPKGV 560

75
 Seq ID NO: C311 Protein Sequence
 Protein Accession #: Bos seq

80
 1 11 21 31 41 51
 MRILKRFLAC IQLLCVCRLD WANGYYRQOR KLVBEIGWSY TGALEQKNG KKYPTCNSPK 60
 QSPINIDEDL TQVNVNKKL KPQGWKTSI ENTFIENHKG TVBINLTNDY RVSGGVSEMV 120
 FKASKITFEH GKCMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSPBEAV KRGKRLALS 180
 ILFEVGTFFW LDFKAIIDGV ESVSFGRQA ALDPPILLNL LPNSTDKYI YNGSLTSPPC 240
 TDTVDWIVFK DTVSISESQL AVFCBVLTMQ QSGYVLMNDY LQNNFREQQY KFSRQVFPSSY 300

Seq ID NO: C312 Protein Sequence
Protein Accession #: XP_031379

Seq ID NO: C313 Protein Sequence
Protein Accession #: NP_002842

1355

5
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PLVIVSALTF ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPIISDDVGAI 840
PIKHFPKHVA DLHASSGFTE EFETLKEFYQ EVQSCITVDLG ITADSSNHPD NKHKRYINI 900
VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960
VEVIVMITNL VEGRRKCDQ YWPADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020
GSQKGRPSGR VVTQYHYTQM PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080
TGTYIVLDSM LQIQHEGTN NIFGFLKHIR SQRYNLVQTE EQYVFIHDTL VEAILSKETE 1140
VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200
VERSRVGISS LSGEGTDYIN ASYIMGYYSQ NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260
MIPDQGNMAE DEFVYWPNDK EPINCESFKV TLMAEEHKCL SNEEKLIQD FILEATQDDY 1320
VLEVRHFQCP KWPNDSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTL 1380
MHQLEKENSU DVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440
AALPDGNIAE SLESVL 1456

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Seq ID NO: C314 Protein Sequence
Protein Accession #: Eos sequence

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MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGA LNQKNWG KKYPTCNSPK 60
QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
MVPKASKITP HWKCKNMSD GSEHSLGQK FPLEMQIYCF DADRFSFEE AVKGRKGLRA 180
LSILFEVGTG ENLDFKAIID GVESVSRFGK QAALDPFILL NLLPNSTDKY YIYNGSLTSP 240
PCTDDTWIVF KDTVSISESQ LAVFCVLTLM QSGYVLMMD YLQNNFREQQ YKFSRQVPS 300
VTGKEEIEHA CSESEPNVQ ADPENYTSLL VWERPRVYV DTMIEKFAVL YQQLDGEDQT 360
KHEFLTDGYQ DLGAILNNLL PNMSYVLQIV AICTNGLYK AICDQLIVDM TNPEDLDFP 420
ELIGTEEIIK EEEGKDIEE GAIVNPGRDS ATNQIRKKEP QISTTTHYNR IGTYNEAKT 480
NRSPTRGSEF SGKGDVPNTS LNSTSQPVTK LATEKDISLT SQTVTELPFH TVEGTSASLN 540
DGSKTVLRSP HMLSGTAES LNTVSIYEY EESLTSFKL DTGAEDSSGS SPATSAIPFI 600
SENISQGYIF SSENPEITTY DVLIPESARN ASEDSTSSGS EESLKDPSME GNWFPSSST 660
ITAQPDVGSR RESFLQNTYT EIRVDESEK TKSPSAGPVM SQGPSVTDLE MPHYSTPAYF 720
PTEVTPHAPT PSSRQDLVST TVNVVYSQTT QPVYNEASNS SHESRIGLAE GLESEKKAIV 780
PLVIVSALTF ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPIISDDVGAI 840
PIKHFPKHVA DLHASSGFTE EFETLKEFYQ EVQSCITVDLG ITADSSNHPD NKHKRYINI 900
VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960
VEVIVMITNL VEGRRKCDQ YWPADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020
GSQKGRPSGR VVTQYHYTQM PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080
TGTYIVLDSM LQIQHEGTN NIFGFLKHIR SQRYNLVQTE EQYVFIHDTL VEAILSKETE 1140
VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200
VERSRVGISS LSGEGTDYIN ASYIMGYYSQ NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260
MIPDQGNMAE DEFVYWPNDK EPINCESFKV TLMAEEHKCL SNEEKLIQD FILEATQDDY 1320
VLEVRHFQCP KWPNDSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTL 1380
MHQLEKENSU DVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440
AALPDGNIAE SLESVL 1456

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Seq ID NO: C315 Protein Sequence
Protein Accession #: Eos sequence

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QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
FKASKITFWH GKCKNMSDGS EHSLEGQKFP LEMQIYCFDA DRPSSFEAV KKGKGLRALS 180
ILFEVGTSEN LDFKAIIDGV ESVSRFGKQA ALDPPILLNL LPNSTDKYYI YNGSLTSPPC 240
TDTVDWIVFK DTVSISESQL AVFCEVLTQM QSGYVLMMDY LQNNFREQQY KFSRQVPSY 300
TGKEEIEHAV CSESEPNVQ ADPENYTSLL VWERPRVYV DTMIEKFAVL YQQLDGEDQT 360
HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYKGY SDQLIVDMPT DNPEDLDFPE 420
LIGTEEIIKE EEEGKDIEE AIVNPGRDSA TNQIRKKEPQ ISTTTHYNR GTKYNEAKTN 480
RSPTRGSEFS GKGDVPNTS NSTSQPVTKL ATEKDISLTS QTVTELPFH TVEGTSASLN 540
GSKTVLRSPH MNLSTAESL NTVSIYEY EESLTSFKL DTGAEDSSGS PATSAIPFIS 600
ENISQGYIFS SENPEITTYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSSSTDI 660
TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVMG SQGPSVTDLE MPHYSTPAYF 720
TEVTPHAPT SSRQDLVST VNVVYSQTTQ PVYNEASNS HESRIGLAE GLESEKKAIV 780
LVIVSALTFI CLVVLVGILI IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPIISDDVGAI 840
IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCITVDLG ITADSSNHPD NKHKRYINIV 900
AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA QGPLKSTAE DFWRMIWEHN 960
EVIVMITNLV EGRRKCDQY WPADGSEYGN NPLVTQKSVQ VLAYYTVRN FTLRNTKIKK 1020
SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFRKAA YAKRHAVGPV VVHCSAGVGR 1080
GTIVLDSML QIQHEGTN NIFGFLKHIR SQRYNLVQTE EQYVFIHDTL VEAILSKETE 1140
LDSHIHAYVN ALLIPGPAG KTKLEKQFQL TSPRLCEGR TISAHCNLP PLGTDPTSA 1200
SRVAGTILLS QSNIQQSDYS AALKQCNREK NRTSSIIPVE RSRVGISSLS GEGTDYINAS 1260
YIMGYYSNE FIITQHPLLH TIKDFWRMIW DHNAQLVVM I PDQGNMAE DEFVYWPNDK 1320
INCESFKVTL MAEEHKCLSN EEEKLIQDPI LEATQDDYVL EVRHFQCPKW PNDSPISK 1380
FELISVKEE AANRDGPMIV HDEHGGVTAG TFCALTTLMH QLEKENSVDV YQVAKMINLM 1440
RPGVFADIEQ YQFLYKVLIS LVGTRQEENP STSLDSNGAA LPDGNIAESL ESLV 1494

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Seq ID NO: C316 Protein Sequence
Protein Accession #: Eos sequence

80

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1      11      21      31      41      51
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MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGA LNQKNWG KKYPTCNSPK 60
QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
FKASKITFWH GKCKNMSDGS EHSLEGQKFP LEMQIYCFDA DRPSSFEAV KKGKGLRALS 180
ILFEVGTSEN LDFKAIIDGV ESVSRFGKQA ALDPPILLNL LPNSTDKYYI YNGSLTSPPC 240

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	TDTVDMIVFK	DTVSISESQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIEHAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTIDGYQD	LGAILNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPEASNSH	420
5	ESRIGLAEG	ESSEKKAIVPL	VIVSALTFIC	LVVLVGILY	WRKCFQTAHF	YLEDSTSPRV	480
	ISTPPTPIFP	ISDDVGAIP	KHFPKHVADL	HASSGFTFEE	ETLKEFYQEV	QSCTVDLGI	540
	ADSSNHDPNK	HKNRYINIVA	YDHSRVKLAQ	LAEDKGKLT	YINANYVDGY	NRPKAYIAAQ	600
	GPKLSTAEFD	WRMIWEHNV	VIVMITNLVE	KGRKCDQYW	PADGSEBYGN	FLVTQKSVQV	660
	LAYYTVRNF	LRNTKIKKGS	QKGRPSGRV	TQYHYTQWP	MGVPEYSLP	LTPVRKAAYA	720
10	KRHAVGPPV	HCSAGVGRG	TYIVLDSMLQ	OIQHEGTVNI	FGPLKHRSQ	RNYLVQTEEQ	780
	YVFIHDTLVE	AILSKEDEV	DSHIHAYVNA	LLIPGPAGKT	KLEKQFQLS	QSNIIQSDYS	840
	AALKQCNREK	NRTSSIIIPVE	RSRVGISSLS	GEGTDYINAS	YIMGYQSN	FIITQHPLH	900
	TIKDFWRMIW	DHNAQLVVM	PDGQNMMAED	FVYWPKNDEP	INCESFKVTL	MAEEHKCLSN	960
	EELKLIQDFI	LEATQDDYVL	EVRFQCPKW	PNPDSPIKST	FELISVIKEE	AANRDGPMIV	1020
15	HDEHGGVTAG	TFCALTLMH	QLEKENSVDV	YQVAKMINLM	RPGVPADIEQ	YQFLYKVLIS	1080
	LVSTRQENP	STSLDSNGAA	LPGDNIAESL	ESL			1113

Seq ID NO: C317 Protein Sequence
Protein Accession #: Eos sequence

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	MRILKRFLAC	IQLLCVCRLD	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNKLKL	KFGQWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
25	FKASKITPHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRPSSPEEAV	KGKGLRALS	180
	ILFEVGTEN	LDPKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDMIVFK	DTVSISESQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIEHAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTIDGYQD	LGAILNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPE	420
30	LIGTEETIKE	EEBEGKIDEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTYKNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITTYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NWFFPSSTDI	660
	TAQPDVSGSR	ESPLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
35	TEVTPHAFIP	SSRQQLVST	VNVVYSQTQ	PVYNEASNS	HESRIGLAEG	LESEKKAIVP	780
	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTFEE	FETLKEFYQE	VQSCTVDLGI	TADSSNHDPN	KHKNRYINIV	900
	AHDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPKLSTAE	FWRMIWEHNV	960
	EVIVMITNLV	EKGRKCDQY	WPADGSEBYG	NFLVTQKSVQ	VLAYYTVRNF	TLRNTKIKKG	1020
40	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFFVRKAAY	AKRHAVGPPV	VHCSAGVGRG	1080
	GTIVLDSML	QQIQHEGTVN	IFGFLKHRS	QRNYLVQTEE	QYVFIHDTLV	EAILSKETEV	1140
	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQL	TLSPRLBCRG	TISACHNLPL	PGLTDPPTSA	1200
	SRVARTILLS	QSNIIQSDYS	AALKQCNREK	NRTSSIIIPVE	RSRVGISSLS	GEGTDYINAS	1260
	YIMGYQSN	FIITQHPLH	TIKDFWRMIW	DHNAQLVVM	PDGQNMMAED	FVYWPKNDEP	1320
45	INCESFKVTL	MAEEHKCLSN	EELKLIQDFI	LEATQDDYVL	EVRFQCPKW	PNPDSPIKST	1380
	FELISVIKEE	AANRDGPMIV	HDEHGGVTAG	TFCALTLMH	QLEKENSVDV	YQVAKMINLM	1440
	RPGVPADIEQ	YQFLYKVLIS	LVSTRQENP	STSLDSNGAA	LPGDNIAESL	ESL	1493

Seq ID NO: C318 Protein Sequence
Protein Accession #: Eos sequence

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	QSPINIDEDL	TQVNVNKLKL	KFGQWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
55	FKASKITPHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRPSSPEEAV	KGKGLRALS	180
	ILFEVGTEN	LDPKAIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYYI	YNGSLTSPPC	240
	TDTVDMIVFK	DTVSISESQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIEHAV	CSSEPEENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
60	HEFLTIDGYQD	LGAILNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPE	420
	LIGTEETIKE	EEBEGKIDEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTYKNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPPT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPEITTYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NWFFPSSTDI	660
65	TAQPDVSGSR	ESPLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTFAYFP	720
	TEVTPHAFIP	SSRQQLVST	VNVVYSQTQ	PVYNEASNS	HESRIGLAEG	LESEKKAIVP	780
	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTFEE	FETLKEFYQE	VQSCTVDLGI	TADSSNHDPN	KHKNRYINIV	900
	AHDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPKLSTAE	FWRMIWEHNV	960
70	EVIVMITNLV	EKGRKCDQY	WPADGSEBYG	NFLVTQKSVQ	VLAYYTVRNF	TLRNTKIKKG	1020
	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFFVRKAAY	AKRHAVGPPV	VHCSAGVGRG	1080
	GTIVLDSML	QQIQHEGTVN	IFGFLKHRS	QRNYLVQTEE	QYVFIHDTLV	EAILSKETEV	1140
	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQL	TLSPRLBCRG	TISACHNLPL	PGLTDPPTSA	1200
	SRVARTILLS	QSNIIQSDYS	AALKQCNREK	NRTSSIIIPVE	RSRVGISSLS	GEGTDYINAS	1260
75	YIMGYQSN	FIITQHPLH	TIKDFWRMIW	DHNAQLVVM	PDGQNMMAED	FVYWPKNDEP	1320
	INCESFKVTL	MAEEHKCLSN	EELKLIQDFI	LEATQDDYVL	EVRFQCPKW	PNPDSPIKST	1380
	DGRNFLCSDN	PYAPTRKRKF	RGCLPGSQDD	QSDARSCLC			1359

Seq ID NO: C319 Protein Sequence
Protein Accession #: XP_002914.4

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	MQDIDIGLEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFR	TRPLEQDQAL	ETAARAEGLS	60
	LDQSMHSQLR	ILDBEHPKGR	YHGLSALKP	IRTTSKHQHP	VDNAGLFSCM	TFSWLSLAR	120
	VAHKKGELSM	EDVMSLSKHE	SSDVNCRRL	RLNQBELNEV	GPDAASLRV	VWIFCRTRLI	180

5	LSIVCLMITQ	LAFSGSPAFM	VKHLLEYTQA	TESNLQYSLL	LVLGILLTEI	VRWSLALTW	240
	ALNYRTGVR	RGAILTMAFK	KILKLNKE	KSLGELINIC	SNDGQRMFEA	AAVGSLLAGG	300
	PVVAILGMIY	NVILIGPTGF	LGSAPFIFY	PAMMFASRLT	AYFRKCVAA	TDERVQKNE	360
	VLTYIKFIKM	YAWKAPFSQS	VQKIREEERR	ILEKAGYFQS	ITVGAPIV	VIASVVTFSV	420
	HMTLGFDLTA	AQAFVTVTVF	NSMTFALKVT	PFSVKSLSEA	SVAVDRPKSL	FLMEEVHMIK	480
	NKPASPHIKI	EMKNATLAWD	SSHSIQNSP	KLTPKMKDK	RASRGKKEKV	RQLQRTHEQA	540
	VLAQKQGHLL	LDSDERPSPE	EEEGKHIHLG	HLRLQRTLHS	IDLEIQEGKL	VGICGSVSGG	600
	KTSLISAILG	QMTLLEGSIA	ISGTFAYVAQ	QAWILNATLR	DNILPGKEYD	EERYNSVLNS	660
10	CCLRPDLAIL	PSSDLTEIGE	RGANLGGQR	QRISLARALY	SDRSIYILDD	PLSALDAHVG	720
	NHIFNSAIRK	HLKSKTVLFF	THQLQYLVD	DEVIFMKEGC	ITERGTHEEL	MNLNGDYATI	780
	FNLLIGETP	PVEINSKKE	SGSQKKSQDK	GPKTGSVKKE	KAVKPEEGQL	VQLEEKQGS	840
	VPWSVYGVI	QAAGGPLAF	VIMALFMLNV	GSTAFSTWWL	SYWIKQSGN	TTVTRGNETS	900
	VSDSMKDNPH	MQYASIAL	SMAVMLILKA	IRGVVFKGT	LRASSRLHDE	LFRRILRSPM	960
	KFFDTTPTGR	ILNRFKMD	EVDVRLPFQA	EMFIQNVILV	FFCVGMIAGV	FWFLVAVGP	1020
15	LVILFSLVHT	VSRLVIRELK	RDNITQSPF	LSHITSSIQG	LATIHAYNKG	QEFHLRYQEL	1080
	LDDNQAPFFL	FTCAMRWLAV	RDLISIALI	TTTGLMIVLM	HQIIPPAYAG	LAIYAVQLT	1140
	GLFQFTVRLA	SETEARFTSV	ERINHYIKTL	SLEAPARIKN	KAPSPDWQPE	GEVTFENAE	1200
	RYRENLPVL	KKVSPTIKPK	EKIGIVGRTO	SGKSSLMAL	FRVLVSGGC	IKIDGVRISD	1260
	IGLADLRSLK	SIIPQEPVLF	SGTVRSNLD	FNQYTEDQIW	DALERTHME	CIAQLPLKLE	1320
20	SEVMENGDNF	SVGERQLLCI	ARALLRHCKI	LILDEATAAM	DTETDLIQE	TIREAFADCT	1380
	MLTIAHRLHT	VLGSDRIMVL	AQQQVVEFDT	PSVLLSNDSS	RFYAMFAAAE	NKVAVKG	1437

Seq ID NO: C320 Protein Sequence
Protein Accession #: NP_005679.1

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	LDSMHSQRL	ILDEEHPKGR	YHGLSALKP	IRTTSKHQHP	VDNAGLPSCM	TFSWLSLAR	120
30	VAHKKGELSM	EDVWSLSKHE	SSDVNCRRL	RLWQEBELNEV	GPDAASLRV	VWIFCRTRLI	180
	LSIVCLMITQ	LAFSGSPAFM	VKHLLEYTQA	TESNLQYSLL	LVLGILLTEI	VRWSLALTW	240
	ALNYRTGVR	RGAILTMAFK	KILKLNKE	KSLGELINIC	SNDGQRMFEA	AAVGSLLAGG	300
	PVVAILGMIY	NVILIGPTGF	LGSAPFIFY	PAMMFASRLT	AYFRKCVAA	TDERVQKNE	360
	VLTYIKFIKM	YAWKAPFSQS	VQKIREEERR	ILEKAGYFQS	ITVGAPIV	VIASVVTFSV	420
35	HMTLGFDLTA	AQAFVTVTVF	NSMTFALKVT	PFSVKSLSEA	SVAVDRPKSL	FLMEEVHMIK	480
	NKPASPHIKI	EMKNATLAWD	SSHSIQNSP	KLTPKMKDK	RASRGKKEKV	RQLQRTHEQA	540
	VLAQKQGHLL	LDSDERPSPE	EEEGKHIHLG	HLRLQRTLHS	IDLEIQEGKL	VGICGSVSGG	600
	KTSLISAILG	QMTLLEGSIA	ISGTFAYVAQ	QAWILNATLR	DNILPGKEYD	EERYNSVLNS	660
40	CCLRPDLAIL	PSSDLTEIGE	RGANLGGQR	QRISLARALY	SDRSIYILDD	PLSALDAHVG	720
	NHIFNSAIRK	HLKSKTVLFF	THQLQYLVD	DEVIFMKEGC	ITERGTHEEL	MNLNGDYATI	780
	FNLLIGETP	PVEINSKKE	SGSQKKSQDK	GPKTGSVKKE	KAVKPEEGQL	VQLEEKQGS	840
	VPWSVYGVI	QAAGGPLAF	VIMALFMLNV	GSTAFSTWWL	SYWIKQSGN	TTVTRGNETS	900
	VSDSMKDNPH	MQYASIAL	SMAVMLILKA	IRGVVFKGT	LRASSRLHDE	LFRRILRSPM	960
45	KFFDTTPTGR	ILNRFKMD	EVDVRLPFQA	EMFIQNVILV	FFCVGMIAGV	FWFLVAVGP	1020
	LVILFSLVHT	VSRLVIRELK	RDNITQSPF	LSHITSSIQG	LATIHAYNKG	QEFHLRYQEL	1080
	LDDNQAPFFL	FTCAMRWLAV	RDLISIALI	TTTGLMIVLM	HQIIPPAYAG	LAIYAVQLT	1140
	GLFQFTVRLA	SETEARFTSV	ERINHYIKTL	SLEAPARIKN	KAPSPDWQPE	GEVTFENAE	1200
	RYRENLPVL	KKVSPTIKPK	EKIGIVGRTO	SGKSSLMAL	FRVLVSGGC	IKIDGVRISD	1260
	IGLADLRSLK	SIIPQEPVLF	SGTVRSNLD	FNQYTEDQIW	DALERTHME	CIAQLPLKLE	1320
50	SEVMENGDNF	SVGERQLLCI	ARALLRHCKI	LILDEATAAM	DTETDLIQE	TIREAFADCT	1380
	MLTIAHRLHT	VLGSDRIMVL	AQQQVVEFDT	PSVLLSNDSS	RFYAMFAAAE	NKVAVKG	1437

Seq ID NO: C321 Protein Sequence
Protein Accession #: NP_005553.1

55	1	11	21	31	41	51	
	MPALWLGCL	CPSLLPAAR	ATSRREVDC	NGKSRQCIFD	RELHRTQNG	FRCLNCNDNT	60
	DGIHCEKCN	GFYRERDR	CLPCNCSKG	SLSARCDNSG	RCSCPKGVGT	ARCDRLPGF	120
60	HMLTDAGCTQ	QRLDLSKCD	CDPAGIAGPC	DAGRCVCKPA	VTGERCDRCR	SGYINLDGGN	180
	PEGCTQCFYC	GHSASCRSSA	EYSVHKITST	FHQDVGWKA	VQRNGSPAKL	QWSQRHQDV	240
	SSAQRDPVY	FVAPAKFLGN	QQVSYGQSLS	FDYRVDRGGR	HPSAHDVILE	GAGLRITAPL	300
	MPLGKTLPCG	LTKTYTFRLN	EHPNNWSPQ	LSYFEYRRL	RNLTLALIRA	TYGEYSTGYI	360
	DNVTILSARP	VSGAPAPWVE	QCICPVGYGK	QPCQDCASGY	KRDSARLGPF	GTICPCNCQG	420
65	GGACDPDTGD	CYSGDENPDI	ECADCPIGFY	NDPHDFRSC	PCPCHNGFSC	SVMPEEEVV	480
	CNNCPGVTG	ARCELADGY	FGDPFGERGP	VRPCQPCQCN	MNVDPASGN	CDRLTGRCLK	540
	CIHNTAGIYC	DQCKAGYFGD	PLAPNPADKC	RACNCPMGS	EPVGCERSGT	CVCKPGFGGP	600
	NCEHGAPSCP	ACYNQVKIQM	DQFMQQLQRM	EALISKAQGG	DGVVPDTELE	GRMQQAQAL	660
	QDILRDAQIS	EGASRSGLG	LAKVRSQENS	YQSRLLDLKM	TVERVALGS	QYQNRVDRTH	720
70	RLITQMQLSL	AESASLGNT	NIPASDHYVG	PNGFKSLAQE	ATRLAESHVE	SASNMEQLTR	780
	ETEDYSKQAL	SLVRKALHEG	VSGSGSPDG	AVVQGLVEKL	EKTKSLAQQL	TREATQAEIE	840
	ADRSYQHSRL	LLDSVSRLOQ	VSDQSFQVEE	AKRIKQKADS	LSTLVTRHMD	EFKRTQKNLG	900
	NWKEEAQQLL	QNGKSGREKS	DQLLSRANLA	KSRAQEAISM	GNATPYEVES	ILKNLREFDL	960
	QVDRKAEAB	EMKRLSYIS	QKVSASDKT	QQAERALGSA	AADAQRAKNG	AGEALEISSE	1020
75	IEQEIGSLNL	EANVTADGAL	AMEKGLASLK	SEMRVEGEL	ERKELEFDTN	MDAVQMVITE	1080
	AQKVDTAKN	AGVTIQDTLN	TLDGLLHMD	QPLSVDEEGL	VLEEQKLSRA	KTQINSQLRP	1140
	MMSELEERAR	QQRGHLHLE	TSIDGILADV	KNLENIRDNL	PPGCYNTQAL	EQ	1193

Seq ID NO: C322 Protein Sequence
Protein Accession #: NP_066924.1

80	1	11	21	31	41	51	
	MANAGLQLLG	FILAPLGNIG	AIVSTALPQW	RIYSYAGDNI	VTAQAMYEG	WMSCVSQSTG	60

QIQCKVFDL LNLSSLTQAT RALMVVGILL GVIAIFVATV GMKCMKLED DEVQKMRMAV 120
 IGGAILLAG LAIVATANY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCLLGA 180
 LLCCSCPRKT TSYTPRPYP KPAPSSGKDY V 211

5 Seq ID NO: C323 Protein Sequence
 Protein Accession #: AAM77876

10 1 11 21 31 41 51
 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKCSA SRIWCSDPSP GIVAFPRLEP 60
 NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFVAHKA FLKNSNLQHI 120
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQKAKSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSTILSCSV AGDPVFNMYW DVGNLVSKHM 240
 NETSHTQGS RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 15 WCIPPTVKGN PKPALQWFFN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTRGH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

20 Seq ID NO: C324 Protein Sequence
 Protein Accession #: NP_006171.1

25 1 11 21 31 41 51
 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKCSA SRIWCSDPSP GIVAFPRLEP 60
 NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFVAHKA FLKNSNLQHI 120
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQKAKSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSTILSCSV AGDPVFNMYW DVGNLVSKHM 240
 NETSHTQGS RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 30 WCIPPTVKGN PKPALQWFFN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTRGH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF ISNDDDSASP 480
 LHHSNGSNT PSSSEGGFDA VIIGMTKIPV IENPQYFGIT NSQLKPDITFV QHIKRHNIVL 540
 KRELGEAGFG KVLAEACYNL CPEQDKILVA VKTLKDASDN ARKDFHREAS LLTNLQHEHI 600
 35 VKFYGVCEBG DPLIMVFEYM KHGDLNKLFLR AHGEDAVLMA EGNPFTLTQ SQMLHIAQOI 660
 AAGMVLASQ HFVHRDLATR NCLVGENLLV KIGDFGMSRD VYSTDYRVG GHTMLPIRMW 720
 PPESIMYRK TTESDVWSLG VVLWEIFTYG KQPHYQLSNN EVIECITQGR VLQRPRTCPQ 780
 EYELMLGCV QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG 822

40 Seq ID NO: C325 Protein Sequence
 Protein Accession #: Eos sequence

45 1 11 21 31 41 51
 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKCSA SRIWCSDPSP GIVAFPRLEP 60
 NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFVAHKA FLKNSNLQHI 120
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQKAKSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPAN LAAPNLTVEE GKSTILSCSV AGDPVFNMYW DVGNLVSKHM 240
 NETSHTQGS RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 50 WCIPPTVKGN PKPALQWFFN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTRGH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

55 Seq ID NO: C326 Protein Sequence
 Protein Accession #: NP_570843.1

60 1 11 21 31 41 51
 MPLKHYLLLL VGCQAWGAGL AYHGCPSSECT CSRASQVECT GARIVAVPTP LPWNAMSLOI 60
 LNTHITELNE SPFINISALI ALRIEKNELS RITPGAFNRL GSLRYLSLAN NKQLVLPGL 120
 FQGLDSLES LLSSNQLLOI QPAHFSQCSN LKELQLHGNH LEYIPDGAFF HLVLTKLNL 180
 GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQO NQIGLLSPGL 240
 FHNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFG PMPNLRLEWL 300
 YDNHISLSD NVFNNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLGNV 360
 65 FRMLANLQNI SLQNNRLRQL PGNIFANVNG LMAIQLQNNQ LENPLGIFD HLKGLCELRL 420
 YDNFWRCDS ILPLRNWLLL NQPRIGTDTV PFCFSPANVR GQSLIIINVN VAVPSVHVE 480
 VPSYPETPMY PDPSPYDPTT SVSSTTELTS PVEDYDILT IQVTDERSVW GMTQAQSGLA 540
 IAAIVIGIVA LACSLAACVG CCCCKRSQA VLMQNKAPNE C 581

70 Seq ID NO: C327 Protein Sequence
 Protein Accession #: NP_002649.1

75 1 11 21 31 41 51
 MRALLARLLL CVLVVSDSKG SNELHQVPSN CDCINGGTCV SNKYFSNIHW CNCPKFGGQ 60
 HCEIDKSKTC YBGNHGFYRG KASTDTMGRP CLPWNATVL QQTYHAHRSD ALQLGLGKH 120
 YCRNPDNRRR PFCYVQGLK PLVQECMVHD CADGKPPSSP PEELKFPCCQ KTLRPRFKII 180
 GGEFTTIENQ PWFAAIYRRH RGSVTVYCG GSLISPCWVI SATHCFIDYP KKEIDIYVYG 240
 RSRLNSNTQS EMKPEVENLI LHKDYSADTL AHNDIALLK IRSKEGRCQA PSRTIQTICL 300
 80 PSMYNDPQFG TSCEITGFGK ENSTDYLYPE QLRMTVVKLI SHRECCQPHY YGSEVTTKML 360
 CAADPQWKTD SQGDSGGPL VCSLQGRMTL TGIVSVGRGC ALKDKPGVYT RVSHFLPWIR 420
 SHTKEENGLA L 431

Seq ID NO: C328 Protein Sequence
 Protein Accession #: XP_087254.1

1 11 21 31 41 51
 5 MQPRECSING MKYQIEINGRL VPEGPTPDSS EGNLSYLSSL SHLNNLSHLT TSSSFRTSPE 60
 NETELIKEHD LFPKAVSLCH TVQISNVQTD CTGDGPWQSN LAPSQLEYA SSPDEKALVE 120
 AAARIGIVFI GNSSETMEVK TLGKLELYKL LHILEFDSOR RRMSVIVQAP SGEKLLFAKG 180
 AESSILPKCI GGEIEKTRIH VDEFALKGLR TLCIAYRKFT SKEYBEIDKR IFEARTALQQ 240
 REEKLAAPVQ FIEKDLILLG ATAVEDRLQD KVRTIEALR MAGIKVWVLT GDKHETAVSV 300
 10 SLSCGHFHT MNILELINQK SDSECAEQLR QLARRITEDH VIQHGLVVDG TSLSLALREH 360
 EKLFMVFCRN CSAVLCCRMA PLQKAKVIRL IKISPEKPIT LAVGDGANDV SMIQEAHVGI 420
 GIMGKEGRQA ARNSDYAIAR FKPLSKLLFV HGHFYIIRIA TLVQYFFYKN VCFITPQFLY 480
 QFYCLFSQQT LYDSVYLTLY NICFTSLPIL IYSLLEQHVD PHVLQNKPTL YRDISKNRLL 540
 SIKTFLYWTI LGFSHAFIFP FGSYLLIGKD TSLLGNGQMP GNWTFGLTVF TVMVTITVTK 600
 15 MALETHFWTW INHLVTWGS I FYFVFSLFY GGILWPLGSS QNMVFPFIQL LSSGSAWFAI 660
 ILMVVTCLFL DIKKVFDRIH LHPTSTKCAQ LTETNAGIKC LDSMCCFPFG EAACASVGRM 720
 LERVIGRCSP THIRSWSAS DFFYTNDRSI LTLSTMDSS C 761

Seq ID NO: C329 Protein Sequence
 Protein Accession #: XP_087461.1

1 11 21 31 41 51
 20 MLPLLAALLA AACPLPFVRG GAADAPGLLG VPSNASVNAS SAASPSPRGC WPRRPPGPPS 60
 ARARRRRRR RRLCNISVQR QMLSSLLVRW GRPRGFQCDL LLFSTNAHGR APFAAFHERV 120
 25 GPPLLIHLG LAAGGAQDDL RLCVGCWVR GRRTGRLRPA AAPSAATAA GAPTALPAYP 180
 AAEPPLPLML QGEPLHFCCL DFSLEELQGE PGWRLNRKPI ESTLVACFMT LVIVVWSVAA 240
 LIWPVPIAG FLPNMGMEQR TTASTAATP AAVPAGTTAA AAAAAAATA AVTSGVATK 299

Seq ID NO: C330 Protein Sequence
 Protein Accession #: XP_051522.2

1 11 21 31 41 51
 35 MDLHLFDYSE PGNFSDISWP CNSSDCIVVD TVMCPNMPNK SVLLYTLSPF YIFIFVIGMI 60
 ANSVVWVNI QAKTTGYDTH CYILNLAIA LWVLTIPVW VVSLVQHQQV PMGELTCKVT 120
 HLIFSINLFG SIFFLTQMSV DRYLSITYFT NTPSSRKKM RRVVCILVWL LAFCVSLPDT 180
 YLKVITVSAS NNETYCRSFY PEHSIKEWLI GMELVSVVLG FAVPFSIIAV FYPLLARAI 240
 40 ASSDQEKHSS RKIIPSYVUV FLVCWLPYHV AVLLDIFSIL HYIPFTCRLE HALFTALHVT 300
 QCLSLVHCCV NPLVYSFINR NYRYELMKAF IFKYSAKTGL TKLIDASRV S ETEYSALEQS 360
 TK 362

Seq ID NO: C331 Protein Sequence
 Protein Accession #: NP_000341.1

1 11 21 31 41 51
 45 MGFVRQIQLL LMKQWTLRKR QKIRFVVELV WPLSLFLVLI WLRNANPLYS HHECHFPNKA 60
 MPSAGMLPWL QGIFCNVNNP CFQSPTPGES PGIVSNYNN S ILARVYRDFQ ELLAQNAPESQ 120
 50 HLGRITWELH ILSQPMOTLR THERIAGRGR IRIRDILKDE ETTLTFLIKN IGLSDSVVYL 180
 LINSQVRPEQ FARGVFDLAL KDIAACEALL ERFIIPSQRR GAKTVRYALC SLSQGTQLWI 240
 EDTLYANVDF FKLPFVLPTL LDSSSQGINL RSWGGLSDM SPRIQEFIRH PSMQDILLWT 300
 RPLMQNGGPE TFKLMGILS DLLCGYPEGG GSRVLSFNWY EDNNYKAFGL IDSTRKDIY 360
 SYDRRTTSFC NALIQSLEEN PLTKIAMRAA KPLLMGKILY TPDSPAARRI LKNNANSTFEE 420
 55 LEHVRLKVA WEEVGQIIFY FFDNSTQMNM IRDTLGNPTV KDFLNRLQGE EGITAEAILN 480
 FLYKGRRESQ ADDMANFDWR DIPNITDRTL RLNVQYLECL VLDKFESYND ETQLTQRAIS 540
 LLEENMFAG VVFPDMYPTW SSLPFHVYK IRMDIDVVEK TNKIKDRYD SGPRADPVED 600
 FRYINGGPAY LQDMVEQGIT RSQVQAEAPV GIYLLQMPYP CFVDDSPMII LNRCPPIPMV 660
 LAWIYSVMT VKSIVLEKEL RLKETLKNQG VSNVAVICTW FLDSPFSIMS SIFLLTIFIM 720
 60 HGRILHSDP FILFLPLAF STATIMLCPL LSTFFSKASL AAACSGVIYF TLYLPHILCF 780
 AWQDRMTAEL KKAVALSLSPV AFGFGTEYLV RFEBOGLGLQ WSNIGNSPTE GDEFSFLLSM 840
 QMMLLDAACT GLLAWYLDQV FPGDYGTPLP WYFLLQESYV LSGEGCSTRE ERALEKTEPL 900
 TEETEDPREP EGIHDSFPER EHPGWVPGVC VKNLVKIFEP CGRPAVDRLN ITFYENQITA 960
 65 FYLHNGAGKT TTLSILTGLL PPTSGTVLVG GRDIETSLDA VRQSLGMCQ HNILFHLITV 1020
 AEHMLFYAQL KGKSOBEAQL EMEAMLEDTG LHHKRNEEAQ DLSSGMQRKL SVAIAPVGA 1080
 KVVILDEPTS GVDPSYRRSI WDLKLYRSG RTIIMPTRHM DEADHQGDRI AIIAQGRLYC 1140
 SGTPLFLKNC FGTGLYTLV RKMKNIQSOR KGSEGTCSGS SKGFSTTCPA HVDDLTPQV 1200
 LDGDNVLEMD VVLHHVPEAK LVEICIGQLI FLLPNKNFKH RAYASLPREL EBTLADLGLS 1260
 70 SFGISDTPL EIFLKVTEDS DSGPLFAGGA QQKRENVNPR HPCLGPREKA GQTPQDSNVC 1320
 SPGAPAAHPE QGPPPEPECP GPOLNTGTQL VLQHVQALLV KRFBORTIRSH KDFLAQIVLP 1380
 ATFVFLALML SIVILPGEY PALTLHPWY GQYTFFSMD EPGSEQFTVL ADVLLNKPFG 1440
 GNRCLKEGWL PEYPCGNSTP WKTPSVSPNI TQLFQKQWT QVNPSPSCRC STREKLTMPL 1500
 75 ECPGAGGLP PPQRTQRSTE ILQDLTDNRN SDFLVKTYPA LIRSSLSKFP WNEQRYGGI 1560
 SIGGLFVVP ITGEALVGL SDLGRIMNVS GGPITREASK EIPDFLKHLE TEDNIKVWFN 1620
 NKGHNAVLSF LAVAHNAIRL ASLPKDRSPE EYGITVISQP LNLTKQLSE ITVLTTSVDA 1680
 VVAICVIFSM SFVPASFVLY LIQERVNKS HLQFISGVSP TTYWVTFNFW DIMNYSVSAG 1740
 LVVGIFIGFQ KAYTSPENL PALVALLLLY GMAVIFPMYP ASFLFDVPST AYVALSCANL 1800
 FIGINSSAIT FIELEFDNNR TLLRFNAVLR KLLIVFPHFC LGRGLLDLAL SQAQVTVYAR 1860
 80 FGEHSANPP HDLIGKQLF AMVVEGVVYF LLTLVORHF FLSQWIAEPT KEPIVDEDD 1920
 VAERQRIT GGNKTDILRL HBLTKIYLG TSSPAVDRLCV GVRPGECFGL LGVNGAGKTT 1980
 TFKMLTGDTT VTSGDATVAG KSILTNISEV HQNMGYCPQF DAIDELLTGR EHLVLYARLR 2040
 GVPAESEIEKV ANWYSKSLG TVYADCLAGT YSGGNKRKLS TAILIGCPP LVLLDEPTTG 2100
 MDQARRMLW NVIVSIIRKG RAVVLTSHSM BECEALCTRL AIMVKGAFCR MGTIQLHLSK 2160
 FGDGVIYTMK IKSFKDILLP DLNPFVQPFQ GNFFGSVQRE RHYNMLQFQV SSSSLARIFQ 2220
 LLLSHKOSTL IBEYSVTQTT LDQVFVNFAK QQTESHDLPL HPRAAGASRQ AQD 2273

Seq ID NO: C332 Protein Sequence
Protein Accession #: NP_006662.2

5
1 11 21 31 41 51
MVPHAILARG RDVCCRNGLL ILSVLSVIVG CLLGFFLRTR RLSPOEISYF QPFGELLMRM 60
LRMMILPLVV SSIMSGLASL DAKTSSRLGV LTVAYYLWTT FMAVIVGIFM VSIHFGSAA 120
10 QKETTEQSGK PIMSSADALL DLIRNMFAN LVEATFKQYR TKTPPVVKSP KVAPEEAPPR 180
RILYGVQOEB NGSHVQNFAL DLTPPEVVY KSEPGTSDGM NVLGIVFFSA TMGIMLGRMG 240
DSGAPLVSCF QCLNESVMKI VAVAVWYFPF GIVFLIAGKI LEMDDPRAVG KCLGFYSVTV 300
VCGLVLRHGLF ILPLLYFFIT KKNPIVFIRG ILQALLIALA TSSSSATLPI TFKCLLENMH 360
IDRRIARFVL PVGATINMDG TALYEAVAAI FIAQVNNYEL DFGQIITISI TATAASIGAA 420
15 GIPQAGLVTM VIVLTSVGLP TDDITLIIAV DWALDRFRM INVGLDALAA GIMAHICRKD 480
FARDTGTEKL LECETKPVSL QEIVAAQONG CVKSVABASE LTLGPTCPHH VPVQVERDEE 540
LPAASLHCT IQISELETNV 560

Seq ID NO: C333 Protein Sequence
Protein Accession #: NP_005680.1

20
1 11 21 31 41 51
MVTGVNYCEA EGPVGPAMWQ DGLSPCFFFT LVPSTERMALG TLALVLALPC RRRERPAGAD 60
SLSMGAGPRI SPYVLQLLLA TLQALPLAG LAGRVGTARG APLPSYLLA SVLESAGAC 120
25 GLWLLVVERS QARQLAMGI WIKPRHSPGL LLLWTVAFPA ENLALVSWNS PQWWHARADL 180
GQQVQFSLWV LRYVVSGLF VLGLWAPGLR PQSYTLQVHE EDQDVERSQV RSAAQQTWR 240
DFGRKLRLLS GYLWPRGSPA LQLVVLICLG LMGLERALNV LVPIFYRNIV NLLTEKAPWN 300
SLAWTVTSYV FLKPLQGGGT GSTGFVSNLR TFLWIRVOQF TSBRELLIF SHLHELRLW 360
HLGRRATGEVL RIADRGTSV TGLLSYLVEN VIPTLADIII GIIYFSMFFN AWFGLIVFLC 420
30 MSLYLTITIV VTEWRTKFRR AMNTQENATR ARAVDSLLNF ETVKYNAES YEVEERYEAI 480
IKYQLEWKS SASVLLNQT QNLVIGLGLL AGSLLCAYFV TEQKLQVGDY VLFGTYYIQL 540
YMLNWFQTY YRMIOQTNFID MENMFDLLKE ETEVKDLPGA GPLRFQKGR IEFENVHFSYA 600
DGRETLQDVS FTVMPQOTLA LVGPGSGAGKS TILRLRFPY DISSGCIRID QODISQVTOA 660
35 SLRSHIGVVP QDTVLFNNDTI ADNIRYGRVT AGNDEVEAAA QAAGIHDAIM APFEGYRTQV 720
GERGLKSGG EKQRVAIART ILKAPGIILL DEATSALDTS NERAIQASLA KVCANRTTIV 780
VAHRLSTVNV AQILVIKDG CIVERGRHEA LLSRGVYAD MWQLQQQOEB TSEDTPQTM 840
ER 842

Seq ID NO: C334 Protein Sequence
Protein Accession #: NP_000667.1

40
1 11 21 31 41 51
MLLETQDALY VALELVIAAL SVAGNVLVCA AVGTANTLQT PTNYFLVSLA AADVAVLFA 60
45 IFFAITISLG FCTDFYGLF LACFVLVLTQ SSIFSLAVA VDRYLAICVP LRYKSLVTGT 120
RARGVIAVLW VLAFGIGLTP FLGWNKSDSA TNNCTEPWDG TTNESCCLVK CLFENVVEMS 180
YMYVFNFGCC VLPPLIMLV IYIKIFLVAC RQLQRTLM D HSRITLQREI HAAKSLAMIV 240
GIFALCNLHV HAVNCVTLEF PAQGNKPKN AMNMAILLSH ANSVVNPIVY AYRNRDFRYT 300
50 FHKIISRYLL CQADVKSNG QAGVQPALGV GL 332

Seq ID NO: C335 Protein Sequence
Protein Accession #: NP_443164

55
1 11 21 31 41 51
MGLGARGAWA ALLGLTLQVL ALLGAHESA AMAETLQHVP SDHTNETSNS TVKPPTSVAS 60
DSSNTTIVTM KPTAASNTIT PGMVSTNMTS TTLKSTPKTT SVSQNTSQIS TSTMVTNHS 120
SVTSAASSVT ITTMHSEAK KGSKFDTGSP VGGIVLTIGV LSLIYIGCKM YYRRRGIRYR 180
60 TIDEHDAII 189

Seq ID NO: C336 Protein Sequence
Protein Accession #: NP_004186.1

65
1 11 21 31 41 51
MAQHGMAGAP RALCGLALLC ALSLGQRPTG GPGCGPGRLL LGTGTARCC RVHTTRCCRD 60
YPGECCSEW DCMCVQPEFH CGDPCCTTCR HHPCCPGQGV QSQGFSGFG QCIDCASGTF 120
SGGHEGHCCK WTDCTQFGFL TVPPGNKTHN AVCVPGSPPA EPLGWLTVVL LAVAACVLLL 180
70 TSAQLGLHIW QLRSCMWPR ETQLLEVPV STEDARSCQF PEEERGERSA EEKRLGLDLW 240
V 241

Seq ID NO: C337 Protein Sequence
Protein Accession #: BAC03767.1

75
1 11 21 31 41 51
MGCDGRVSG LARNLQPTLT YWSVFFSFLG CIAFLGPTLL DLRCQTHSSL PQISWVFFSQ 60
QLCLLGSAL GGVFKRTLAQ SLWALETSSL AISLVFAVIP FCRDVKVLAS VMALAGLAMG 120
80 CIDTVANMQL VMYQKDSAV FLQVLEFPVG FGALLSPLIA DPFLSEANCL PANSTANTTS 180
RGHLFHVSRV LGQEHVDAKP WSNQTPPGLT PKDGAGTRVS YAFWIMALID LPVPMVIML 240
LSKERLLTCC PQRRPLLLSA DELALETQPP EKEDASSLPP KFQSHLGHED LPSCCQRKRL 300
RGAPYSFFAI HITGALVLFM TDGLTGAYSA FVYSYAVEKP LSVGHRVAGY LPSLFWGFIIT 360
LGRLLSIPIS SRMKPATMVF INVVGVVVTF LVLLIPSYNV VFLFVGTSAL GLFLSSTFFS 420
MLAYTEDSIQ YKGCATTVLV TGAGVGEMVL QMLVGSIFQA QGSYSFLVCG VIFGCLAFTF 480

YILLFFHRM HPGLPSVPTQ DRSIGMENSE CYQR

514

Seq ID NO: C338 Protein Sequence
Protein Accession #: NP_002194.1

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1	11	21	31	41	51	
MGPERTGAAP	LPILLVLALS	QGIILNCCLAY	NVGLPEAKIF	SGPSSEQFGY	AVQQFINPKG	60
NWLLVGSPWS	GFPENRMGDV	YKCFVDLSTA	TCEKLNLTQS	TSIPNVTEMK	TNMSLGLILT	120
RNMGTGGFLT	CGPLMAQCGQ	NQYYTTGVC	DISPDFQLSA	SFSPATQPCP	SLIDVVVVCD	180
ESNSIYPWDA	VKNFLKFKVQ	GLDIGPTKTQ	VGLIQYANNP	RVVFNLTATK	TKEEMIVATS	240
QTSQYGGDLT	NTFGATQYAR	KYAYSASAGG	RRSATKVMV	VTDGESHGDS	MLKAVIDQCN	300
HDNILRFRTA	VLGLNLRNAL	DTKNLIKEIK	AIASIPTERY	FFNVSDAAL	LEKAGTLGEQ	360
IPSIETVQG	GDNFQMEMSQ	VGFSADYSSQ	NDILMLGAVG	AFGWSGTIVQ	KTSHGHLIPP	420
KQAFDQILQD	RNHSSYLGSY	VAAISTGEST	HFVAGAPRAN	YTGQIVLYSV	NENGNITVIQ	480
AHRGDQIGSY	FGSVLCSDV	LKDTITDVL	VGAPMYMSDL	KKEEGRVYLF	TIKKGILGOH	540
QFLEGGEGIE	NTRFGSAIAA	LSDINMDGPN	DVIVGSPLEN	QNSGAVYIYN	GHQGTIRTKY	600
SQILGSDGA	FRSHLQYFGR	SLDGYGDLNG	DSITDVSIGA	FGQVVQLWSQ	SIADVAIEAS	660
FTPEKITLVN	KNAQIILKLC	PSAKFRPTKQ	NNQVAIVYNI	TLDADGFSR	VTSRGLFKEN	720
NERCLQKNMV	VNQACSCEPH	IYIQEPSDV	VNSLDLRVDI	SLENPGTSPA	LEAYSETAKV	780
PSIPFHKDSY	EDGLCISDLV	LDVRQIPAAQ	EQPFIVSNQN	KRLTFSVTLK	NKRESAYNTG	840
IVVDFSENLF	FASPSLPVDG	TEVTQVVAAS	QKSVACDVGY	PALKREQQVT	FTINFDFNLQ	900
NLQNASLSF	QALSESQEEEN	KADNLVNLKI	PLLYDAEHL	TRSTNINPYE	ISSDGNVPSI	960
VHSFEDVQK	FIFSLKVTG	SVPVSMATVI	IHIPQYTKK	NPLMYLTGQV	TDKAGDISCN	1020
ADINPLKIQ	TSSSVSKSE	NFRHTKELNC	RTASCNVTC	WLKDVHMKGE	YFVNVTIRW	1080
NGTFASSTFQ	TQVLTAAAEI	NTYNPEIYVI	EDMTVTIPLM	IMKPDKEAEV	PTGVIIGSII	1140
AGILLLLALV	AILWKLGGFF	KRYEKMKNP	DEIDETTELS	S		1181

Seq ID NO: C339 Protein Sequence
Protein Accession #: NP_113648.1

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1	11	21	31	41	51	
MYRPRARAAP	EGRVGCAVP	STVLLLLAYL	AYLALGTGVF	WTLEGRAAQD	SSRSFQDKW	60
ELLQNFCTLD	RPAALDSLIR	VQOAYKNGAS	LLSNTTSMGR	WELVGSFFFS	VSTITTIGY	120
NLSPNTMAAR	LFCIFFALVG	IPLNLVVLNR	LGHLMQQGVN	HWASRLGGTW	QDPDKARWLA	180
GSGALLSGLL	LFLLPLPLLF	SHMEGWSYTE	GFYFAPITLS	TVGFGDYVIG	MNPSQRYPLW	240
YKNMVSILW	FGMAWLALII	KLILSQLETP	GRVCSCHHS	SKEDFKSQSW	RQGFDPREPES	300
HSPQGGCYPE	GPMGIHQHLE	PSAHAAGCCK	DS			332

Seq ID NO: C340 Protein Sequence
Protein Accession #: NP_004145.1

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1	11	21	31	41	51	
MEWDNGTGQA	LGLPPTTCVY	RENFKQLLLP	PVYSAVLAAG	LPLNICVITQ	ICTSRRALTR	60
TAVYTLNLAL	ADLLYACSLP	LLIYNYAQGD	HWPFQDFACR	LVRFLFYANL	HGSILPLTCI	120
SPQRYLGI	PLAPWHKRG	RRAAMLVCVA	VWLAVTTQCL	PTAIFATGI	QRNRTVCYDL	180
SPPALATHYM	PYGMALTVIG	FLLPFAALLA	CYCLLACRLC	RQDGPAPFVA	QERRGKAARM	240
AVVVAAAFAR	SFLPFHITKT	AYLAVRSTPG	VPCTVLEAFA	AAYKGTTPPA	SANSVLDPII	300
FYPTQKFKFR	RPHELLQKLT	AKWQRQGR				328

Seq ID NO: C341 Protein Sequence
Protein Accession #: NP_009128.1

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1	11	21	31	41	51	
MQRPGPRLWL	VLQVMGSCAA	ISSMDMERPG	DGKCQPIEIP	MCKDIGYNTM	RMPNLMGHEN	60
QREAAIQLHE	FAPLVEYGC	GHLRFFLCSL	YAPMCTEQVS	TPIPACRVMC	EQARLKCSPI	120
MEQFNFKWPD	SLDCRKLPNK	NDPNYLCEA	PNNGSDEPTR	GSGLFPPLFR	PQRPHSAQEH	180
PLKDGQGRG	GCDNPGKFEH	VEKSASCAPL	CTPGVDVYWS	REDKRFAPVW	LAIWAVLCFF	240
SSAFTVLTFL	IDPARFRYPE	RPIIFLSMCY	CVYSVGYLIR	LPAGAESIAC	DRDSGQLYVI	300
QEGLESTGCT	LVFLVLYYPG	MASLLMWVVL	TLTWFLAAGK	KWGHEATEAN	SSYFHLAANA	360
IPAVKTIILIL	VMRRVAGDEL	TGVCYVGSMD	VNALTGFVLI	PLACYLVIGT	SFILSGFVAL	420
FHIRRMVMTG	GENTDKLEKL	MVRIGLFSVL	YTVPATCVIA	CYFYERLAMD	YWKILAAQHK	480
CKNNQTKTL	DCLMAASIPA	VEIFMVKIFM	LLVVGITSGM	NIWTSKTLQS	WQQVCSRRLK	540
KKSRRRPASV	ITSGGIYKKA	QHPQKTHHGK	YEIPAQSPTC	V		581

Seq ID NO: C342 Protein Sequence
Protein Accession #: NP_005752.1

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1	11	21	31	41	51	
MEVSRRKAPP	RPPRPAAPLP	LLAYILLALAA	PGRGADEFVW	RSEQAIGAIA	ASQEDGVFVA	60
SGSCLDQLDY	SLEHSLRLY	RDQAGNCTEP	VSLAPPARPR	PGSSFSKLLL	PYREGAAGLG	120
GLLLTGWTFD	RGACEVRPLG	NLSRNSLRNG	TEVVSCHPOG	STAGVVYRAG	RNRNRVLAFA	180
ATYVLPPEPT	ASRCNPAASD	HDYTAIALKDT	EGRSLATQEL	GRKLCEGAG	SLHFVDAFLW	240
NGSIYFPYYP	YNYTSGAATG	WPSMARIAQS	TEVLFQGGAS	LDOGHGHDPG	RRLLSSSLV	300
EALDVWAGVF	SAAAGEGQER	RSPTTALCL	FRMSEIQARA	KRVSWDFKTA	ESHCKEGDQP	360
ERVQPIASST	LIHSDLTSVY	GTVMNRTVL	FLGTGQGQLL	KVILGENLTS	NCPEVIYBIK	420
EETPVFYKLV	PDPVKNIYII	LTAGKEVARI	RVANCNKHK	CSECLTATPD	HCGWCHSLQR	480
CTFQGDVCHS	ENLENWLDIS	SGAKKCPKIQ	IIRSSKEKTT	VTMVGFSFPR	HSKOMVKNVD	540
SSRELQCNKS	QPNRTCTCSI	PTRATYKDV	VNVMPSPGS	WNLSDRFNFT	NCSSLKECPA	600
CVETGCWACK	SARRCIHPFT	ACDPSDYERN	QECCPVAVEK	TSGGGRPKEN	KGNRTNQALQ	660
VFYKISIEPQ	KVSTLGSNSV	IVTGANPTRA	SNITMILKGT	STCDKDVIVQ	SHVLNTHMK	720

5 FSLPSSRKEM KDVCIQFDGG NCSSVGSLSY IALPHCSLIF PATTWISGGQ NITMGRNFD 780
 VIDNLIISHE LKGNINVSEY CVATYCGFLA PSLKSSKVRT NVTVKLRVQD TYLDCGTLOQ 840
 REDPRPTGYR VESEVDTELE VKIQKENDNF NISKKDIEIT LEHGENGLN CSFENITRNQ 900
 DLTTILCKIK GIKTASTIAN SSKKVRVKLG NLELYVEQES VPSTWYFLIV LPVLLVIVIF 960
 AAVGVTRHKS KELSRKQSQQ LELLESELRK EIRDGFALQ MDKLDVVDVF GTVPFLDYKH 1020
 10 FALRTFFPES GGFTHIPTED MNRDANDKN ESLTALDALI CNKSFLVTVI HTLEKQKNFS 1080
 VKDRCLPASF LTIALQTKLV YLTSILEVLT RDLMEQCSNM QPKMLLRTE SVVEKLLTNW 1140
 MSVCLSGFLR ETVGEPFYLL VTTLNQKINK GPVDVITCKA LYTLNEDWLL WQVPEFSTVA 1200
 LNVVFEKIPE NESADVCRNI SVNVLDCDTI GQAKEKIFQA PLSKNGSPYG LQLNEIGLEL 1260
 QMGTRQKELL DIBSSSVILE DGITKLNTIG HYEISNGSTI KVPKCIANFT SDVEYSDDHC 1320
 15 HLILPDSEAF QDVQGRHRG KHKFKVKEMY LTKLLSTKVA IHSVLEKLF R SWSLPSNSRA 1380
 PFAIKYFFDF LDAQAENKKI TDDPVVHIWK TNSLPLRFWV NILKNPQFVF DIKKTPHIDG 1440
 CLSVIAQAFM DAPSLTEQQL GKEAPTNNKL YAKDIPTYKE EVKSYKPAIR DLPLLSSEM 1500
 EEFLTQESKK HENEFNEEVA LTEIYKIYVK YFDEILNKLE RERGLEEAQK QLLHVKVLFD 1560
 EKKKCKWM 1568

Seq ID NO: C343 Protein Sequence
 Protein Accession #: NP_002176.1

20 1 11 21 31 41 51
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 MTILGTTFGM VPSLLQVVSQ ESGYAQNGDL EDABLDYDYP SCYSQLEVNG SQHSILTCAP 60
 DPDVNTTNLE FEICGALVEV KCLNFRKLQE IYFIETKKFL LIGKSNICVK VGEKSLTCKK 120
 25 IDLTTIVKPE APFDLSVIYR EGANDFVVT FNTSHLQKKYV KVLMDHVAYR QEKDENKWT 180
 VNLSSKTLTL LQRKLQPAAM YEIKVRSIPD HYFKGFSEW SPSYVFTPE INNSSGEMDP 240
 ILLTISILSF FSVALLVILA CVLWKKRIKP IWPVSLPDHK KLEHLCKKP RKNLNVSPNP 300
 ESPLDQIHR VDDIQARDEV EGFLQDTFPQ QLEESKQRL GGDVQSPNCP SEDVVVTPE 360
 FGRDSSLTCL AGNVACDAP ILSSSRSLDC RESGKNGPHV YQDLLSLGT TNSTLPPPPFS 420
 30 LQSGILTLPN VAQQPILTS LGSNQEEAYV TMSSFYQNG 459

Seq ID NO: C344 Protein Sequence
 Protein Accession #: NP_002713.1

35 1 11 21 31 41 51
 | | | | | |
 NAAARLCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPEQMAQYA ADLRRYINML 60
 TRPRYGRHK EDTLAFSEWG SPAAVPREL SPLDL 95

40 Seq ID NO: C345 Protein Sequence
 Protein Accession #: NP_115934.1

1 11 21 31 41 51
 | | | | | |
 45 MTWRHHVRL FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSHPGE 60
 VTGSAGWGP EEPLPYSRAP GEGASARPC CRNGGTCVLG SPCVCPAHT GRYCEHDQRR 120
 SECGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHAGP SAGGAPSLLL 180
 LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRCGRPGLG HRL 223

50 Seq ID NO: C346 Protein Sequence
 Protein Accession #: NP_006524.1

1 11 21 31 41 51
 | | | | | |
 55 MARSLVCLGV IILLSAFSGP GVRGGPMPKL ADRKLCADQE CSHPISSMAVA LDYMAPDCR 60
 FLTIHRGQVV YVPSKLKGRG RLFWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD 120
 VKTDKWDPHYC Q 131

60 Seq ID NO: C347 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | | |
 65 MTQVTEKSTE HPEKITSTTE KTRTPPEKPT LYSEKTICTK GKNTFVPEKP TENLGNLTIT 60
 TETIKAPVKS TENPEKTAHV TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSPTLI 120
 TSRTKLSSIT SEATGNESHP YLNKDGSKQG IHAGQMGEND SPPAWAIVIV VLVAVILLLV 180
 FLGLIFLVSY MMRTRRTLQ NTQYNDAEDE GGPNSYPVYL MEQQLNGMQ IPSR 235

70 Seq ID NO: C348 Protein Sequence
 Protein Accession #: NP_543146.1

1 11 21 31 41 51
 | | | | | |
 75 MTQVTEKSTE HPEKITSTTE KTRTPPEKPT LYSEKTICTK GKNTFVPEKP TENLGNLTIT 60
 TETIKAPVKS TENPEKTAHV TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSPTLI 120
 TSRTKLSSIT SEATGNESHP YLNKDGSKQG IHAGQMGEND SPPAWAIVIV VLVAVILLLV 180
 FLGLIFLVSY MMRTRRTLQ NTQYNDAEDE GGPNSYPVYL MEQQLNGMQ IPSR 235

80 Seq ID NO: C349 Protein Sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
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	MWRLAFCCW	GLALVSGWAT	FQOMSPSRNF	SFRLFPETAP	GAPGSIPAPP	APGDEAAGSR	60
	VERLQAFRR	RVRLLRELSE	RLELVPLVDD	SSSVGEVNF	SELMFVRKLL	SDFPVVPTAT	120
	RVAIVTFSSK	NYVVPVRDVI	STRRARQHKC	ALLLQEIPI	SYRGGTYTK	GAPQQAQIL	180
5	LHARENSTKV	VFLITDGYSN	GGDPRIIAAS	LRDSGVIEFT	FGIWQGNIRE	LNDMASTPKE	240
	EHCYLLHSFE	SFEALARRAL	HEDLPSGSFI	QDDMVHCYSL	CDEGKDCDDR	MGSCKCGTHT	300
	GHFECICEKG	YYGKGLQYEC	TACPSGTYPK	EGSPGGISSC	IPCDENHITS	PPGSTSPEDC	360
	VCREGYRASG	QTCELVHCPA	LKPPENGYFI	QNTCNHFNFA	ACGVRCHPGF	DLVGSSIIIC	420
	LFNGLWSGSE	SYCRVTRCPH	LRQPKHGHS	CSTREMLYKT	TCLVACDEGY	RLEGSCKLTC	480
10	QGNQMDGPE	PRCVERHCST	FQMPKDVII	PRNCGKPAK	FGTICVSCR	QGFILSGVKE	540
	MLRCTTSGKW	NVGVQAACVK	DVEAPQINCP	KDIBAKTLEQ	QDSANVTWQI	PTAKDNGSEK	600
	VSVHVPAPT	PPYLFPIGDV	AIVYTATDLS	GNQASCIFI	KVIDAEPFVI	DWCRSPPPVQ	660
	VSEKVAASW	DEPQSDNSG	AELVITRSHT	QGDLPQOET	IVQYTATDPS	GNNRTCDIHI	720
	VIKGSPCEIP	FTPVNGDFIC	TPDNTGVNCT	LTCLEGYDFT	EGSTDKYICA	YEDGVWKEPT	780
15	TTWPDCAK	RFANHGKFSF	EMFYKAARCD	DTDLMKKFSE	AFETTLGKMV	PSFCSDAEDI	840
	DCRLEENLTK	KYCLEYNVDY	ENGFAIGPGG	WGAANRLDYS	YDDELDTVQE	TATSIGNAKS	900
	SRIKRSAPLS	YKIKILIFNI	TASVPLPDER	NDTLENNQ	RLIQTLETIT	NKIKRTLNKD	960
	PMYSFQLASE	ILIADSNLSL	TKKASPFPCRP	GSVLGRMCV	NCPLGTYYNL	EHTFCESCRI	1020
	GSYQDEGQL	ECKLCPSGMY	TEYIHSRNI	DCKAQCKQGT	YSYSGLETCE	SCPLGTYQPK	1080
20	FGSRSCLCSP	ENTSTVKRGA	VNISACGVPC	PEGKFSRSLG	MPCHPCPRDY	YQPNAGKAFK	1140
	LACPFYGTTP	PAGSRSITEC	STSVLNIITF	GGFGHLELLN	CPSEVFHECF	FNPCHNSGTC	1200
	QQLGRGYVCL	CPLGYTGLKC	ETDIDECSP	PCLNNGVCKD	LVGEFICECP	SGYTQORCEE	1260
	NINECSSSPC	LNKGICVDGV	AGYRCTCVKG	FVGLHCETE	NECQSNPCLN	NAVCEDQVGG	1320
	FLCKCPGFL	GTRCGKNVDE	CLSQPCKNGA	TCKDGANSFR	CLCAAGFTGS	HCELNINEQC	1380
25	SNPCRNQATC	VDELNSYSKC	CQPGFSGKRC	ETBQSTGFNL	DFEVSGIYGY	VMLDGLMPSL	1440
	HALTCTFNMK	SDDMNYGTP	ISYAVDNGSD	NTLLLTIDYNG	WVLYVNGREK	ITNCPSVNDG	1500
	RWHHIAITWT	SANGIWKVYI	DGKLSDDGGAG	LSVGLPIPGG	GALVIGQEQD	KKGEGFSPAE	1560
	SFVGSISQLN	LWDYVLSPPQ	VKSLATSCPE	ELSKGNVLAW	PDFLSQIVGK	VKIDSKSIFC	1620
	SDCPRLGGSV	PHLRTASELD	KPGSKVNLFC	DPGFQLVGNP	VQYCLNQGW	TQPLFHCERI	1680
	SGVPPPLEN	VFHSADDFYA	GSTVTYQCN	GYLLGDSRM	FCTDNGSWNG	VSPSCLDVDE	1740
30	CAVGSDCSEH	ASCLNVDGSY	ICSCVPPYTG	DGKNCAEPIK	CKAPGNPENG	HSSGEIYTVG	1800
	AGVTFSCQEG	YQLMGVTKIT	CLESGEWNHL	IPYCKAVSCG	KPAIPENGCI	BELAFTFGSK	1860
	VTYRNCSSPC	LAGDKESSCL	ANSSWSHSP	VCEPVKCSSP	ENINNGKYL	SGLTYLSTAS	1920
	YSCDTGYSLQ	GPSIIECTAS	GINDRAPPAC	HLVFCGEPPA	IKDAVITGN	FTFRNTVTYT	1980
35	CKEGYTLA	LITIECLADGK	WSRSDQCLA	VSCDEPIVD	HASPTAHL	PGDIAFYCS	2040
	DGYSLADNSQ	LLCNAQKQW	PPEGQDMPC	IAHFCEKPPS	VSYSILESVS	KAKPAAGSVV	2100
	SFKCMEGFVL	NTSAKIECMR	GGQWNPSPMS	IQCIPIVRCGE	PPSIMNGYAS	GSNYSFGAMV	2160
	AYSQNKGYI	KGEKSTCEA	TQWSSPIPT	CHPVSCGEPP	KVENGFLHT	TGRIFSEVR	2220
	YQCNPGYKSV	GSPFVQCQAN	RHWHSSEPLM	CVPLDCGKPP	PIQNGFMKGE	NFEVGSKVQF	2280
40	FCNEGVELVG	DSSWTCQKSG	KWNKSNPKC	MPAKCPEPPL	LENQLVLKEL	TTEVGVTFS	2340
	CKEGHVLQGP	SVLKLPSQ	WNDSFPVCKI	VLCTPPLIS	FGVPIPSAL	HFGSTVKYSC	2400
	VGGFELRNS	TTLQPDGTW	SSPLPECVPV	ECQPPEEIPN	GIIDVQGLAY	LSTALYTCKP	2460
	GFELVGNNT	LCGEGHWLG	GKPTCKAIEC	LKPKELNGK	FSYTDLHYGQ	TVTYSQNRGF	2520
	RLEGPSALTC	LETGDWDVDA	PSCNAIHCD	PQPIENGFE	GADYSYGAI	IYSCFPGFQV	2580
45	AGHAMQTCBE	SGWSSSIPTC	MPIDCGLPH	IDFGDCTKLK	DDQGYFEQED	DMMEVPYVTP	2640
	HPPYHLGAVA	KTWENTKESP	ATHSSNFLYG	TMVSYTCNPG	YELGNPVL	CQEDGTWNGS	2700
	APSCISIECD	LPTAPENGFL	RFTETSMGSA	VQYSCKPGHI	LAGSDLRCL	ENRKWSGASP	2760
	RCEAISCKKP	NPMVNGSIKG	SNYTYLSTLY	YECDFGVVLN	GTERRTQDD	KNWDEDEPIC	2820
	IPVDCSSPPV	SANGQVRGDE	YTFQKEIEYT	CNEGFLLEGA	RSRVCLANGS	WSGATPDCVP	2880
50	VRCATPPQLA	NGVTGGLDYG	FMKEVTFHCH	EGYILHGAPK	LTCQSDGNWD	ABIPLCKPVN	2940
	CGPPEDLAHG	PNGFSGFIHG	GHIQYQCFPG	YKLHGNSSRR	CLNSGWSGSG	SPSCLPCRS	3000
	TPVIBYGTVN	GTFDFCGKAA	RIQCFCGFKL	LGLSEITCEA	DGQWSSGFP	CBHTSCGSLP	3060
	MINAFISET	SSWKENVITY	SCRSGYVIQ	SSDLICTEKG	VNSQYPVCE	PLSCGSPSPV	3120
	ANAVATGEAH	TYESEVKLRC	LEGYTMOTDT	DTFTQKQDGR	WPPERISCSP	KKCPLEMIT	3180
55	HILVHGDDFS	VNRQVSVSCA	EGYTFEGVNI	SVCQLDGTWE	PPFSDSCSP	VSCGKPSPE	3240
	HGFVNSKYT	FESTIYQCE	PGYELEGNRE	RVCQENRQWS	GGVAICKETR	CSTPLEPLNG	3300
	KADIENRTTG	PNVVSQNRG	YSLEQPSSEH	CTENGTSWHP	VPLCKPNPCP	VFPVIPENAL	3360
	LSEKEFYVDQ	NVSIKCREGF	LLQHGHIITC	NPDETWTQTS	AKCEKISCGP	PAHVENAIAR	3420
	GVHYQYGM	TYSCYSGYML	EGFLRSVCLB	NGTWTSPPIC	RAVCRFPQCN	GGICQRPNAC	3480
60	SCPEGWGRLL	CEEPICILPC	LNGGRCVAPY	QCDCPPGWTG	SRCTAVCQS	PCLNGGKCVR	3540
	PNRCHCLSSW	TGHNCSR					3557

Seq ID NO: C350 Protein Sequence
Protein Accession #: FGENESH predicted

65	1	11	21	31	41	51	
	MRFSVSGMRT	DYPRSVLAPA	YVSVCLLLLC	PREVIAPAGS	EPWLQCPAPR	CGDKIYNPLE	60
	QCCYNDAIVS	LSETRQCGPP	CTFWPCFELC	CLDSFGLTND	FVVLKLVQGV	NSQCHSSPIS	120
70							129
	SKCERGRIC						

Seq ID NO: C351 Protein Sequence
Protein Accession #: AAH35671.1

75	1	11	21	31	41	51	
	MVPGARGGGA	IARAAGRGLL	ALLLAVSAPL	RLQAEISLGDG	CGHLVYQDS	GTMTSKNYPG	60
	TYPNHTVCEK	TITVPKGRKL	ILRLGLDLIE	SQTCASTDYLL	FTSSSDQYGP	YCGSMTVPKE	120
	LLNLNTSEVT	REFSGSHISG	RGFLLTYASS	DHPDLITCLE	RASHYLKTEY	SKFCPAGCRD	180
80	VAGDISGNMV	DGYRDTSLLC	KAAIHAGIIA	DELGGQISVL	QRKQISRYEG	ILANGVLSRD	240
	GSLSDKRFLP	TSNGCSRSL	FEPDQIRAS	SSWQSVNESG	DQVHWSFGQA	RLQDQGPSWA	300
	SGDSSNNHKK	REWLIDILGE	KKKITGIRTT	GSTQSNFNFY	VKSFVMNFKN	NNSKWKTYKG	360
	IVNNREKVQF	GNSNFRDPVQ	NNFIPPIVAR	YVRVVPQTWH	QRALKVELI	CGQITQGNDS	420
	LVRKTSQST	SVSTKQEDET	ITRPIPSEET	STGINITTVA	IPLVLLVVLV	PAGMGIFAAF	480
	RKKKKKGSFY	GSAAEQKTDC	WKQIKYPPAR	RQSAEPTISY	DNEKEMTQKL	DLITSMDMAG	539

Seq ID NO: C352 Protein Sequence
Protein Accession #: Eos sequence

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1 11 21 31 41 51
MGFGAGQRLR FVPAPRSSAE EAARPGQLRL GIRRGAEALA KLAPSGVMVP GARGGGALAR 60
AAGRGLLALL LAVSAPLRLQ AEELGDGCGH LVTYQDSGTM TSKNYPGTYP NHTVCEKTIT 120
10 VPKGKRLILR LGDLIDIESQT CASDYLLFTS SSDQYGPYCG SMTVPKELLN NTSEVTVRFE 180
SGSHISGRGF LLTYASSDHP DLITCLERAS HYLKTEYSKF CPAGCRDVAG DISGNMVDGY 240
RDTSLCLKAA IHAGIIADEL GGQISVLQK GISRYEGILA NGVLSRDGSL SDRFLFTSN 300
GCSRSLSPFP DGQIRASSSW QSVNESGDQV HWSPGQARLQ DQGPSWASGD SSNNHKPREW 360
LEIDLGEKKK ITGIRTTGST QSNFNFYVKS FVMNFKNNNS KWKTYKGIVN NEEKVFQGN 420
15 NFRDPVQNNF IPPIVARYVR VVPQTHQRI ALKVELIGCQ ITQGNDSLVM RKTQSSTSVS 480
TKKEDETITR PIPSEETSTG INITTVAIPL VLLVVLVPAG MGIFAAPRRK KKGSPYGSA 540
BAQKTDCKWQ IKYPPARHQE AEFTISYDNE KEMTQKLDLI TSDMAG 586

20 Seq ID NO: C353 Protein Sequence
Protein Accession #: FGENSEH predicted

1 11 21 31 41 51
MFQRQERFLD LSSAEVAAM ILHQHPDIIN KGDGCGHLVT YQDSGTMTSK NYPGTYPNHT 60
25 VCKRTITVPK GKRLILRLGD LDIESQTCAS DYLLFTSSSD QYGMQKEEBT EVLCLSVAGA 120
QRVDIPVQLL PSFLEGWKGH ADARGPYCGS MTPVKELLN TSEVTVRFES GSHISGRGFL 180
LYASSDHPD LITCLERASH YLKTEYSKFC PAGCRDVAGD ISGNMVDGYR DTSLLCKAAI 240
HAGIIADELG GQISVLQKRG ISRYEGILAN GVLSRDGSL SDRFLFTSN CSRSLSFEPD 300
GQIRASSSWQ SVNESGDQVH WSPGQARLQD QGPSWASGDS SSNNHKPREW BIDLGEKKKI 360
30 TGIRTGSTQ SNFNFYVKSF VMNFKNNNSK WKTYKGIVNN BEKVFGQNSN PRDPVQNNFI 420
PPIVARYVRV VPQTHQRIA LKVELIGCQI TQGNDSLVMR KTSQSTSVST KKEDEITITR 480
IPSEETSTDA MPVQIVGDHT QMISQRENLG PDEGKIPFKG TAESMVRVVF AVVVNDLGLM 540
FLAHTPEEDI DHYCNKQIKY PFARHQSAEF TISYDNEKEM TQKLDLITSD MARYQQPLMI 600
35 GTGTVTRKGS TFRPMDTAE EAGVSTDAAG HYDCPQRAGR HEYALPLAPP EPEYATPIVE 660
RHVLRHHTFS AQSGYRVPQP QPGHKHSLSS GGFSPVAVGV AQDGDYQRPB SAQPADRGYD 720
RPAVSALAT ESHGPDSDQKP PTHPGTSDSY SAPRDCLTPL NQTAMTALL 769

40 Seq ID NO: C354 Protein Sequence
Protein Accession #: NP_004607.1

1 11 21 31 41 51
MAGVSACIKY SMFTFNFLFW LOGILILALA IWVRVSNDSD AIFGSEDVGS SSYVAVDILI 60
45 AVGAIIMILG FLCCCGAIKE SRCMLLFFI GLLLILLQV ATGILGAVPK SKSDRIVNET 120
LYENTKLLSA TGESEKQFE AIVFQEEFK CCGLVNGAAD WGNMFQHYPE LCACLDKQRP 180
CQSYNGKQVY KETCISFIKD FLAKNLIIVI GISPLAVIE ILGLVFSMVL YCQIGNK 237

50 Seq ID NO: C355 Protein Sequence
Protein Accession #: NP_004608.1

1 11 21 31 41 51
MCTGGCARCL GGTLIPLAFF GFLANILLFF PGGRVIDDND HLSQBIWFFG GILGSGVIMI 60
55 FPALVFLGLK NNDCCGCCGN EGCGKRFAMF TSTIFAVVGF LGAGYSFIIS AISINKGPKC 120
LMANSTWGVF PHDGYLVNDE ALMNKCREPL NVVPWNLTLP SILLVVGGIQ MVLCAIQVVN 180
GLLGTLGDCD QCCGCCGGDG PV 202

60 Seq ID NO: C356 Protein Sequence
Protein Accession #: NP_002372.1

1 11 21 31 41 51
MPRPAPARRL PGLLLLLLWPL LLLPSAAPDP VARPGFRRLR TRPGGSGSPGR RPSPAAPDGA 60
65 PASGTSEPGR ARGAGVCKSR PLDLVFIIDS SRSVRPLEFT KVKTFSVRII DTLDIGPADT 120
RVAVVNYAST VKIEFQLQAY TDKQSLKQAV GRITPLSTGT MSGLAIQTAM DEAFVTEAGA 180
REPSSNIPKV AIVTDGRPQ DQVNEVAARA QASGIELYAV GVDRADMASL KMMASEPLEE 240
HVFYVETYG VIEKSSSRFQE TPCALDPCVL GTHQCQHVCI SDGEGKHCE CSQGYTLNAD 300
KKTCSALDRC ALNTHGCEHI CVNDRSGSYH CECYEGYTLN EDRKTCQAQD KCALGTHGCO 360
70 HICVNDRTGS HHCECYEGYT LNADKKTCSV RDKCALGSHG CQHICVSDGA ASYHCDYCPG 420
YTLNEDKKT CATEEARRLV STEDACGCEA TLAQDKVSS YLQRLNTKLD DILEKIKINE 480
YQQRH 486

75 Seq ID NO: C357 Protein Sequence
Protein Accession #: NP_057723.1

1 11 21 31 41 51
MARGSLRRL RLLVLGLWLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRRAPH 60
80 SDFCLGCAAA PPAPFRLWLP ILGGALSITP VLGLLSGFLV WRCRRREKFP TPIETBTGGE 120
GCPAVALIQ 129

Seq ID NO: C358 Protein Sequence
Protein Accession #: NP_001810.1

1 11 21 31 41 51
 5 MQPTLLLSLL GAVGLAAVNS MPVDNRNHNH GMVTRCIIEV LSNALSKSSA PPITPECRQV 60
 LKTSRDOVD KETTENENTK FEVRLLRDPD DASEAHSSSS RGEAGAPGEE DIQGPTKADT 120
 EKWAEGGGHS RERADFPQWS LYPDSQVSE EVKTRHSEKS QREDEEEBEG ENYQKGERGE 180
 DSSEKHLLEE PGETQNAFLN ERKQASAIKK EELVARSETH AAGHSQEKTH SREKSSQESG 240
 SEAGSQENHP QESKGQPRSQ ESEEGEEDA TSEVDKRRTR PRHHHGRSRP DRSSQGSLLP 300
 SEEKGHPQEE SEESNVSMAS LGEKRDHST HYRASEEPE YGEEIKGYPG VQAPEDLEWE 360
 10 RYRGRGSEY RAPRPQSEES WDEEDKRNYP SLELDKMAHG YGEESEERG LEPGKRHRHR 420
 GRGGEPRAYF MSDTREKRF LGEHHRVQE NQMDKARRHP QGAWKELDRN YLNYGEGAP 480
 GKWQQQDLQ DTENREEAR FQDKQYSSH TAEKRLGE LFNPHYDPLQ WKSSHFERED 540
 NMNDNFLEGE EENELTLNEK NFFPEYNYDW WEKKPFSBDV NWGYEKRLA RVPKLDLKRQ 600
 YDRVAQLDQL LHYRKSAEF PDFYDSEEPV STQBAENK DRADQTVLTE DEKKELENLA 660
 15 AMDLELQKIA EKFSQRG 677

Seq ID NO: C359 Protein Sequence
 Protein Accession #: XP_093082.1

1 11 21 31 41 51
 20 MKLLCEGLKQ PNCVLQTLRW YRCLISSASC GALAAVLSTS QWLTELEPSE TKLEASALKL 60
 LYGGKDPNC KLQKLNLPFS LSVTAALKPV GMVNCSGFS GSVLQSHFGY CQDSSPKCDL 120
 CKLLWPSTRV AAACDQSPK SFLSGLNWA GRLEAVEEVL GLGLVQPGD PASQGGGHC 180
 25 NYGSFRDLVD LEVKAEPSEL KGMQLQRP LQVLLCKIF SLKLFLEIAL PNPFGQVSV 240
 QVTIPDGFVN VTVGSNVLI CIYTTTVASR EQLSIQWSFF HKKEMEPISS PWEKGKPDV 300
 BAVKGLDGG QAEQLIYFSQ GQQAIVAGQF KDRITGSNDP GNASITISHM QPADSGIYIC 360
 DVNNPDPFLQ NQKILNVSV LVKPSKPLCS VQGRPETGHT ISLSCLSLG TSPFVYVWHK 420
 LEGRDIVPVK ENFNPTTGIL VIGNLTNFEQ GYQCTAINR LGNSSCEIDL TSSHPVVGII 480
 30 VGALIGSLVG AAIISVVCV ARNKAKAKAK ERNSKTIAEL EPMTKINPRG ESEAMPREDA 540
 TQLEVTLPSS IHETGPDITQ EPDYEPKPTQ EPAPEPAPGS EPMAPVDLDI ELELEPETQS 600
 ELEPEPEPEP ESEPGVVVEP LSEDEKGVVK A 631

Seq ID NO: C360 Protein Sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 35 MVFAFWKVP ILSCLAGQVS VVQVTIPDGF VNVTVGSNVT LICITYTTVA SREQLSIQWS 60
 FFHKKEMEP SSFWEKGWP DVEAVKGLD GQQAELQIYF SQGQAIVAG QFKDRITGSN 120
 40 DPGNASITIS HMQPADSGIY ICDVNNPDPF LGQNGGILNV SVLVKPSKPL CSVQGRPETG 180
 TITISLCLSA LGTPSPVYVY HKLEGRDIVP VKENFNPTTG ILVIGNLTNF EQGYQCTAI 240
 NTLGNSSCEI DLTSSHEPVG IIVGALIGSL VGAIIISV CFARNKAKAK AKERNKTIA 300
 ELEPMTKINP RGESEAMPRE DATQLEVTLP SSIHETGPD ITQEPDYEPK TQEPAPAP 360
 45 GSEPMAPVDL DLELEPET QSELEPEPEP EPSEPGVVV EPLSEDEKGV VKA 413

Seq ID NO: C361 Protein Sequence
 Protein Accession #: NP_003011.1

1 11 21 31 41 51
 50 MVSVMVSTML SGLLFWLASG WTPAFAYSPP TDRVSEADI QRLHGVMEQ LGIARPRVEY 60
 PAQAMNLVG PQSIEGGAHE GLQHLGPPGN IPNIVAEITG DNIPKDFSED QGYPPDPNPC 120
 PVKTTDGLCL ENTPTDAEFS REFQLHQHLE DPEHDYPGLG KWNKLLLYEK MKGGERRRR 180
 55 SVNPLYQQR LDNVVAKKSV PHPSDEKDP E 211

Seq ID NO: C362 Protein Sequence
 Protein Accession #: NP_076926.2

1 11 21 31 41 51
 60 MTTMQGMEQA MPGAGPGVPQ LGNMAVIHSH LNKGLQEKFL KGEPKVLGVV QILTALMSLS 60
 MGITMCMAS NTYGSNPISV YIGYTINGSV MFIISGLSI AAGIRTTKGL VRGSLGMNIT 120
 SSVLAASGIL INTFLAFYS FHHPYCNYG NSNNCHGTMS ILMGLDGMVL LLSVLEPCIA 180
 65 VLSLAFGCKV LCCTPGGVVL ILPSHSHMAE TASPTPLNEV 220

Seq ID NO: C363 Protein Sequence
 Protein Accession #: NP_002082.1

1 11 21 31 41 51
 70 MRGSELPLVL LALVLCLAPR GRAVPLPAGG GTVLTIMYPR GNHWAVGHLM GKKSTGESS 60
 VSERGSLKQ LREYIRWEEA ARNLLGLIEA KENRNEQPPQ PKALGNQPS WDSSESSNF 120
 DVGSGKGVGR LSAPGSQREG RNPQLNQ 148

Seq ID NO: C364 Protein Sequence
 Protein Accession #: NP_036393.1

1 11 21 31 41 51
 80 MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60
 EFAAKFIVPY DWASNYVDL ITEQADIALT RGAEVKRCG HSQSELQVFW VDRAVALKML 120
 FVKESHNMK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHLS ALVTPAGKSY 180
 EQQAQQTISL ASQDPKIVT MILSAVHIQ FDIISDFVS BEHKCPVDER EQLEETPLI 240
 LGLILGLVIM VTLAIYVHH KMTANQVQIP RDRSQYKMG 280

Seq ID NO: C365 Protein Sequence
Protein Accession #: NP_003217.1

5 1 11 21 31 41 51
| | | | |
MLGLVLALLS SSSAEYVGL SANQCAVPAK DRVDCGYPHV TPKECNRGCG CFDSRIPGVP 60
WCFKPLTRKT ECTF 74

Seq ID NO: C366 Protein Sequence
Protein Accession #: NP_002984.1

10 1 11 21 31 41 51
| | | | |
MSLPSSRAAR VPGPSGSLCA LLALLLLLTG PGPLASAGPV SAVLTELRCT CLRVTLRVNP 60
KTIGKLQVFP AGPQCSKVEV VASLKNKGQV CLDPEAPFLK KVIQKILDSG NKKN 114

Seq ID NO: C367 Protein Sequence
Protein Accession #: NP_005233.2

20 1 11 21 31 41 51
| | | | |
MRSPSAWLL GAAILLAASL SCSGTIQGTN RSSKGRSLIG KVDGTSHTVG KGVTVETVFS 60
VDEFSASVLT GKLTTFPLPI VYTIIVFVVG PSNGMALWVP LFRTKKKHPA VIYMANLALA 120
25 DLLSVIWFPL KIAYHIHANN WIYGEALQNV LIGFFYGNMY CSILFMTCLS VQRYWVIVNP 180
MGHSRKQANI AIGISLAIWL LILLVTIPLY VVKQTIFIPA LNITTCHDVL PEQLLVGDMF 240
NYFLSLAIGV FLFPALFAS AYVLMIRMLR SSAMDENSEK KRKRAIKLIV TVLAMYLICF 300
TPSNLLLVVR YFLIKSQQS HVYALYIVAL CLSTLNSCID PFVYFVSHD FRDHAKNALL 360
30 CRSVRTVKQM QVSLTSKHS RKSSSYSSSS TTVKTSY 397

Seq ID NO: C368 Protein Sequence
Protein Accession #: NP_003460.1

35 1 11 21 31 41 51
| | | | |
MAEAKTHWLG AALSLIPLIF LISGAZAAAF QRNQLLQKEP DLRLNVQKP PSPEMIRALE 60
YIENLRQAH KEESPDPYNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRIILEALRQ 120
AENEPQSAK ENKPYALNSE KNFPMDSDD YETQQWPERK LKHMQFPPMY EENSERNPFK 180
40 RTNEIVEEQY TPQSLATLES VFQELGKLTG PNNQKRERMD EEQKLYTDE DDYKANNIA 240
YEDVVGEDW NVEVEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSQGLGI QEEDLRKESK 300
DQLSDDVSKV IAYLRLVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIETSRNLQI 360
PFDLIEMLK TGEKPNGSVE PERELDLPVD LDDISEADLD HPDLFQNRML SKSGYPKTPG 420
RAGTEALFDG LSVEDIALLL GMSAANQKT SYFFNPNQCE KVLRLPYGA GRSRSNQLPK 480
AAWIPHVENR QMAYENLNDK DQELGEYLAR MLVKYPEIIN SNQVKRVPGQ GSSEDQLQEE 540
45 EQIBQAIKEH LNQGSSETD KLAPVSKRFP VGPPKNDITP NRQYWDLDL MKVLEYLNQE 600
KAEKGRHIA KRAMENM 617

Seq ID NO: C369 Protein Sequence
Protein Accession #: NP_112217.1

50 1 11 21 31 41 51
| | | | |
MPCAQSWLA NLSVVAQLLN FGALCYGRQP QPGFVRFPDR ROEHFIKGLP EYHVVGPRV 60
DASGFSLSYG LHYPIITSSRR KRDLGSEEDW VYYRISHEEK DLFPNLTVMQ GFLSNSYIME 120
55 KRYGNLSHVK MMASAPLCH LSGTVLQQT RVGTAALSAC HGLTGFFQLP HGDFPIEPVK 180
KHPLVEGGYH PHIVYRRQKV PETKBPCTGL KDSVNIQKQ ELNREKNERH NLPBSLSRR 240
SISKERWVET LUVADTKMIE YHGSSEVESY ILTIMNMVGT LFNHPSIGNA IHIVVRLIL 300
LREEEQGLKI VHHAECTLSS PCKWQKSNP KSDLNPVHHD VAVLLTRKDI CAGFNRCET 360
LGLSHLSGMC QPHRSCTNINE DSGPLAFTI AHELGHSPFI QHDGKENDCE PVGRHPYIMS 420
60 RQLQYDTPFL TWSKCSSEYI TRFLDRGWGF CLDDIPKKG LKSKVIAPGV IYDVHQCQL 480
QVGNATFCQ EYENVQTLW CSVKGFCSRK LDAAADGTQC GEKKWCMAGK CITVGGKPE 540
IPGGWGRWSP WSHCSRTCGA GVQSAERLCN NPEPKFGKY CTGERKRYRL CNVHPCRSEA 600
PTFRMQCSE FDTVPYKNEH YHWFFIFNPA HPCELYCRPI DGQFSEKMLD AVIDGTPCFE 660
GNSRNVCIIN GICKMVGCDY EIDSNATEDR CGVCLDGSS CQTVRKMFQK KEGSGYVDIG 720
65 LIPKARDIR VMEIEGAGNF LAIRSEDPEK YYLNGGFIIQ WNGNYKLAGT VFQYDRKIDL 780
EKLMTGPTN ESWIQLLPQ VTNPGIKYEV TIQKDLGND VEQMYFQYQ HWTECSVTG 840
TGIRRTAHC IKKGRGMVKA TFCDPETQFN GRQKKCHEKA CPPRWAGWE EACSAICGPH 900
GEKRTVLICI QTMVDEQAL PPTDQHLK PRTLLSCNRD ILCPDWTVG NWSECSVSCG 960
70 GGVRIKSVTC AKNHDEFCDV TRKPNRSLC GLQCPSSRR VLKPNKGTIS NGKNPFTLKP 1020
VPPPTSRPRM LTTPTGPESM STSTFAISSP SPTTASKEGD LGGKQWQDSS TQPELSSRYL 1080
ISTGTSQPI LTSQSLSIQ SEENVSSSDT GPTSEGLVA TTTSGSLSS SRNPITWVPT 1140
PFYNTLTGKP EMRIHSGSGE EREQPEDKE SNPVIWTKIR VPGNDAPVES TEMPLAPPLT 1200
PDLRSRSHWP PFSTVMEGLL PSQRPTTSET GTPRVEGMVT EKPAANTLLPL GGDHQPEPSG 1260
75 KTANRNHLKL PNMNMQTKSS EPVLTEDAT SLITEGFLN ASNYQLTNG HGSAHWIVGN 1320
WSECSTTCGL GAYWKRVECT TQMSDCAAI QRPDPAKRCH LRPCAGWKG NWSKCSRNCS 1380
GGFKIREIQ VDSRDHRNLR PFHQFLAGI PPPLSMSCNP EPCEAWQVE WSQCSRSQCG 1440
GVQERGVFCP GGLCDWTKRP TSTMSCNEL CCHWATGNWD LCSTSCGGF QKRIVQCVP 1500
80 BGNKTEDQD CLCDHKRFP EFKKCNQAC KKSADLLCTK DKLSASFQCT LKAMKKCSVP 1560
TVRAECCFSC PQTHITHYR QRRQLLQKS KEL 1593

Seq ID NO: C370 Protein Sequence
Protein Accession #: NP_001053.1

1 11 21 31 41 51

5	1	MRQSHQLPLV	GLLLFSFIPS	QLCEICEVSE	ENYIRLKPLL	NTMIQSNYNR	GTSAVNVVLS	60
	11	LKLVGIQIQI	LMQKMIQIQI	YVVKSRRLSDV	SSGELALIL	ALGVCNRAEE	NLIYDYHLTD	120
	21	KLENKFAQBI	ENMEAHNGTP	LITNYQLSLD	VLALCLFNNG	YSTAEVVNHF	TPENKNYYPG	180
	31	SQFSVDTGAM	AVLALTCVKK	SLINGQIKAD	EGSLKNISYI	TKSLVEKILS	EKKENGLIGN	240
	41	TFSTGEMQA	LFVSSDYNE	NDWNCQQTIN	TVLTEISQGA	FSNPNAQAQV	LPALMGKTFI	300
10	51	DINKSSCVS	ASGNFNISAD	EPITVTPPDS	QSYISVNVSV	RINETYFTNV	TVLNGSVPLS	360
	61	VMEKAQKMD	TIFGFTMEER	SWGPIYTCIQ	GLCANNDRDT	YWELLSGGEP	LSQAGSYVW	420
	71	RNGENLEVRW	SKY					433
	81							
	91							
Seq ID NO: C371 Protein Sequence Protein Accession #: NP_004582.1								
15	1	MCCTKSLLLA	ALMSVLLHL	CGESEASNF	DCCLGYTDRI	LHPKFIVGFT	RQLANEGCDI	60
	11	NAIIFHTKKK	LSVCANPKQT	WVKYIVRLLS	KVKQNM			96
	21							
	31							
	41							
Seq ID NO: C372 Protein Sequence Protein Accession #: NP_037403.1								
20	1	MAGSPILLWP	RAGGVGLLVL	LLGLFRPFP	ALCARPVKEP	RGLSAASPPL	AETGAPRRFR	60
	11	RSVPRGEAAG	AVQELARALA	HLLAEERQER	ARAEQAED	QOARVLAQLL	RVWGAPRNSD	120
	21	PALGLDDDPD	APAAQLARAL	LRARLDPAAL	AAQLVPAPVP	AAALRPRFPV	YDDGPAQPD	180
	31	EEAGDETDFD	DELLRYLLG	RILAGSADSE	GVAAPRRRLR	AAEDHVGSEL	PPEGVLGALL	240
	41	RVKLETFAP	QVPARRLLFP					260
Seq ID NO: C373 Protein Sequence Protein Accession #: NP_002236.1								
25	1	MLQSLAGSSC	VRIVERHRS	WCFGLVLGY	LLYLVFQAVV	FSSVELPYED	LRLQELRKLK	60
	11	RRFLEHECL	SEQQLBQFLG	RVLEASNYGV	SVLSNASGNW	NWDFTSALFF	ASTVLSTTGY	120
	21	GHTVPLSDGG	KAPCIISYVI	GIPFTLLFLT	AVVQRITVHV	TRRPVLYFHI	RWGFSGQVVA	180
	31	IVBAVLLGFV	TVSCFFFIPI	AVFSVLEDDW	NFLESFYPCF	ISLSTIGLGD	YVPGEYNQK	240
	41	FRELKIGIT	CYLLGLLIAM	LVLLETFCEL	HELEKKFRMF	YVKDKDEDDQ	VHIEHDQLS	300
30	51	FSSITDQAAG	MKEDQKQNEP	FVATQSSACV	DGPANH			336
	61							
	71							
	81							
	91							
Seq ID NO: C374 Protein Sequence Protein Accession #: NP_005463.1								
35	1	METTINGTETW	YESLHVLKA	LNATLHSNLL	CRPGPLGPD	NQTEERRASL	PGRDDNSYMY	60
	11	ILFVMPLEFAV	TVGSLILGYT	RSRKVDKRS	PHYVYIKNRV	SMI		103
	21							
	31							
	41							
Seq ID NO: C375 Protein Sequence Protein Accession #: NP_005236.1								
40	1	MGRHLALLLL	LLLLFQHFQD	SDGSQRLEQT	PLQFTHLEYN	VTQENSAAK	TYVGHFVRMG	60
	11	VYITHPAWEV	RYKIVSGDSE	NLFKAEEYIL	GDQCFRLIRT	KGNTAILNR	EVKDHYYTLV	120
	21	KALEKNTNVE	ARTKVRVQVL	DTNDRPLFS	PTSYSVSLPE	NTAIRTSIAR	VSATDADIGT	180
	31	NGEYFYSPKD	RTDMFAIHPT	SGVIVLTGRL	DYLETCLYEM	EILAADRGMK	LYGSSGSISS	240
	41	AKLTVHIEQA	NECAPVITAV	TLSPELDRD	PAYAITVDD	CDQANGDIA	SLSTVAGDLL	300
45	51	QQFTVRSFP	GSKEYVKAI	GDIDWDSHP	GYNLTQAKD	KGTTPQFSSV	KVHVTSQPF	360
	61	KAGFVKFEKD	VYRAEISEFA	PENTPVVMVK	AIPAYSHLRY	VFKRTFGKAK	FSLNYNTGLI	420
	71	SILEPVKRRQ	AAHFELEVT	SDRKASTKVL	VKVLGANSNP	PEFTQTAYKA	AFDENVPIGT	480
	81	TIMSLSAVDP	DEGENGYVTY	SIANLNHVPP	AIDHFTGAVS	TSENLDYELM	PRVYTLRIRA	540
	91	SDWGLPYRRE	VEVLATITLN	NLNDNTPLFE	KINCEGTIPR	DLGVGEQITT	VSAIDADELQ	600
50	101	LVQYQIEAGN	ELDLFSLNPN	SGVLSLKRSL	MDGLGAKVSF	HSLRITATDG	ENFATPLYIN	660
	111	ITVAASHKLV	NLQCEETGVA	KMLAEKLLQA	NKLHNQGEVE	DIPFDSSHVN	AHIPQFRSTL	720
	121	PTGIQVKENQ	PVGSSVIFMN	STDLDTGFGN	KLVAVSGGN	EDSCFMIDME	TGMLKILSPL	780
	131	DRETTDKYTL	NITVYDLGIP	QKAAWRLLHV	VVDANDNPP	EPLQESYFVE	VSEDKEVHSE	840
	141	IIQVEATDKD	LGPNGHVYS	ILTDITDTSI	DSVTGVVNIA	RPLDRELQHE	HSLKIEARDQ	900
55	151	AREEPQLFST	VVKVSLSDV	NDNPPTFIPP	NVRVKVREDL	PEGTVIMWLE	AHDEPLGQSG	960
	161	QVRYSLLDHG	EGNFDVDKLS	GAVRIVQQLD	FERKQVYNLT	VRAKDKGKEV	SLSSTCYVEV	1020
	171	EVVDVNEENH	PPVFSSFVEK	GTVKEDAPVG	SLVMTVSAHD	EDAGRDGEIR	YSIRDGSGVG	1080
	181	VFKIGESTGV	IETSDRLDRE	STSHYWLTVF	ATDQGVVPLS	SFBIYIEVE	DVNDNAPQTS	1140
	191	EPVYYPEIME	NSPKDVSUVQ	IEAFDPSDS	NDKLMYKITS	GNPQGFSSIH	PKTGILTTTS	1200
60	201	RKLDRQQDE	HILEVTVTDN	GSPPKSTIAR	VIVKILDEND	NKPQFLQKPY	KIRLPEREKQ	1260
	211	DRERNARREP	LRVIAITDKD	EGPNABISYS	IEDGNEHGKF	FIEPKTGVS	SKRPSAAGEY	1320
	221	DILSIKAVDN	GRPQKSSSTR	LHIEWISKPK	QSLEPISPEE	SPTFTVMES	DPVAHMIGVI	1380
	231	SVEPPGIPLV	FDITGGNYDS	HFDVDRGTGT	IIVAKPLDAE	QKSNYNLTVE	ATDGTITILT	1440
	241	QVFIKVIDTN	DHRPQFSTSK	YEVVIPEDTA	PETEILQISA	VDQDEKNKLI	YTLQSSRDPL	1500
65	251	SLKKFRIDPA	TGSLYTSEKL	DHEAVSPAHL	TVMVRDQDVP	VKNRFARIVV	NVSDTNDHAP	1560
	261	WFTASSYKGR	VYASAAVGSV	VLQVTALDKD	KGKNAEVLVS	IESGNIGNIG	NSFMIDPVLG	1620
	271	SIKTAKELDR	SNQASYDLMV	KATDKGSPPM	SEITSVRIFV	TIADNASPKF	TSKEYSVELS	1680
	281	ETVSGISFVG	MYTAHSQSSV	VYEIKDGNIG	DAFDINPHSG	TIITQKALDF	ETLPIYTLII	1740
	291	QGTNAGLST	NTTVLVHLQD	ENDNAPVFMQ	AEYTGILISES	ASINSVVLTD	RNVPLVIRAA	1800

	DADKDSNALL	VYHIVEPSVH	TYFAIDSSTG	AIHTVLSLDY	EETSIFHFTV	QVHDMGTPRL	1860
	FAEYANVTV	HVIDINDCP	VFAKPLYEAS	LLLPYTKGVK	VITVNATDAD	SSAFSOLIYS	1920
	ITEGNIGKEF	SMDYKTGALT	VQNTTQLRSR	YELTVRASDG	RFAGLTSVKI	NVKESKESHL	1980
5	KFTQDVYSAV	VKENSTEAE	LAVITAIGSP	INEPLFYHIL	NPDRRFKISR	TSGLVSTTGT	2040
	PFDREQQEAF	DVVVEVIEEH	KPSAVAHVVV	KVIVEDQNDN	APVFNLPY	AVVKVDTEVG	2100
	HVIRYVTAVD	RDSGRNGEVH	YYLKEHHEHF	QIGPLGEISL	KKQFELDTLN	KEYLVTTVAK	2160
	DGGNPAPSAE	VIVEITVMNK	AMPVFEKPFY	SABIAESIQQ	HSPVHVQAN	SPBGLKVPYS	2220
	ITDGPFSQF	TINFNTGVIN	VIAPLDPEAH	PAYKLSIRAT	DSLTGAHAEV	FVDIIVDDIN	2280
10	DNPPVFAQQS	YAVTLSEASV	IGTSVVQVRA	TDSSEPNRG	ISYQMFNGHS	KSHDFPHVDS	2340
	STGLISLLRT	LDYEQSRQHT	IFVRAVDGGM	PTLSSDVIPT	VDVTDLNGNP	PLFBEQQIYEA	2400
	RISHAPHGH	FVTCVKAYDA	DSSDIDKLQY	SILSGNDHGH	FVIDSATGII	TLNLHRHAL	2460
	KPFYSLNLSV	SDGVFRSSTQ	VHVTVIGGNL	HSPAFIQNEY	EVELAENAPL	HTLVMEVKT	2520
	DGDSGIYGHV	TYHIVNDPAK	DRFYINERGQ	IFPLEKLDRE	TPAEKVISVR	LMADAGGKV	2580
	AFCVNVILT	DDNDNAQFPR	ATKYEVNIGS	SAAKGTSVVK	SASDADEGSN	ADITYAIEAD	2640
15	SESIVENLEI	NKLSGVITTK	ESLIGLENEF	FTFFVRAVDN	GSPSKESVVL	VYVKILPEPM	2700
	QLPKFSEPPY	TFTVSEDVVP	GTEIDLIRAE	HSGTVLYSLV	KGNTPESNRD	ESPFIDRQSG	2760
	RLKLEKSLDH	ETTKWYQFSI	LARCTQDDHE	MVASVDVSIQ	VKDANDNSPV	FESSPYEAFI	2820
	VENLPGGSRV	IQIRASDADS	GTNGQVMYSL	DQSQSVEVIE	SFAINMETGW	ITTLKELDHE	2880
	KRDNYQIKV	ASDHGEKIQ	SSTAIVDVTV	TDVNDSPPRF	TABIYKGTVS	EDDPQGGVIA	2940
20	ILSTTDADSE	EINRQVTYFI	TGGDPLGQFA	VETIQNEWKV	VYKKPLDREK	RDNYLLTITA	3000
	TDGTFSSKAI	VEVKVLDAND	NSPVCCKTLY	SDTIPEDVLP	GKLIMQISAT	DADIRSNAEI	3060
	TYTLLSGSAE	KFKLNPDTGE	LKTSTPLDRE	EQAVYHLLVR	ATDGGGRFCQ	ASIVVTLEDV	3120
	NDNAPEFSAD	PYAITVFENT	EPGTLTLTRQ	ATDADAGLNR	KILYSLIDSA	DGQFSINELS	3180
25	GIQLEKPLD	RKLQAVYTLS	LKAVDQGLER	RLTATGTIVV	SVLDINDNPP	VFEYREYGAT	3240
	VSEDILVGE	VLQVYAASRD	IEANAEITYS	IISGNEHGKF	SIDSKTGAVP	IENLOYESS	3300
	HEYLYTVEAT	DGGTPSLSDV	ATVNVNVTDI	NDNTPVFSQD	TYTIVISEDA	VLEQSVITVM	3360
	ADDADGFSNS	HIIYGIIDGN	QGSSTPIDPV	RGEVKVTKLL	DRETISGYTL	TVQASDNGSP	3420
	PRVNTTNYI	DVSDVNDNAP	VFSRGNYSVI	IQENKPVGFS	VLQLVVTDED	SSHNGPPFFF	3480
	TIVTGNDEKA	FEVNPQGVLL	TSSAIKRKEK	DHYLLQVKVA	DNGKPLSSL	TYIDIRVIEE	3540
30	SIYPPAILPL	EIFITSSGEE	YSGGVIGKIH	ATDQDVYDTL	TYSLDPQMDN	LFSVSTGGK	3600
	LIAHKKLDIG	QYLLNVSVTD	GKFTTVADIT	VHIRQVTQEM	LNHTIARFA	NLTPPEFVGD	3660
	YWRNQRALR	NILGVRNDI	QIVSLQSEEP	HPHLDVLLFV	EKPGSAQIST	KQLLHKINSS	3720
	VTDIEIIGV	RILNVFQKLC	AGLDCPWKFC	DEKVSVDSEV	MSTHSTARLS	FVTPRHHRRA	3780
35	VCLCKEGRCP	PVHGGCEDDP	CPBGSECVSD	PWEEKHTCVC	PSGRFCQCPG	SSSMILTGN	3840
	YVKYRLTENE	NKLEMKLTM	LRTYSTHAVV	MYARGTDYSI	LEIHHGRLQY	KPDCGSGPGI	3900
	VSVSQIQVND	GQWHAVALEV	NGNYARLVLD	QVHTASGTAP	GTLLKTLNLDN	VYFPGGHIRQ	3960
	QGRHGRSPQ	VGNFRGCMO	SIYLNQELP	LNSKPRSYAH	IESVDVSPG	CFLTATEDCA	4020
	SNPCQNGGVC	NPSAGGYC	KCSALYIGTH	CEISVNPCSS	NPCLYGGTCV	VNDGGFVCQC	4080
40	RGLYTQGRQC	LSPYCKDEPC	KNGGTCFDSL	DGAVCQCDSG	FRGERCQSDI	DECSGNPCLE	4140
	GALCENTHGS	YHCNCSHEYR	GRHCEDAAPN	QYVSTPWNIG	LAEGIGIVVP	VAGIFLLVVV	4200
	FVLCKRMISR	KKKHQAEPKD	KHLGPATAFL	QRPFYDSKLN	KNIYSDIPPQ	VPVRPISYTP	4260
	SIPSDSRNML	DRNSFEGSAI	PEHPEFSTFN	PESVHGHRKA	VAVCSVAPNL	PPPPSPNSPS	4320
	DSDSIQKPSW	DFDYDTKVD	LDPCLSKKPL	BEKPSQPYSA	RESLSEVQSL	SSPQSESCDD	4380
45	NGYHMDTSDW	MPSVPLPDIC	EPFNVEVIDE	QTPLYSADPN	AIDTDYYPGG	YDIESDPPFP	4440
	PEDFPAABEL	PFLPPEFSNQ	FESIHPPRDM	PAAGSLGSSS	RNRQRFLNLR	YLPNFYPLDM	4500
	SEPQTGTGTE	NSTCREPHAP	YPGQYQRHFE	APAVESMPMS	VIASASCSD	VSACCEVESE	4560
	VMSDYESGD	DGHFEVETIP	PLDSQQHTEV				4590

Seq ID NO: C376 Protein Sequence
Protein Accession #: NP_055035.1

	1	11	21	31	41	51	
55	MCYKGCARCI	GHSVLGLALL	CIAANILLYF	PNGETKYASE	NHLSRFVWFF	SGIVGGGLLM	60
	LLPAFVPIGL	BQDDCCGCGC	HENCGKRCAM	LSSVLAALIG	IAGSGYCVIV	AALGLAEGPL	120
	CLDSLQGMNY	TPASTBQYQL	LDTSTWSECT	EPKHIVEWNV	SLFSILLALG	GIEFLCLLIQ	180
	VINGVLGGIC	GFCCSHQQQY	DC				202

Seq ID NO: C377 Protein Sequence
Protein Accession #: NP_003750.1

	1	11	21	31	41	51	
65	MSTENVGKPK	SNLGERGRAR	SSTFLRVVQP	MFNHSIFTSA	VSPAARIRF	ILGEEDDSFA	60
	PPQLFTLDEL	LLAVDQGEHE	WKETARWIKP	EEKVEQGGER	WSKPHVATLS	LHSLFELRTC	120
	MEKGSIMLDR	EASSLPQLVE	MIVDHIQIETG	LLKPELKDKV	TYTLLRKHRR	QTKKSNLRLS	180
	ADIGKTVSSA	SRMPTNPONG	SPAMTHRNLT	SSSLNDISDK	PEKQDLKPKF	MKRLPRDAEA	240
	SNVLGRSEVD	LDTFFIAPVR	LQQAIVMLGAL	TEVPVPTREF	FILLGPKGKA	KSYHEIGRAI	300
70	ATLMSDEVFH	DIAYKAKDRH	DLIAGIDEFL	DEVIVLPPGE	WDPAIRIEPP	KSLPSSDKRK	360
	NMYSGGENVQ	MNGDTPHDGG	HGGGGHGDCE	ELQRTGRFCG	GLIKDIKKA	PPFASDFYDA	420
	LNIAQLSAIL	PIYLATVTNA	ITPGGLLGD	TDMQGVLES	FLGTAVSGAI	FCLPAQPLT	480
	ILSSTGVLV	PERLLFNFSK	DNNFDLYEPR	LWIGLWSAPL	CLILVATDAS	FLVQYPTFT	540
	BEGFSSLSIF	IPIVDAPFKM	IKLADYYPIN	SNFKVGYNTL	PSCTCVPPDP	ANISISNDIT	600
75	LAPEYLPMS	STDYHNTTF	DWAFLSKKEC	SKYGNLVGN	NCNFVEDITL	MSPIFLGTY	660
	TSSMALKKPK	TSPYPTTAR	KLISDPAIL	SILIFCVIDA	LVGVDTPKLI	VPSEFKPTSP	720
	NRGWEVPPFG	EPPNWWCLAA	AIPALLVTIL	IFMDQQTAV	IVNRKHEKIK	KGAGYHLDLF	780
	WYALLMWICS	LMALPWVAA	TVISIAHIDS	LKMETETSAP	GEQPKFLGVR	EQRVGTGLVF	840
80	ITGLSVFMA	PILKPIPMFV	LYGVPLYMGV	ASLNGVQFMD	RLKLLMLPLK	HQPDFIYLRH	900
	VPLRRVHLFT	FLQVLCALL	WILKSTVAAI	IPVVMILALV	AVRKGMDYLF	SQHDLSFLDD	960
	VIPEKDKKKK	EDBKDKKKK	GSLDSNDSDS	DCPYSEKVP	IKIPMDIMEQ	QPLFSDSKPS	1020
	DRERSPTLE	RQDSTC					1035

Seq ID NO: C378 Protein Sequence
Protein Accession #: NP_000949.1

1 11 21 31 41 51
 5 MSTPGVNSSA SLSPLRLNSP VTIPAVMFIF GVVGNLVAIV VLCKSRKEQK ETTFTYTLVCG 60
 LAVTDLLGTL LVSPVTIATY MKGQWPGGQP LCEYSTFILL FFSLSGLSII CAMSVERYLA 120
 INHAYFYSHY VDKRLAGLTL FAVYASNVLF CALPNMGLGS SRLQYPDITWC FIDWTTNVTA 180
 HAAYSYMYAG FSSFLILATV LCNVLVCGAL LRMHRQPMRR TSLGTEQHHA AAAASVASRG 240
 HPAASPALPR LSDFRRRRSF RRIAGAEIQM VILLIATSLV VLICISPLV RVFVNQLYQP 300
 10 SLEREVSKNP DLQAIRIASV NPILDPIYI LLRKTVLVSKA IEKIKCLPCR IGGSRRESG 360
 QHCSDSQRTS SAMSQHSRSF ISRELKEISS TSQTLPLDLS LPDLSENGLG GRNLLPGVPG 420
 MGLAQEDTTS LRLTRISETS DSSQQQDSES VLLVDEAGGS GRAGPAPKGS SLQVTFPSET 480
 LNLSEKCI 488

15 Seq ID NO: C379 Protein Sequence
 Protein Accession #: NP_002650.1

1 11 21 31 41 51
 20 MGHPPLLELL LLLHTCPVAS WGLRCMQCKT NGDCRVEECA LGQDLCRTTI VRLWEBGEEL 60
 ELVEKSCTHS EKTNRITLSYR TGLKITSLTE VVCGLDLNCQ GNSGRAVTVS RSRYLECISC 120
 GSSDMSCEERG RHQSQCQCRP EEQCLDVVTH WIQEGEGRRP KDRHRLRCGG YLPGCPGSG 180
 FHNNDTFHFL KECNTTKCNE GPILLELENLP QNGRCQYCK GNSTHGCSSE ETFLIDCRGP 240
 MNQCLVATGT HEPKNSQSYM RGCATASMCQ HAHLGDAFSM NHIDVSCCTK SGCNRPDLV 300
 25 QYRSGAAPQP GPAHLSLTIT LLMTARLWGG TLLWT 335

Seq ID NO: C380 Protein Sequence
 Protein Accession #: BAB55406.1

1 11 21 31 41 51
 30 MDEFSGQVDP LASVILPPNL LENLSPEDSV LVRRQAFTFF NKTGLPQDVG PQRKTLVSYV 60
 MACSIGNITI QNLKDPVQIK IKHTRTQEVH HPICAFWDLN KNKSFQGMNT SGCVAHRSD 120
 ASETVCLCNH FTFGVLMDL PRSASQLDAR NTKVLTFISY ICGISAIPI AATLLTYVAF 180
 35 EKLRDYPSPK ILMNLSTALL FLNLLFLLDG WITSPNVDGL CIAVAVLLHP PLLATFTWVG 240
 LEAIIHMYIAL VKVFNTYIRR YILKFCIIGW GLPALVVSVV LASRNNNEVY GKESYKKEG 300
 DEFQIQDPV IFYVTCAGYF GVMFPLNIAM FIVVMVQICG RNGKRSNRTL REEVLNRLS 360
 VVSLTFLLGM TWGFAFPFAG PLNIPFMYLF SIFNSLQGLF IFIFHCAMKE NVQKQWRRL 420
 COGRFRLADN SDWSKTATNI IKKSSDNLKG SLSSSSIGSN STYLTSKSKS SSTYTPKRNS 480
 40 HTDNVSYEHS FNKSGSLRQC FHGQVLVKTG PC 512

Seq ID NO: C381 Protein Sequence
 Protein Accession #: NP_000565.1

1 11 21 31 41 51
 45 MTVARPSVPA ALPLLGLPR LLLVLLCLP AVWGDCGLPP DVPNAQPALE GRTSPPEDTV 60
 ITYKCESEFV KIPGEKDSVI CLKGSQWSDI BEFCNRSCEV PTRLNSASLK QPYITQNYFP 120
 VGTVVEYECR PGYRREPSLS PKLTCLQNLK WSTAVEFCKK KSCPMPGEIR NGQIDVPGGI 180
 50 LFGATISFSC NTGYKLFST SSFCLISGSS VQWSDPLEC REIYCPAPPQ IDNGIIQGER 240
 DHYGRQSVT YACNKGFTMI GEHSIYCTVN NDEGEWSGPP PEBCRGKSLTS KVPPTVQKPT 300
 TVNVPTTEVS PTSQKTTTCT TTPNAQATRS TPVSRTRKHF HETTPNKGSG TTSGITRLLS 360
 GHTCFTLTGL LGTLVTMGLL T 381

55 Seq ID NO: C382 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 60 MDTSLRGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
 PSNLSVFTSY LDLSMNISQ LLPNLPLSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVL 120
 LQNNQLRHVP TEALQNLRLS QSLRLDANHI SYVPPSCPSG LHSRLRLWLD DNALTEIPVQ 180
 AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLTLD 240
 65 LNYNNLDEFP TAIRTLNLK ELHFYDNPIQ FVGRSAFQHL PELRTLTLNG ASQITEFPDL 300
 TGTANLESIT LTGAQISSLP QTVCNQLFNL QVLDLSYNLL EDLPSEFSVQ KLQKIDLRN 360
 EIYBIKVDTF QQLSLRSIN LAWNKIAIHH FNAFSTLPSL IKLDLSSNLL SFPFITGLHG 420
 LTHLKLTKNH ALQSLISSEN FPBLKVIEMP YAYQCCAFGV CENAYKISNQ WNKGDNSMD 480
 DLHKGADAGM QAQDERDLED FLIDFREDLK ALHSVQCSFS PGPFKPCERL LDGWLIRIGV 540
 70 WTIAVLALTC NALVTSTVFR SPLYISPIKL LIGVIAAVNM LTGVSSAVLA GVDFTFGSF 600
 ARHGAWWENG VGCHVIGFLS IPASESSVFL LTLAALERGF SVKYSKPFET KAPFSSLKVI 660
 ILLCALLATG MAAVPLLGGS KYGASPLCLP LPFGPESTWG YMVALLILMS LCPLAMTIAY 720
 TKLYCNLDKG DEINWDCSM VKHIALLLFT NCILNCPVAF LSFSSLINLT PISPEVIKFI 780
 LLVVVPLPAC LNPLLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DDVEKQSCDS 840
 75 TQALVTPTSS SITYDLPPSS VPSPAYFVTE SCHLSSVAEV PCL 883

Seq ID NO: C383 Protein Sequence
 Protein Accession #: NP_003658.1

1 11 21 31 41 51
 80 MDTSLRGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
 PSNLSVFTSY LDLSMNISQ LLPNLPLSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVL 120
 LQNNQLRHVP TEALQNLRLS QSLRLDANHI SYVPPSCPSG LHSRLRLWLD DNALTEIPVQ 180
 AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLTLD 240
 LNYNNLDEFP TAIRTLNLK ELGFHSNNIR SIPEKAPVGN PSLITIHFDY NPIQFVGRSA 300

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FQHLPELRTL TLNGASQITE FFDLTGTANL ESLTLTGAQI SSLPQTVQCNQ LPNLQVLDLS 360
YNLLEDLPSE SVQCQLKQID LRHNEIYEIK VDTFOQLLSL RSLNLAWNKI AIIHPNAFST 420
LPSLIKLDLS SNLLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFPPELV IEMPAYQCC 480
AFGVCEWAYK ISNQMNKGDN SSMDDLHKKD AGMFQAQDER DLREDPLDPE EDLKALHSVQ 540
CSPSPGPFKP CEHLLDGNLI RIGVWTIAVL ALTCLALVTS TVFRSPLYIS PIKLLIGVIA 600
AVNMLTGVSS AVLAGVDAFT FGSFARHGAW WENGVGCHVI GFLSIFASES SVFLLTLAAL 660
ERGFVSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGEF 720
STMGYMVALI LLNSLCFLMM TIATYTKLYCN LDKGDLNLIW DCSMVRHIAL LLFTNCILNC 780
PVAFLSPSSL INLTISPSEV IKFILLVVVP LPACLNPPLY ILFNPFPKED LVSLRKQTYV 840
WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PFSSVPSPAY PVTESCHLSS 900
VAFVFCF 907

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Seq ID NO: C384 Protein Sequence
Protein Accession #: NP_003497.1

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1 11 21 31 41 51
MEMFTLLTLC IFLPLLRGHS LFTCEPITVP RCMQAMYNMT FFPNLMGHYD QSIAAVEMEH 60
FLPLANLECS PNLETFLCKA FVPTCIEQIH VVPPCRKLCE KVYSDCKKLI DTFGIRNPPEE 120
LECDRLQYCD ETVPVTFDPH TEFLGSPQKKT EQVQRDIGFW CPRHLKTSGG QGYKFLGIDQ 180
CAPPENMYF KSDLEFAKS FIGTVSIFCL CATLFTFLTF LIDVRRFRYP ERPIIYYSVC 240
YSIVSLMYFI GFLLGSTAC NKADEKLELG DTVVLGSQNK ACTVLFMLLY FFMAGTVWW 300
VILTITWFLA AGRKWSCEAI BQKAVWFHAV AWGTPGFLTV MLLALNKVEG DNISGVCVFG 360
LYDLASRYF VLLPLCLCFV VGLSLLLAGI ISLNHVRQVI QHDGRNQKLI KKFMRIGVF 420
SGLYLVPLVT LLGCYVYEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALFMKY 480
LMTLIVGISA VFVVGSKKTK TEWAGFPKRN RKRDPISER RVLQSECEFF LKHNSKVHKH 540
KKHYKPSHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQBTLEIQ TSPETSMREV 600
KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660
TGLAQSNLQ VPSSESPSSL KGSTSLLVHP VSGVRKEQGG GCHSDT 706

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Seq ID NO: C385 Protein Sequence
Protein Accession #: NP_000573

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1 11 21 31 41 51
MRIAIVICFCL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLAPQTL 60
PSKSNESHSH MDDMDDDDDD DHVDSQDSID SNDSDDVDDT DDSHQSDSH HSDESEDLVT 120
DFPTDLPAE VFTPVVPTVD TYDGRGDSV YGLRSKSKKF RRPDIQYDA TDEDITSHME 180
SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240
NEHSDVIDSQ ELSKVSREFH SHEFHSHEDM LVVDPKSKEE DKHLKFRISH ELDSASSEVN 300

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Seq ID NO: C386 Protein Sequence
Protein Accession #: NP_002812

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1 11 21 31 41 51
MGAARGSPAR PRRLPLLSVL LLPLLGSTQT AIVFIKQPS QDALQRRAL LRCEVEARGP 60
VHVYWLIDGA PVQDTERFPA QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE EARSANAFN 120
IKWIEAGPVV LKHPASEAEI PQQTQVTLRC HIDGHPRPTY QWFRDGTPLS DGQSNHTVSS 180
KERNLTLRPA GPEHSGLYSC CAHSAGGQAC SSQNFSLIA DESFARVVLA PQDVVVARYE 240
EAMFHCQPSA QPPSLQWLF EDETPTITNS RPFHLRRATV FANGSLLLTQ VRPRNAGIYR 300
CIGQGQGRGP IILEATLHLA EIEDMPLFEP RVFTAGSEER VTCPLPKGLP EPSVWWEHAG 360
VRLPTHGRVY GRGHELVLAN IASDAGVYT CHAANLAGQR RQDVNITVAT PWSNLKKPQD 420
SQLBEGKPGY LDCLTQATPK PTVVWYRNQM LISEDSRFEV PKNGTLRINS VEYDGTWYR 480
CMSSTPAGSI EAQARVQVLE KLKFTFPPOP QQCMFEDKEA TVPCSATGRE KPTIKWERAD 540
GSSLPENVTD NAGTLHFARV TRDDAGNYTC IASNGPQQQI RAHVQLTVAV FITFKVEPER 600
TTYVQGHATL LQCEAQGDPK FLIQWKGKDR ILDPFTKLGR MHIFQNGSLV IHDVAPEDSG 660
RYTCIAGNSC NTKHTEAPLY VVDKPVPEES EGPSPPPYK MIQTIGLSVG AAVAYIIAVL 720
GLMPYCKMKH KAKRLQKQPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN 780
KRHSTDOKH PPRSLQPIIT TLGKSEFGEV FLAKAQGLEE GVAETLVVK SLQTKDEQQQ 840
LDFRRELEMP GKLNHANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKSQ 900
PLSTKQKVAL CTQVALGMEH LSNRFVHKD LAARNCLVSA QRQVKVSAIG LSKDVYNSEY 960
YHFRQAWVPL RWMSPBAILE GDPSTKSDVW AFGVLMWEVF THGEMPHGGQ ADDEVLAIDLQ 1020
AGKARLPQPE GCPSKLYRLM QRCWALSPKO RPSFSEIASA LGDSTVDSKP 1070

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Seq ID NO: C387 Protein Sequence
Protein Accession #: NP_002300.1

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75

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1 11 21 31 41 51
MKVLAAGVVP LLLVLVHKHG AGSPLPITPV MATCAIRHPC HNNLMNQIRS QLAQLNGSAN 60
ALFILIYYTA GEFPFNLDK LCGFNVTDFP PFHANGTEKA KLVELYRIVV YLGTSLGNIT 120
RDQKILNPSA LSLHSLNAT ADILRGLLEN VLCRLCSKYH VGHVDVTYGP DTSGKDVFPK 180
KKLGCCQLGK YKQIIAVLAQ AF 202

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Seq ID NO: C388 Protein Sequence
Protein Accession #: XP_097508

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1 11 21 31 41 51
MGRPRLTLVC HVSIIISARD LSMNNLTQL PGLFHHLRPL EELRLSGNHL SHIPQAFSG 60
LYSLKILMLQ NNQLGGIPAE ALWELPSLQS LRLDANLISL VPERSFEGLS SLRHLWLDN 120
ALTEIPVRAL NNLPALQAMT LALNRISHIP DYAFQNLTSV VVLHLHNNRI QHLGTHSFEG 180
LHNLETLDLN YNKLQEPFVA IRTLGRQLQL GFHNNNIKAI PEKAFMGNPL LQTIHFYDNP 240

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IQFVGRSAFQ YLPKLHTLSL NGAMDIQEPF DLKGTTSLEI LTLTRAGIRL LPSGMCQQLP 300
RLRVLELSHN QIEELPSLHR CQKLEEIQLQ HNRIWEIGAD TFSQLSSLOA LDLSNNAIRS 360
IHPEAFSTLH SLVKLDLTDN QLTTLPLAGL GGLMHLKLG NLALSQAFSK DSFPKLRILE 420
VPYAYQCCPY GMCASFYKAS QWEAEADLHL DDEESSKRPL GLLARQAEH YDQDLDELQL 480
EMEDSKPHPS VQCSPTPGPF KPCYELPESW GIRLAVMAIV LLSVLCNGLV LLTVFAGGPV 540
PLPPVKFVVG AIAGANTLTG ISCGLLASVD ALTFQGFSEY GARWETGLGC RATGFLAVLG 600
SEASVLLTL AAVQCSVSVS CVRAYGKSPS LGSVRAGVLG CLALAGLAAA LPLASVGEYG 660
ASPLCLPYAP PEGQPAALGF TVALVMNSF CFLVVAGAYI KLYCDLPRGD FEAVWDCAMV 720
RHVAMLIFAD GLLYCPVAPL SFASMLGLFP VTPEAVKSVL LVVLPPLACL NPLLYLLFNP 780
HFRDDLRLRL FRAGDSGSLA YAAAGELEKS SCDSTQALVA FSDVDLILEA SEAGRPPGLE 840
TYGFPSVTLI SCQPGAPRL EGSCHVEPEG NHFGNPQPSM DGELLLRAEG STPAGGGLSG 900
GGGFQPSGLA FASHV 915

Seq ID NO: C389 Protein Sequence
Protein Accession #: NP_570901

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1 11 21 31 41 51
MASLVSELG LLLAVLVVTA TASPPAGLLS LLTSGQGALD QEALGGLLNT LADRVHCTNG 60
PCGKCLSVED ALGLGEPEGS GLPPGFVLEA RYVARLSAAA VLYLSNPEGT CEDTRAGLWA 120
SHADHLLALL ESPKALTPGL SWLLQRMQAR AAGQTPKTAC VDIPQLLEA VGAGAPGSAG 180
GVLAALLDHV RSGSCFHALP SPQYFVDFVF QHSSEVPMT LAELSALMQR LGVGREAHSD 240
HSHRHGASS RDPVPLISSS NSSSVMDTVC LSARDVMAAY GLSEQAGVTP BAWAQLSPAL 300
LQQQLSGACT SQSRPPVQDQ LSQSERYLYG SLATLLICLC AVFGLLLTLC TGCGRVAHYI 360
LQTFLSLAVG ALTGDVAVLH TPKVLGLHTH SEEGLSPOPT WRLLAMLGL YAFFLFENLF 420
NLLLPDPED LEDGPCGHSS HSHGGHSHGV SLQLAPSELR QPKPPHEGSR ADLVAEESPE 480
LLNPEPRRLS PELRLPYMI TLGDVAVHFA DGLAVGAAPA SSWKTGLATS LAVFCHELPH 540
ELGDFAAALH AGLSVRQALL LNLASALTAF AGLYVALAVG VSESEAWIL AVATGLFLYV 600
ALCDMLPAML KVRDPRPWL FLLHNVGLLG GWTVLLLLSL YRDDITF 648

Seq ID NO: C390 Protein Sequence
Protein Accession #: NP_061844

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1 11 21 31 41 51
MANASEPGGS GGGEAAALGL KLATLSLLLC VSLAGNVLFA LLIVRERSLH RAPIYLLLDL 60
CLADGLRALA CLPAVMLAAR RAAAAAGAPP GAGCKLLAF LAALFCFHAA FLLLGVGVT 120
YLATAHRFY AERLAGWPCA AMLVCAAWAL ALAAAFPPVL DGGGDEEDAP CALEQRPDGA 180
PGALGFLLL AVVVGATHLV YLRLLFFIHD RRRMRPARLV FAVSHDWTFF GPATGQAAA 240
NWTAGFGRGP TFPALVGRIP AGPGRGARRL LVLEEFKTEK RLCKMFYAVT LLLFLLWGPY 300
VVASYLRVLV RGAVPQAYL TASVWLTFAQ AGINPVVCFE FNRELRDCFR AQFPCCQSPR 360
TTQATHPCDL KGIGL 375

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Seq ID NO: C391 Protein Sequence
Protein Accession #: NP_005622

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1 11 21 31 41 51
MAAARPARGP ELPELLGLLLL LLLGDPGRGA ASSGNATGPG PRSAGGSARR SAAVTGPPPP 60
LSHCGRAPAC EPLRYNCLG SVLPYGATST LLAGDSDSQE EAHGKLVLS GLRNAPRCWA 120
VLOPLLCAVY MPKCENDRVE LPSRTLQCAT RGPCAIVERE RGWDFLRCCT PDRFPPEGCTN 180
EVQNKFNSS GQCEVPLVRT DNPKNWYEDV ECGIQCCNP LFTAEHQDM HSYIAAPGAV 240
TGLCTLFTLA TFVADWRNSN RYPAVILFYV NACPFVGSIG WLAQFMDGAR REIVCRADGT 300
MRLGEPSTNE TLSCVIIFVI VYALMAGVV WFVVLTYAMH TSFKALGTTY QPLSGKTSYF 360
HLLTSLFFV LTVALLAVA VDGDVSGIC FVGKMYRYR AGFVLAPIGL VLIUGGYFLI 420
RGVMTLFSIK SNRPGLLSEK AASKINETML RLIGIFGLAF GFVLITFSCH FYDFPNQAEW 480
ERSFRDYLVC QANVTIGLEPT KQPIPDCEIK NRPSLLVEKI NLFAMFGTGI AMSTVWVTKA 540
TLIIWRRTY RLITGQSDDEP KRIKSKMIA KAFSKREHLL QNPQGLSFS MHTVSHDGPV 600
AGLAFDLNEP SADVSSAWAQ HVTOMVARRG AILPDQISVT PVATPVPPPE QANLWLVAE 660
ISPELQKRLG RKIKGRKRK EVCPLAPPE LHPPAPAPST IPRLPQLPRQ KCLVAAGAWG 720
AGDSCRQAW TLVSNPFCPE PSPPQDPFLP SAPAPVAWAH GRRQQLGPIH SRTNLMDEL 780
MDADSD 788

70
75
80

Seq ID NO: C392 Protein Sequence
Protein Accession #: BAC04382

1 11 21 31 41 51
MGARSARGA LLLALLLCWD FRLSQAGRKR SGEVLPSDFP SAPAEPLPYF LQEPQDAYIV 60
KNKPVELRCR AFPATQIYFR CMGEWVSQND HVTQEGLEDA TLGARGGLRV REVQIEVSRQ 120
QVEELFGLD YWCQCVAWSS AGTTKSRAY VRIAYLRKNF DQEPKGKEVP LDBEVLLQCR 180
PPEGVPVAVV EWLKNEDVID PTQDTNPLLT IDENLIIRQA RLSDTANYTC VAKNIVAKRR 240
STTATVIVV NGWSSWAEW SPCSNRCGRG WQKTRTCTN PAFPLNGAFC EGQAQKRTAC 300
TTICPVDGAW TEWSKWSACS TECAHWSRE CMAPPNGG RDCSGTLDS KNCTDGLCMQ 360
NKKTLSDPNS HLEASGDAA LYAGLVVAIF VVVAILMAVG VVVYRRNCRD FDTITDSSA 420
ALTGGFHPVN FKTARPSNPQ LLHPSVFPDL TASAGIYRGP VYALQDSTDK IPMTNSPLLD 480
PLPSLKVEVY SSSTTSGSGP LADGADLGV LPFGTYPSPF ARDTHFLHLR SASLGSQQLL 540
GLPRDPGSSV SGTFGCLGGR LSIPGTGVS LVPNGAIPQG KFYENYLLIN KAESTLPLSE 600
GTQTVLSPSV TCGPTGLLLC RPVILTMFHC AEVSARDWIF QLKTOAQHGH WEEVVTLEE 660
TLATPCYCQL EPRACHILL QLGTVVPTGE SYRSARKRL QLAVFAPALC TSLEYSRLRV 720
CLEDTPVALK EVLELERTLG GYLVEEPKPL MFKDSYHNLRL LSLHDLPHAH WRSKLLAKYQ 780
EIPFYHIWSG SQKALHCTFT LERHSLASTE LTCKICVRQV EGEGQIFQLH TTLAETPAGS 840
LDTLCSAPGS TTTQGLGPA FKIPLSIRQK ICNSLDAPNS RGNDRWMLAQ KLSMDRYLNY 900
FATKASPTGV ILDLWEALQQ DGDGLNSLAS ALEEMGKSEM LVAVATDGDC 950

Seq ID NO: C393 Protein Sequence
Protein Accession #: NP_004616

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MNRKARRCLG HLFSLSLGMVY LRIGGFSSVV ALGASTICNK IPGLAPRQRA ICQSRPDAIL 60
VIGEGSQMGL DEQCFQFRNG RWNCSALGER TVFGKELKVG SREAAPTYAI IAAGVAHAIT 120
10    AACTQGNLSD CGCDKEKQGG YHRDEGWKMG GCSADIRYGI GFAKVFVDAR EIKQNARTLM 180
      NLHNNAGRKL ILEENMKLEC KCHGVSGSCT TKTCTWTLPO FRELGTVLKO KYNEAVHVEP 240
      VRASNRKPT FLKIKKPLSY RKPMDTDLVY IEKSPNYCEE DFTVGSVGTQ GRACNKTAPO 300
      ASGCDLMCCG RGYNTHQYAR VWQCNCCKFH CCYVKCNTCS ERTEMYTCK 349

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Seq ID NO: C394 Protein Sequence
Protein Accession #: NP_003777

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15      1      11      21      31      41      51
      |      |      |      |      |      |
MDALCGSGEL GSKFWDNLS VHTENPDLT CFONSLAWV PCIYLMVALP CYLLYLRRHC 60
20    RGYIILSHLS KLMKVLGVLL WCVSWADLFY SFHGLVHGRA PAPVFFVTPL VVGVTMLLAT 120
      LLTIYERLQG VQSSGVLIIF WFLCVCAIV PFRSKILLAK AEGEISDPFR FTTFYIHFAI 180
      VLSALILACF REKPPFFSAK NVDPNPYPET SAGFLSRLFF WFTKMAIYG YRHPLREKDL 240
      WSLKEEDRSQ MVVQQLLEAW RKQEKQTARH KASAAPGKNA SGEDEVLLGA RPRPKPSFL 300
25    KALLATFGSS FLISACFKLI QDLLSFNPQ LLSILIRFIS NPMAPSWGPF LVAGLMFLCS 360
      MMQSLILQHY YHYIFVTGVK FRTGIMGVII RKALVITNSV KRASTVGEIV NLMSSVDAQRF 420
      MDLAPFLNLL WSAPLQIILA TYFLWQNLGP SVLAGVAFMV LLIPLNGAVA VKMRAPQVKQ 480
      MKLKDSRIKL MSBILNGIKV LKLYAWEPSP LKQVEGIRQG ELQLLRTAAY LHTTTTFTWM 540
      CSPFLVTLIT LWVYVVDPN NVLDAAEKAFV SVSLFNILRL PLNMLPQLIS NLTAQASVSLK 600
30    RIQQLSQEE LDPQSVERTK ISPGYAITIH SGTFTWAQDL PPTLHSLDIQ VPKGALVAVV 660
      GPVGCCKSSL VSALLGEMEK LEGKVHMKGS VAYVPOQAWI QNCTLQENVL PGKALNPTRY 720
      QQTLEACALL ADLEMLPGGD QTEIGERGIN LSGGQRQVRS LARAVYSADAD IFLLDDPLSA 780
      VDSHVAKHIF DHVIGPEGVL AGKTRVLVTH GISFLPQTDI IIVLADGQVS EMGPYPALLQ 840
      RNGSFANFLC NYADEDEQGH LEDSWTALEG AEDKEALLIE DTLSNHTDIT DNDPVTYVVO 900
35    KQFMRLQSLA SSDGEGQGRP VPRRHLPSE KVQVTEAKAD GALTQEEKAA IGTVELSVFW 960
      DYAKAVGLCT TLAICLLYVG QSAAGANV WLSAWTNDAM ADSRQNTSL RLGVYALGI 1020
      LQGLFVNLAA MAMAAGGQA ARVLHQAALL NKIRSPQSF DTTPSGRILN CFSKDIYVVD 1080
      EVLAPVILML NSFFNAIST LVVIMASTPL FTVVILPLAV LVTLVQRFYA ATSRQLKRL 1140
40    SVSRSPYISH FSETVTGASV IRAYNRSRDF EIISDTKVDA NQRSCYPYII SNRWLSIGVE 1200
      FVGNVCVFLA ALFAVIGRSS LNPGLVLGSLV SYSLQVTFAL NWMIRMMSDL ESNIVAVERV 1260
      KEYSKTETES PWVVEGSRPP EGWPPRGEVE PRNYSVRYRP GLDLVLRDLS LVHVGGEKVG 1320
      IVGRTPGAGKS SMTLCLFRIL EAAKGEIRID GLNVADIGLH DLRSQTLTIIP QDPILFSGTL 1380
      RMNLDPFGSV SEEDIWALE LSHLETFSVS QPAGLDFQCS EGGENLSVQO RQLVCLARAL 1440
45    LRKSRILVLD BATAAIDLET DNLQIATIRT QFDTCTVLTII AHRNTINDY TRVLVLDKGV 1500
      VAEPDSPANL IAARGIFYGM ARDAGLA 1527

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Seq ID NO: C395 Protein Sequence
Protein Accession #: NP_004617

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50      1      11      21      31      41      51
      |      |      |      |      |      |
MRARPQVCEA LFLALALQTG VCYGIKWLAL SKTPSALALN QTOHCKOLEG LVSAQVQLCR 60
      SNLELMHTTV HAAREVMKAC RRAFPADMRWN CSSIELAPNY LLDLERGTRE SAPVYALSAA 120
      AISHAIARAC TSGDLPGCSC GPVPGEPGP GNRWGGCADN LSYGLLMGAK PSDAPMKVVK 180
55    TGSQANKLMR LINSSEVGRQA LRASLEMKCK CHGVSGSCSI RTCWKGQLQL QDVAAADLKTR 240
      YLSATKVVHR PMGTGRHLVP KDLDIRPVKD SELVYLQSSP DFCMKNEKVG SHGTQDRQCN 300
      KTSNGSDSCD LMCCGRGYNP YTDVVVERCH CKYHWCYVT CRRCERTVER YVCK 354

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Seq ID NO: C396 Protein Sequence
Protein Accession #: NP_114072

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60      1      11      21      31      41      51
      |      |      |      |      |      |
MEWGYLLEVT SLLAALALI QSSGAAAAASA KELACQETV PLCKGIGYNY TYMPNQFNHD 60
      TQDEAGLEVH QFWPLVEIQ SPDLKFFLCS MYTPICLEDY KKPLPPCRSV CERAKAGCAP 120
65    LMRQYGFAMP DRMRCDLFE QGNPDTLCMD YNRTDLTTAA PSPPRRLPPP PPGEQPPSGS 180
      GHGRPPGARF PHRGGGRGGG GGDAAAAPPAR GGGGGGKARP PGCGAAPCEP GCQCRAPMVS 240
      VSSEHPLYN RVKTGQIANC ALPCHNPFPS QDERAFTVFW IGLMSVLCFV STFATVSTFL 300
      IDMERFKYPE RPIIFLSACY LFVSVGYLVR LVAGHEKVAC SGGAFGAGGA GGAGGAAAGA 360
70    GAAGAGAGGP GGRGEYELG AVSQHVRYET TGPALCTVVF LLYVFFGMAS SIWWVILSLT 420
      WFLAAGMKMG NEAIAAGSYQ FHAAAWLVPS VKSIIVLALS SVDGDPVAGI CVVGNQSLDN 480
      LRGFVLAPLV IYLFITGMFL LAGFVSLFRI RSVIKQDQGP TKTHLEKILM IRLGLFTVLY 540
      TVPAVAVVAC LFYEQHNRRP WEATHNCPLI RDLQPDQARR PDYAVFMLKY FMCLVVGITS 600
      GVVWSGKTL ESWRSLCTRC CWASKGAAGV GGAGATAAGG GGGPGGGGGG GPGGGGGPGG 660
75    GGGSLYSDVS TGLTWRSCTA SSVSYPKQMP LSQV 694

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Seq ID NO: C397 Protein Sequence
Protein Accession #: XP_050625

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80      1      11      21      31      41      51
      |      |      |      |      |      |
MLQPGSLLL LFLASHCCLG SARGFLFLGQ PDFSYKRSNC KPIPANLQLC HGIEYQNMRL 60
      PNLLGHETMK EVLEQAGAWI PLVMKQCHPD TKKFLCSLEA FVCLDDDET IQPCHSLCVQ 120
      VKDRCAPVMS AFGPPFMDL ECDRPPQDND LCIFLASSDH LLPATEAPK VCEACKNKND 180
      DDNDIMETLC KNDPALKIKV KEITYINRDT KIILETKSKT IYKLVGVSER DLKKSVLWLK 240

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DSLQCTCEEM NDINAPYLVN GQKQGGLVI TSVKRWQKGQ REFKRISRSI RKLQC 295

Seq ID NO: C398 Protein Sequence
Protein Accession #: NP_001297.1

1	11	21	31	41	51	
MSMGLBITGT	ALAVLGLWGT	IVCCALPMWR	VSAFIGSNII	TSQNIWEGWL	MNCVVQSTGQ	60
MQCKVYDSSL	ALPQDLQAAR	ALIVVAILLA	AFGLLVALVG	AQCTNCVQDD	TARAKITIVA	120
GVFLLLAALL	TLVPVWSAN	TIIRDFYNPV	VPEAQKREMG	AGLYVGWAAA	ALQLLGGALL	180
CCSCPPEKK	YTATKVYSA	PRSTGPGASL	GTGYDRKDYY			220

Seq ID NO: C399 Protein Sequence
Protein Accession #: NP_036581.1

1	11	21	31	41	51	
MESRKDITNQ	EELWKMKPRR	NLEEDDYLHK	DTGETSMLKR	PVLLHLHQTA	HADEFDCPSE	60
LQHTQELFPQ	WHLPIKIAAI	IASLTFLYTL	LREVIHPLAT	SHQQYFYKIP	ILVINKVLPM	120
VSITLLALVY	LFGVIAAIVQ	LENGTKYKCF	PHWLDKWMLT	RKQFGLLSFF	PAVLHAIYSL	180
SYPMRRSYRY	KLLNWAYQQV	QQNKEDAWIE	HDVWRMEIYV	SLGIVGLAIL	ALLAVTSIPS	240
VSDSLTWREF	HYIQSKLGIV	SLLLGTHIAL	IFAWNKWIDI	KQFVWYTPPT	FMAIAVFLPIV	300
VLIFKSLPL	PCLRRKILKI	RHGWEDEVTKI	NKTEICSQL			339

Seq ID NO: C400 Protein Sequence
Protein Accession #: NP_001766.1

1	11	21	31	41	51	
MANCEFSPVS	GDKPCCRLSR	RAQLCLGVSI	LVLILVVVLA	VVPRWRQTN	SGPGTTKRFP	60
ETVLARCVMY	TEIHPEMRHV	DQSVWDAFK	GAPISKHPCN	ITEEDYQPLM	KLGTQTVPCN	120
KILLWSRIKD	LAHQPTQVQR	DMFTLEDTL	GYLADDLTWC	GEFNTSKINY	QSCPDWRKDC	180
SNMPVSVFWK	TVSRFPABAA	CDVVHVMLNG	SRSKIFDKNS	TFGSVEVHNL	QPEKVQTLA	240
WVIHGGREDS	RDLQDPTIK	ELESIIISKRN	IQFSCKNYIR	PKFLQCVKN	PRDSSCTSEI	300

Seq ID NO: C401 Protein Sequence
Protein Accession #: XP_120513.2

1	11	21	31	41	51	
MVSCFPSSGL	RETNEVVKCF	YALRAFMRFM	SSEAAMLGES	RTPKPKHRA	TTRAKIFKRF	60
PSEGESNSNR	LVEELAVIHT	YSDDPAPTTS	PSSVQPREFG	VMQGAPEARF	GSRTPPAAAE	120
ASSPHLGIGE	AACQSGARAA	APRAGARRCQ	PORQAAAAAA	TAQHTLPHA	RTRADPAGRR	180
RRHPRSPAPG	GEGTCSGPA	PRRRMEEMQ	PAEAGPSVVK	YKQSPSYSV	LKTFPSKRPA	240
LAKRYERPTL	VELPHGLHRT	PAQPPFPASPA	ASSSSSFAAV	VELGAPPRPP	RRGFRARGTI	300
PLLLPAPGVA	GTLPLPPPTSS	SPPSPRPRPW	BAAAPRGGTS	HTHMWRSQST	LPGSDTMVSV	360
FGLMAQRRLQ	HLRLQCFWQ	ILGSWGTWPC	QQDWLEKEGQ	VAULLPRSEG	NTAPKKSRLI	420
LDAPAAQCQR	VLSLNCGGK	LDSNHSQSM	ISCVKQEGSS	YNERQEHCHI	GKGVHSQTS	480
NVDIEMQYMQ	RKQQTSAFLR	VFTDSLQNYL	LSGSFPTPNP	SSASEYGHLA	DVDPLSTSPV	540
HTLENISLDS	TASLCKSRHL	SREPPVKSDP	FNPLQALAG	GASRPFSGAQ	QSIAYRVNSE	600
LEDGIRSVVP	LSCEALEMDL	TSLSGSKQLN	NYPVYITSKQ	WDEAVNSSKK	DGRRLRLRYLI	660
RFVFTDELK	YSCGLGKRKR	SVQSGETGPE	RRPLDPVKVT	CLRGTASFRS	VSPSVISPHR	720
IGCGSPRTSV	QPSVF					735

Seq ID NO: C402 Protein Sequence
Protein Accession #: BAA92562.1

1	11	21	31	41	51	
METTIVLSGIN	FEYKGMTGWE	VAGDHIYTAA	GASDNDFMIL	TLVVPGRFRP	QSVMAADTENK	60
EVARITFVFE	TLCSVNCELY	FMVGVSRTN	TPVETWKGSK	GKQSYTYIE	ENTITSPTWA	120
PQRTTFHEAS	RKVTNDVAKI	YSINVTNVMN	GVASYCRFCA	LEASDVGSSC	TSCPAGYYID	180
RDSGTCHSCP	PNTILKAHQF	YGVQACVPCG	PGTKNNKIHS	LCYNDCTFSR	NTPTRTFNYN	240
FSALANTVTL	AGGPSFTSKG	LKYFRHFTLS	LCOGQGRKMS	VCTDNVTDLR	IPEGESGFSK	300
SITAYVCQAV	IIPPEVTGYK	AGVSSQFVSL	ADRLIGVTTD	MTLDGITSPA	ELPHLESIGI	360
PDVIFFYRSN	DVTQSCSSGR	STTIRVRCSP	QKTVPGSLLL	PQTCSDGTCD	GCFHFLWES	420
AAACPLCSVA	DYHAIVSSCV	AGIQKTTYVW	REPKLCSGGI	SLPEQRVTIC	KTIDFWLKVG	480
ISAGTCTAIL	TLVLTCTYFWK	KNQRLEYKYS	KLVMNATLKD	COLPAADSCA	IMEGEDVEDD	540
LIFTSKSLP	GKIKSPTSQ	PAPVTISLSE	DS			572

Seq ID NO: C403 Protein Sequence
Protein Accession #: NP_055139.1

1	11	21	31	41	51	
MALQGISVVE	LSGLAPGRXC	AMVLADFGAR	VVRVDRPGSR	YDVSRLGRGK	RSLVLDLKQP	60
REPRAAASVQ	AVGCAAGALP	PRCHGETPAG	PRDSAAAGSK	AYLCQAEWIN	PVQESFCRLA	120
GHDINYLALS	GVLSKIGRSG	ENPYAPLNLV	ADFAGGGLMC	ALGIIMALPD	RTRTDKGQVI	180
DAMNVEGTAY	LSSFLNKTQK	SSLWEAPRGQ	NMLDGGAPFY	TTYRTADGEF	MAVGAIEPQF	240
YELLINGLGL	KSDLEPNQMS	TDDWPEMKKK	FADVFAKTKK	AEWCQIPDGT	DACVTFVLTP	300
EEVVHHDHMK	ERGSFITSEE	QDVSPRLAPL	LIANTPAIPSS	KGDPFFIGEHT	EEILEEFGPS	360
REEIYQLNSD	KIIESNKVKA	SL				382

Seq ID NO: C404 Protein Sequence

Protein Accession #: XP_091332.1

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1      11      21      31      41      51
5  MQRWTLWAAA FTLHSAQAF PQTDISISPA LPELPLPSLC PLFWMEFKGH CYRFFPLNKT 60
   WAEADLYCSE FSVGRKSAKL ASIHSEENV FVYDLVNSCV PGIPADVWTG LHDHRQEGQF 120
   EWTGSSYDY SYWDGSPDD GVHADPEED CVQIWRPPTS EQLQAPPEQL PLISSEATDV 180
   YLPEDFPAEP KLMDQSWVSR KSLKPSKSHL MEPPTPVAKH QKAKTRHRSI RGVWVPSGKA 240
10 GSWKERMNAD YGRRKRSAPR QEGRLRCRER RLRAASGQGR PEGQRKQRQ ERQERGWEEL 300
   GGVSPFMRGA AQHGHLGAGS QRGAAPCEGE NHQAPELGST WRGRLQPPQT AALCHFALEK 360
   LFGNAHGLAA AFVQPALQVQ EEKNNRTRFS GAYFTMSDPT CDQDSKEQSL RRGREAEKD 420
   GPYRLVKKKR GPVACPSSFE LQSGGEVCLD PPVELRAGTW IAREPP 466

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Seq ID NO: C405 Protein Sequence
Protein Accession #: XP_054869.2

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1      11      21      31      41      51
20 MHTCCPPVTL EQDLHRKMS WMLQTLAFV TSLVLSAET IDYYGEICDN ACPCEEKDI 60
   LTVSCENRGI ISLSEISPPR FPIYHLLLSG NLLNRLYPNE FVNYTGASIL HLGSNVIQDI 120
   ETGAFHGLRG LRRHLNANNK LELLRDDTFL GLENLEYLQV DYNYSVIEP NAFGKLHLLQ 180
   VLILANDNLS SLPNMLFRFV PLTHLDLRGN RLKLLPYVGL LQHMDKVVEL QLBENPWNC 240
   CELISLKDWL DSISYSALVG DVVCETPFRL HGRDLDEVSK QELCPRLIS DYEMRPQTPL 300
   STTGYLHTTP ASVNSVATSS SAVYKFPPLK PKGTRQPNKP RVRPTSRQPS KDLGYSNYGP 360
25 SIAYQTKSPV PLECPACSC NLQISDLGLN VNCQERKIES IAELOPKPYN PKMYLTENY 420
   IAVVRTDFL EATGLDLLHL GNNRISMIQD RAFGDLNLR RLVLNCRNRI RLSPELFYGL 480
   QSLQYLFLQY NLIREIQSGT FDPVFNQLQL FLNNLLQAM PSGVPSGLTL LRLNLRNHF 540
   TSLPVSGVLD QLSLIQIDL HDNPDWCTCD IVGMKLWVEQ LKVGVLVDEV ICKAPKKFAE 600
   TDMRSIKSEL LCPDYSVVV STPTPSIQV PARTSAVTPA VRLNSTGAPA SLGAGGGASS 660
30 VPLSVLILSL LLVFMVSFV AAGLFVLVMK RRKKNQSDHT STNNSDVSSF NMQYSVYGGG 720
   GGTGGHPAHV VHRHGPALPK VKTPAGHVYE YIPHLGHMC KNPIYRSRG NSVEDYKDLH 780
   ELKVITYSSNH HLQQQQPPF PPQQPQQPPF PQLQLQPGEE ERRESHLRS PAYSVSTIEP 840
   REDLLSPVQD ADRFYRGILE PDKHCSTTPA GNSLPEYKPF PCSPAAYTFS PNYDLRRPHQ 900
   YLHPGAGDSR LREPVLISFP SAVFVEPNRN EYLELAKLN VEPDYLEVLE KQTTFSQF 958

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Seq ID NO: C406 Protein Sequence
Protein Accession #: NP_000784.2

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1      11      21      31      41      51
40 MGILSVLLLI TLQILPVFFS NCLFLALYDS VILLKHVLL LSRKSTRGE WRRMLTSEGL 60
   RCVWKSFLLD AYKQVKGLED APNSSVVHVS STEGGDNSGN GTQEKIAEGA TCHLLDFASP 120
   ERPLVVNFGS ATUPPFTSQL PAFRKLVEEF SSVADFLVY IDEAHPSDGN AIPGDSLSL 180
   EVKKHQQED RCAAAQQLLE RFSLPQCRV VADRMDNNAN IAYGVAPERV CIVQRQKIAY 240
45 LGKGKPFYSN LQEVHRWLEK NPSKRUKTR LAG 273

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Seq ID NO: C407 Protein Sequence
Protein Accession #: NP_006540.2

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1      11      21      31      41      51
50 MSSCVSSQPS SNRAAPQDEL GGRGSSSSSES QKPCEALRGL SLSIHLGME SFIVVTECEP 60
   GCAVDLGLAR DRPLEADGQE VPLDSSGSQA RPHLSGRKLS LQERSQGGLA AGGSLDMNGR 120
   CICPSLPYSP VSSPQSSPRL PRRPTVESHH VSITGMQDCV QLNQYTLKDE IGKGSYGWVK 180
   LAYNENDNTY YAMKVLKSKK LIRQAGFPFR PPRGTRPAP GGCIPRGPPI EQVYQETAIL 240
55 KKLDDHNVVK LVEVLDDPNE DHLVMVFELV NQGPVMEVPT LKPLSEDQAR FYFQDLIKGI 300
   EYLHYQKIIH RDIKPSNLLV GEDGHKIAD FGVSENEFKGS DALLSNTVGT PAFMAPESLS 360
   ETRAKIPSGA LDVWAMGVTL YCFVFGQCPP MDERIMCLHS KIKSQALEPP DQPDIAEDLK 420
   DLITRMLDIN PESRIVVPEI KLHPVVTREG AEPLPSDEN CTLVEVTEEE VENSVKHIPS 480
60 LATVILVKTM IRKRSFGNPF EGSRRREERSL SAPGNLLTKK PTRECELSSE LKEARQRRQP 540
   PGRPAFRGG GGSALVRGSP CVESCWAPAP GSPARMHPLR PEEAMEPE 588

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Seq ID NO: C408 Protein Sequence
Protein Accession #: NP_061116.2

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1      11      21      31      41      51
65 MGLSLPKKKG LILCLWSKFC RWFQRRSWA QSRDEQNLIQ QKRINESPLL LAAKNDVQA 60
   LNKLLKYEDC KVRQRGAMGE TALHIAALYD NLEAAMVME AAPVLVFEPM TSELYEGQTA 120
70 LHIAVNVQNM NLVRALLARE ASVSARATGT AFRSPCNLI YFGEHPLSFA ACVNSEIIVR 180
   LLIEHGADIR AQDSLGNLVL HILILQPNKT FACQMYNLLI SYDRHGDHLQ PLDLVFNHGG 240
   LTPPKLAGVE GNTVMPQHLM QKRKHTQWY GPLTSTLYDL TRIDSSGDEQ SLELEIITTK 300
   KREARQILDQ TPVKELVSLK WKRYGRPYFC MLGAIYLLYI ICTMCCIIYR PLKPRTNNT 360
75 SPRDNTLLQK KLQBAVMTP KDDIRLVGEL VTVIGAIIL LVEVPDIFRM GVTRFPQGTI 420
   LGGPFVHLII TYAFMVLVTM VMRLISASGE VVPMFALVL GWCNMVYFAR GFQMLGPPTI 480
   MIQRMIPGDL MRFCWLMVAV ILGFASAPYI IFQTEDPREL GHFYDYPMAL PSTFELPLTI 540
   IDGPANYNDV LPFMYSTIYA APAILATLLM LNLIAMMGD THWRVAHERD ELWRAQIVAT 600
   TVMLERKLPR CLWPRSGICG REYGLGDRWF LRVEDRQDLN RQRIQRYAQA FHTRGSEDL 660
80 KDSVEKLELG CFPSPHLSLP MPSVSRSTSR SSANWERLRQ GTLRRLRGI INRGLEDGES 720
   WEYQI 725

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Seq ID NO: C409 Protein Sequence
Protein Accession #: NP_068710.1

1 11 21 31 41 51
 MQKVTILGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSEW 60
 5 RSSGEGAGRG WGSPPPLTTQL SPTGAKCKCK FGQKSGHHPG ETPPLITPGS AQS 113

Seq ID NO: C410 Protein Sequence
 Protein Accession #: NP_005962.1

1 11 21 31 41 51
 10 MQKVTILGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSAK 60
 CKCKFGQKSG HHPGETPPLI TPGSAQS 87

Seq ID NO: C411 Protein Sequence
 Protein Accession #: NP_004952.1

1 11 21 31 41 51
 20 MLSKVLPLVL GILLILQSRV RGPQTBSKNE ASSRDVVYGP QPQPLENQLL SEETKSTETS 60
 TGSRVGLKPE ASRILNTILS NYDHKLRPGI GEKPTVVTV E IAVNSLGPLS ILDMEXTIDI 120
 IFSQTWYDER LCYNDTFESL VLNGNVVSQ L WIPDTFFRNS KRTHEHEITM PNQMVRIYKD 180
 GKVLVYTRMT IDAGCSLHML RPFMDSHSCP LSPSSFSYPE NEMIVKWENF KLEINEKNSW 240
 25 KLFQDFDTGV SNKTEIITP VGDFMVMTIF FNVSRFPYV AFQNYVPSSV TMLSVWSFW 300
 IKTESAPART SLGITSVLTM TTLGTFSRKN FPRVSYITAL DFYIACFPV CPCALLEFAV 360
 LNFLLYNTK AHASEKLEHP RINSRAHART RARSACARQ HQEAPVCQIV TTEGSDGEER 420
 PSCSAQQPPS PGSPGPRSL CSKLACCWCW KRFFKYFCMV PDCGSTWQQ GRLCIHVYRL 480
 DNYSRVVPFV TFFFFNVLYW LVCLNL 506

Seq ID NO: C412 Protein Sequence
 Protein Accession #: NP_068819.1

1 11 21 31 41 51
 35 MEYTIIDIIFS QTWYDERLCY NDTFESLVN GNVVSQLWIP DTFFRNSKRT HEHEITMPNQ 60
 MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120
 INEKNWSKLF QLDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTM 180
 LSWVSFWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFPVFCFC 240
 ALLEPAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE APVCQIVTTE 300
 40 GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCWCWCRF KKYFCMVPCD EGSTWQQARL 360
 CIHVRLDNY SRVVPVPTFF FPNVLYWLVC LNL 393

Seq ID NO: C413 Protein Sequence
 Protein Accession #: NP_068822.1

1 11 21 31 41 51
 45 MEYTIIDIIFS QTNWKRTHS HEITMPNQMV RIYKDGKVLY TIRMTIDAGC SLHMLRFPMD 60
 SHSCPLSFSS FSYPENEMIY KWENFKLEIN EKNSWKLFQF DFTGVSNKTE IITTPVGDPM 120
 50 VMTIFFNVSR RFGYVAFQNY VPSSVTMIS WVSFWIKTES APARTSLGIT SVLMTTLGT 180
 FSRKNFPRVS YITALDFYIA ICFVFCFAL LEPAVLNFI YNQTKAHASP KLRHPRINSR 240
 AHARTRARS ACARQHQRAF VCQIVTTEGS DGEERPSCSA QQPPSPGSPE GPRSLCSKLA 300
 CCEWCKRFKK YFCMVPCDCEG STWQQGRLCI HVYRLDNYSR VVPVPTFFFF NVLYWLVCIN 360
 L 361

Seq ID NO: C414 Protein Sequence
 Protein Accession #: NP_068830.1

1 11 21 31 41 51
 60 MEYTIIDIIFS QTWYDERLCY NDTFESLVN GNVVSQLWIP DTFFRNSKRT HEHEITMPNQ 60
 MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120
 INEKNWSKLF QDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTM 180
 LSWVSFWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFPVFCFC 240
 65 ALLEPAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE APVCQIVTTE 300
 GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCWCWCRF KKYFCMVPCD EGSTWQQGRL 360
 CIHVYRLDNY SRVVPVPTFF FPNVLYWLVC LNL 393

Seq ID NO: C415 Protein Sequence
 Protein Accession #: NP_068591.1

1 11 21 31 41 51
 70 MPAVSGPGPL FCLLLLLLDP HSPBTGCPPL RRFYKLSFK GPRALPGAG IPFWSHHGDA 60
 ILGLEEVRLT PSMNRNSGAV WSRASVPFSA WEVEVQMRVT GLGRRGAGM AVWYTRGRGH 120
 75 VGSVLGLAS WDGIGIFFDS PAEDTQDSPA IRVLASDGH I PSEQPGDGAS QGLGSCHWDF 180
 RNRPHPRFR IYVQGLRLM SLNSGLTFS D PGEFCVDVGP LLLVPGGFFG VSAATGTIAD 240
 DHDVLSPLTF SLSEPSPEVP PQPFLEMQLL RLARQLEGLW ARLGLGTRED VTPKSDSEBQ 300
 GEGRLFDLE ETLGRHRRIL QALRGLSKQL AQAERQWKQ LGPPGQARPD GGWALDASCQ 360
 80 IPSTPGRGGH LSMSLNKD SA KVGALLHGQW TLLQALQEMR DAAVRMAAEA QVSYLEFVGIE 420
 HHFLELDHIL GLLQELRGP AKAAAKAPRP PQQPPRASSC LQGFIFLYL LIQTVGFFGY 480
 VHFRLQELNKS LQECSTGSL PLGPAPHTPR ALGILRRQPL PASMPA 526

Seq ID NO: C416 Protein Sequence
 Protein Accession #: XP_117036.1

5	1	11	21	31	41	51	
	MERRTRGALG	SRPPPPPLPA	LRHLCTGLQA	AGMAWPGTLW	RHTCQGRAXA	AEGPFWGLFRP	60
	HRCFPREAGQA	PVGSPSETQG	VAHVCSRARV	SVDREPGGG	AYAMHVTPRW	KGCHRHSGRT	120
	VRGSVSWKRP	EQAAPETGRG	PAVARGSGDG	NECGWG			156
Seq ID NO: C417 Protein Sequence							
Protein Accession #: XP_167803.2							
10	1	11	21	31	41	51	
15	MPGKGQRKTA	TNKPGLPGA	PGVGIGGHCL	YVLECKCFIK	NKTKTHHHKK	KNFAAKRNEE	60
	KLKKKKQEK	KNHTKPFHHT	YPLSQDFLP	AKSYFCGNP	CPLMQGLF		108
Seq ID NO: C418 Protein Sequence							
Protein Accession #: NP_079056.1							
20	1	11	21	31	41	51	
25	MFRIVERYEM	PRHEVYVLLI	RNIFLKISII	GILCYWLNT	VALSGEECWE	TLIGQDIYRL	60
	LLMDVFVSLV	NSFLGEFLRR	IIGMQLITSL	GLQEFDIARN	VLELIYAQTL	VWIGIFFCPL	120
	LPPIQMIMLF	IMFYSKNISL	MMNFQPPSKA	WRASQMMTFP	IFLLFFPSPT	GVLCTLAITI	180
	WRLKPSADCG	PFRGLPLFIH	SIYSWIDTSL	TRPGYLMVVW	IYRNIGSVH	FFILTILIVL	240
	IIITYLYNQIT	EGRKIMIRLL	HEQIINEGKD	KMFLIEKLIK	LQDMEKKANP	SSLVLERREV	300
	EQQGFHLHGE	HDGSLDLRSR	RSVQEGNPRA				330
Seq ID NO: C419 Protein Sequence							
Protein Accession #: Eos sequence							
30	1	11	21	31	41	51	
35	MLSDDHVNEI	IIQVENVSSG	VQSHPPSNQI	FQEKVLLDSS	INMVLISIDI	DVIDSQTVSK	60
	RNDQKGNQVL	RFSTSLNESM	SQTLHSLECM	GIDTPGSSHE	TVQGGKLIAS	LIPMTSRDRI	120
	KAIRNQPRMT	EKKRNLKIV	DKEKSKQTHR	ILQLNCCIQC	LNSISRAYRR	SKNSLSEILN	180
	SISLWQKTLK	IIGGKFGTSV	LSYFNFLRWL	LKFNIPSPIL	NFSFIIIPQF	TVAKKNTLQF	240
	TGLEFFTGVG	YPRDTVMYVG	FYTNSTIQHG	NSGASYNMQL	AYIFTIGACL	TTCFFSLLFS	300
	MAKYFRNNFI	NPHIYSGGIT	KLIPQWDFTV	THEKAVKLKQ	KNLSTEIREN	LSELRQENSK	360
	LTPNQLLTRF	SAYMVAVVVS	TGVAIACCAA	VYLAENLE	FLKTHSNPGA	VLLLPFVWSC	420
40	INLAVPCIYS	MFRIVERYEM	PRHEVYVLLI	RNIFLKISII	GILCYWLNT	VALSGEECWE	480
	TLIGQDIYRL	LLMDVFVSLV	NSFLGEFLRR	IIGMQLITSL	GLQEFDIARN	VLELIYAQTL	540
	VWIGIFFCPL	LPPIQMIMLF	IMFYSKNISL	MMNFQPPSKA	WRASQMMTFP	IFLLFFPSPT	600
	GVLCTLAITI	WRLKPSADCG	PFRGLPLFIH	SIYSWIDTSL	TRPGYLMVVW	IYRNIGSVH	660
	FFILTILIVL	IIITYLYNQIT	EGRKIMIRLL	HEQIINEGKD	KMFLIEKLIK	LQDMEKKANP	720
45	SSLVLERREV	EQQGFHLHGE	HDGSLDLRSR	RSVQEGNPRA			760
Seq ID NO: C420 Protein Sequence							
Protein Accession #: NP_002241.1							
50	1	11	21	31	41	51	
55	MGGDLVLGLG	ALRRKRRLLE	QEKSLAGWAL	VLAGTGIGLM	VLHAEMLWFG	GCSWALYLF	60
	VKCTISISTP	LLLCLIVAFH	AKEVQLFMTD	NGLEDWRVAL	TGRQAAQIVL	ELVVCGLHPA	120
	PVRGPPCVOD	LGAPITSPQP	WPGFLQGGEA	LLSLAMLLRL	YLVPRAVLLR	SGVLLNASYR	180
	SIGALNQVRP	RHWFAKLYM	NTHPGRLLLG	LTGLWLITTA	WVLSVAERQA	VNATGHLSDT	240
	LWLIPITFLT	IGYGDVVPQT	MWGKIVCLCT	GVMGVCTAL	LVAVVARKLE	FNKAERHVEN	300
	FMDIQYTKK	MEKESARVLQ	EAMMFYKHTR	RKESHAARRH	QRKLAAAINA	PROVRLKHRK	360
	LREQVNSMVD	ISKMMILYD	LQQLSSSSRR	ALEKQIDTLA	GKLDALTELL	STALGPRQLP	420
60	EPSQQSK						427
Seq ID NO: C421 Protein Sequence							
Protein Accession #: NP_079533.1							
65	1	11	21	31	41	51	
70	MGGKQRDEDD	EAYGKPVKYD	PSFRGPIKNR	SCTDVICCVL	FLLFILGYIV	VGIVAWLYGD	60
	PRQVLYPRNS	TGAYCGMGEN	KDKPYLLYFN	IFSCILSSNI	ISVAENGLQC	PTPQVCVSSC	120
	PEDPWTVGKN	EPSQTVGEVF	YTKNRNFCLE	GVPWNMTVIT	SLQELCPSF	LLPSAPALGR	180
	CPFWNTITPP	ALPGITNDTT	IQQGISGLID	SINARDISVK	IFEDFAQSWY	WILVALGVAL	240
	VLSLLFILLL	RLVAGPLVLV	LILGVLGVLA	YGIYYCWEEY	RVLADKQASI	SQLGFTTNLS	300
	AYQSQVETWL	AALIVLAVLE	AILLVLVIFL	RQRIRIAIAL	LKEASKAVGQ	MMSTMIFYPLV	360
	TFVLLLICIA	YWMATLYPL	PTQPATLGYV	LWASNISSPG	CEKVPINTSC	NPTAHLVNSS	420
	CPGLMCPVQG	YSSKGLIQRS	VFNLIQYGV	GLFWTLNWL	ALGQCVLAGA	PASFYWAFHK	480
	PQDIPTFPLI	SAFIRTLRYH	TGSLAFGALI	LTLVQIARVI	LEYIDHKLRG	VQNPVARCIM	540
75	CCFKCCLWCL	EKFIFKLNRN	AYIMIAIYK	NPCVSAQNAF	MLMARNIVRV	VVLDKVTDLL	600
	LFFGKLLVVG	GVGVLSFFFP	SGRIPGLGKD	FKSPHLYYTW	LPIMTSILGA	YVIASGFPSV	660
	FGMCVDTLFL	CFLIEDLRNN	GSLDRPYMS	KSLKILGKK	NEAPPDNKKR	KK	712
Seq ID NO: C422 Protein Sequence							
Protein Accession #: NP_057264.1							
80	1	11	21	31	41	51	
	MGSNSGQAGR	HIYKSLADDG	PFDSVEPPKR	PTSRILMHSM	AMFGREFCYA	VEAAYVTPVL	60

5 LSVGLPSSLY SIVWFLSPIL GFLQLQFVVG ASDHCRSRWG RRRPYILTGL VMMLVGMALY 120
 LMGATVVAAL IANPRRKLVM AISVTMIGVV LFDFAADFID GPIKAYLFDV CSHQDKKEKGL 180
 HYHALFTGFG GALGYLLGAI DWAHLELGRLL LGTEFQVMFF PSALVLTLCF TVHLCSISEA 240
 PLTEVAKGIP PQQTPODPPPL SSDGMVEYGS IEKVKNGYVN PELAMQGAKN KNEAEQTRRA 300
 MTLKSLRLAL VNMPPHYRYL CISHLIGWTA FLSNMLFFTD PMGQIVYRGD PYSAHNSTEF 360
 LIYERGVEVG CWGFCINSVF SSLYSYFQKV LVSYIGLKG L YFTGYLLFGL GTGPIGLFPN 420
 VYSTLVLCSL FGVMSSTLYT VPFNLITEYH REEEKERQQA PGGDFFDMSVR GKGMDCATLT 480
 CMVQLAQILV GGLGLFLVNT AGTVVVVVIT ASAVALIGCC FVALFVRYVD 530

10 Seq ID NO: C423 Protein Sequence
 Protein Accession #: NP_003264.1

15 1 11 21 31 41 51
 | | | | | |
 MEGFGGVGGR GTRGFAAKGV WRGRAEEGPV LGAAERGFMV STGSRRRVFE GPGGGGLRWT 60
 PGKGTGRQRG AWGPRAEEDGV RRRTLGMPRG SRRDVRAPCG PAGSWGARGG RRRDGPSSRR 120
 RGSATAAARH HVPPAPGGPF GPRAPAGSTR VPARAGGAVE PTGAAAVARL ARPAGGALPT 180
 AGAQAGGPAR GRSGESEWA RRGKGRPGPY QSPGPAVAE GQELKDKSRL RYPINGPQAL 240
 20 VLTALLVGLG MSAGLPLGAL PEMLLPLAFV ATLTAIFISL FLYMKAQVAP VSALAPGGNS 300
 GNPIYDFPLG REINPRICPF DFKYFCELRP GLIGWVLINL ALLMKEAELR GSFSLAMWLV 360
 NGPQLLYVGD ALWHEEAVLT TMDITHDGF FMLAFGDMAW VPFTYSLQAQ FLLEHPQPLG 420
 LPMASVICLI NATGYIIFRG ANSQKNTFRK NPSDPRVAGL ETISTATGRK LLVSGWGMV 480
 RHPNYLGLDI MALAWSLPCG VSHLLPYFYL LYPTALLVHR EARDERSACR STAWPGRSTA 540
 25 GHVCLTASCT STRAAPPPQV GHVPTHPPAH PGPAGASTHLG LKGLHPTQP 589

Seq ID NO: C424 Protein Sequence
 Protein Accession #: NP_056535.1

30 1 11 21 31 41 51
 | | | | | |
 MGRLLRAARL PPLLSPLLLL LVGGAFGLGAC VAGSDEPGFE GLTSTSLDL LPTGLEPLD 60
 SEEPSBTMGL GAGLGAPGSG FPSENEESR ILQPPQYFWE EEEELNDSSL DLGPTADYVF 120
 PDLTEKAGSI EDTSQAQELP NLPSPLPKMN LVEPPWHMPP REEEEEE EEREKEVEK 180
 35 QEEEEEEELL PVNGSQEEAK PQVRDFSLTS SSQTPGATKS RHEDSGDQAS SGVEVESSMG 240
 PSLLLPSTVT TTVTPGQDS TSQEAETVL PAAGLGVEFE APQEAASEAT AGAAGLSGQH 300
 EEPVLPSPFP QTTAPSGAEH PDEDPLGSRT SASSPLAPGD MELTPSSATL QGEDLNQQLL 360
 EGQAEEAQR IPWDSQVIC KDWSNLGKN YIILNMTENI DCEVFRQHRG PQLLALVEEV 420
 LPRHGSQHHG AWHISLSKPS EKEQHLLMTL VGEQGVVPTQ DVLSMLGDIR RSLEEIGIQN 480
 40 YSTTSSQCAR ASQVRSYDGT LFPVVLVIGA ICIIIIALGL LYNCWQRRLP KLKHVSHGEE 540
 LRFVENGCHD NPTLDVASDS QSEMQEKPIS LNGGGALNGP GSWGALMGK RDPESDVPE 600
 EDTHL 605

Seq ID NO: C425 Protein Sequence
 Protein Accession #: NP_001188.1

45 1 11 21 31 41 51
 | | | | | |
 MSEVRPLSRD ILMETLLYEQ LLEPPTMEVL GMTDSEEDLD PMEDFDSLEC MEGSDALALR 60
 LACIGDEMVD SLRAPRLAQL SEVAMHSLGL APIYDQTEDI RDVLSRFMDG FTTIKENIMR 120
 50 FWRSPFNGSV VSCQVLLAL LLLLALLLPL LSGGLHLLK 160

Seq ID NO: C426 Protein Sequence
 Protein Accession #: AAF76225.1

55 1 11 21 31 41 51
 | | | | | |
 MATPLPPSP RHLRLRLRL SGLVLGAALR GAAAGHPDVA ACPGSLDCL KRRARCPFGA 60
 HACGCLQPF QEDQQGLCVF RMRRPPGGGR PQPRLEDEID FLAQELARKE SGQSTPPLPK 120
 60 DRQRLPEPAT LGFSARGQGL ELGLPSTPGT PTPPTHTSLG SPVSSDPVEM SPLEPRGGQG 180
 DGLALVLILA FCVAGAAALS VASLCWCRLQ REIRLTQKAD YATAKAPGSP AAPRISPGDQ 240
 RLAQSAEMYH YQHQRQMLC LERHKEPPKE LDTASSDEEN EDGDFTVYEC PGLAPTGE 300
 VRNPLFDHAA LSAPLPAPSS PPALP 325

65 Seq ID NO: C427 Protein Sequence
 Protein Accession #: NP_004436.1

70 1 11 21 31 41 51
 | | | | | |
 MVCSLWVLLL VSSVLALIEV LLDITGETSE IGWLTYPGG WDEVSVLDDQ RRLTRTFEAC 60
 HVAGAPPGTG QDNWLQTHFV ERRGAQRAHI RLHFSVRACS SLGVSGGTCR ETFTLYYRQA 120
 EEPDSPDSVS SMHLKRWTKV DTIAADESFP SSSSSSSSS SAAMAVGPHG AGORAGLQLN 180
 VKERSFGPLT QRGFYVAFQD TGACIALVAV RLFSYTCPAV LRSFASFPET QASGAGGASL 240
 75 VAAVGTCTVAH AEPEEDGVGG QAGGSPFRLH CNBEGKMWVA VGGCRCQPGY QPARGDKACQ 300
 ACPRGLYKSS AQNAPCSPCP ARSHAPNPA FVCPCLBGFY RASDPPBPAP CTGPPSAPQS 360
 LWFVQGSAL MGRWRLPREL GGRGDLLENV VCKEGRQES PASGGGGTCH RCRDEVHFD 420
 RQRGLTESRV LVGGLRAHVP YILEVQAVNG VSELSFDPQP AAAINVSTSH EVPSAVPVVH 480
 QVSRASNSIT VSWPQPDQTN GNILDYQLRY YDQAEDESHS FTLTSETNTA TVTQLSPGHI 540
 YGFQVRARTA AGHGPYGGKV YFQTLPGQEL SSQLEPRLSL VIGSILGALA FLLLAITVL 600
 80 AVVFQKRKRG TGYTEQLQY SSPGLGVXY IDPSTYEDPC QAIRELAREV DPAYIKIEV 660
 IGTGSPGVR QGRLLQPRGR EYTVAIQALW AGGAESLQMT FLGRAAVLQG FQHPNILLRE 720
 GVVTKSRLPM VLTEFMEELG LDFSLRQREG QPSSQLQVAM QRGVAAAMQY LSSFAFVHRS 780
 LSAHSLVNS HLVCCKVARLG HSPQGPSCLL RWAAPVIAH GKHTTSSDVV SPGILMWEV 840
 SYGERPYNDM SEQEVNLAIE QEFRLPPPPG CPPLGLHLLM DTWQKDRARR PHFDQLVAAP 900
 DKMIRKFDTL QAGGDPGERP SQALLTPVAL DFPCLDSPQA WLSAIGLECY QDNFSEKPLC 960

TFSDVAQLSL EDLPALGITL AGHQKLLHH IQLLQHLRQ QGSVEV

1006

Seq ID NO: C428 Protein Sequence
Protein Accession #: XP_043340.2

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10

1	11	21	31	41	51	
MPDFRRFDI	YRKVPKDLTQ	PTYTGAIISI	CCCLFILFLF	LSELTGFITT	EVVNELYVDD	60
PDKDSGGKID	VSLNLSLPLN	HCELVGLDIQ	DEMGRHEVGH	IDNSMKIPLN	NGAGCRFEGQ	120
FSINKVPGNF	HVSTHSATAQ	PQNPDMTHVI	HKLSFGDTLQ	VQNIHGAFNA	LGGADRLTSN	180
PLASHDYILK	IVPTVYEDKS	GKQRYSYQYT	VANKEYVAYS	HTGRIIPAIW	FRYDLSPITV	240
KYTERRQPLY	RFITTICAI	GGTFTVAGIL	DSCIPTASEA	WKKIQLGKMH		290

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Seq ID NO: C429 Protein Sequence
Protein Accession #: NP_002142.1

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25

1	11	21	31	41	51	
MAQKEGGRTV	PCCSRPKVAA	LTAGTLLLLT	AIGAASWAIV	AVLLRSDQEP	LYPVQVSSAD	60
ARLMVFDKTE	GTWRLLCSSR	SNARVAGLSC	EEMGFLRALT	HSELDVRTAG	ANGTSGFFCV	120
DEGRLPHTQR	LLEVISVDCD	PRGRFLAAIC	QDCGRRRLPV	DRIVGGRTDS	LGRWPWQVSL	180
RYDGAHLCCG	SLLSGDWILT	AAHCFPERNR	VLSRWRVPAG	AVAQASPHGL	QLGVQAVVYH	240
GGYLPFRDPN	SEENSNDIAL	VHLSSPLPLT	EYIQPVCLPA	AGQALVDGKI	CTVTGWGNTQ	300
YYGQAGVLQ	EARVPIISND	VCGADFYGN	QIKPKMPCAG	YPEGGIDACQ	GDGGPFVCE	360
DSISRTPRRR	LCGIVSWGTS	CALAQKPGVY	TKVSDFREWI	FQAIKTHSEA	SGMVTQL	417

Seq ID NO: C430 Protein Sequence
Protein Accession #: BAA92562.1

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1	11	21	31	41	51	
METTIVLSGIN	FEYKGMTGWE	VAGDHIYTAA	GASDNDFMIL	TLVVPGRFP	QSVMA DTENK	60
EVARITTFVE	TLCVSNCELY	FMVGVNSRTN	TPVETWKGSK	GKQSYTYIIE	ENTTTSFTWA	120
FQRTTFHEAS	RKYTNDVAKI	YSINVTNVMN	GVASYCRPCA	LEASDVGSSC	TSCPAGYYID	180
RDSGTCHSCP	PNTILKAHQ	YGVQACVPCG	PGTKNNKIHS	LCYNDCTFSR	NTPTRTFNYN	240
FSALANTVTL	AGGPSFTSKG	LKYPHHFTLS	LCGNQGRKMS	VCTDNTVDLR	IPEGESGFSK	300
SITAYVCQAV	IIPPEVTGYK	AGVSSQPVSL	ADRLIGVTID	MTLDGITSFA	ELPHLESGLI	360
PDVIFFYRSN	DVTQSCSSGR	STTIRVRCSP	QKTVPGLSL	PGTCSGDTGC	GCNFHFLWES	420
AAACPLCSVA	DYHAIVSSCV	AGIQKTTYVW	REPCLCSGGI	SLPEQRVTIC	KTIDFNLKVG	480
ISAGTCTAIL	LTVLTCYFWK	KNQKLEYKYS	KLVMNATLKD	CDLPAADSCA	IMGEDVEDD	540
LIFTSKSLF	GKIKSFTSKQ	PAPVTISLSE	DS			572

Seq ID NO: C431 Protein Sequence
Protein Accession #: NP_004855.1

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50

1	11	21	31	41	51	
MPGQELRTVN	GSQMLLVLLV	LSWLPHGGAL	SLAEASRAS	PGPSELHSED	SRFRELKRY	60
EDLLTRLRAN	QSWEDSNTDL	VPAPAVRIIT	FEVRLGSGGH	LHLRISRAAL	PEGLPEASRL	120
HRALFRLSPT	ASRSWDVTRP	LRRQLSLARP	QAPALHLRLS	PPPSQSDQLL	AESSSARPQL	180
ELHLRPAAR	GRRRARARNG	DDCPLGPGRC	CLRLTVRASL	EDLGWADWVL	SPREVQVTMC	240
IGACPSQFRA	ANMHAQIKTS	LHRLKPDTEP	APCCVPASYN	FMVLIQKTD	GVSLQTYDDL	300
LAKDCHCI						308

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Seq ID NO: C433 Protein Sequence
Protein Accession #: NP_443090.1

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1	11	21	31	41	51	
MEDPSGAREP	RARPRERDFG	RRPHPDQGR	HDRPRDRPGD	PRRKRSSDGN	RRRDGDRDPK	60
RDQERDGNRD	RNRDRERERE	RERDPDRGPR	RDTRDAGPR	AGEHGVWEKE	RQSRTRDGAR	120
GLTWDAAPF	GPAPWEAPEP	POPORKGDPG	RRRPESEKPS	ERYLPSTPRP	GREVEVEYQS	180
EAEGLLLECHK	KYKLTCTGRAC	CQMLEVLLNL	LILACSSVS	SSTGGYTGIT	SLGGIYYYP	240
GGAYSGFDGA	DGEKAQQLDV	QFYQLKLPV	TVAMACSGAL	TALCCLFVAM	GVLRVPWHCP	300
LLLVTGELL	MLIAGGYIPA	LYFYFHYLSA	AYGSPVCKER	QALYQSKGYS	GFPGCSFHGAD	360
IGAGIFALG	IVVFALGAVL	AIKGYRKVRK	LKEKPAEMFE	P		401

Seq ID NO: C435 Protein Sequence
Protein Accession #: Eos sequence

70

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1	11	21	31	41	51	
MGAAGRQDFL	FKAMLTISWL	TLTCFPGATS	TVAAGCPDQS	PELQPNWPGH	DQDHHVHIGQ	60
GKTLILLTSSA	TVYSIHISBG	GKLVKIDHDE	PIVLRTREIL	IDNGGELHAG	SALCPFGGNF	120
TILLYGRADE	GIQPDYPYGL	KYIGVGKGG	LELHGQKKLS	WTFLNKTLHP	GGMAEGGYFF	180
ERSWGHGRVI	VHVIDPKSGT	VIHSDRFDTY	RSKKESERLV	QVLNAVDPGR	ILSVAVNDEG	240
SRNLDDMARK	AMTKLGSKHF	LHLGFRHPWS	FLTVKGNPSS	SVEDHIEYHG	HRGSAARVP	300
KLPTTEHGEY	FNVSLSSEWV	QDVENTEWFD	HDKVSQTKGG	EKISDLWKAH	PGKICNRPID	360
IQATTIDGYN	LSTEVVYKKG	QDYRFACYDR	GRACRSYRVR	FLCGKPVRPK	LTVTIDTNVN	420
STILNLEDNV	QSWKPGDTLV	IATDYSMYQ	AEFPQVLPCR	SCAPNQVKVA	GKPMYLIHGE	480
EIDGVDMAE	VGLLSRNIIV	MGEMEDKCYP	YRNHICNFPD	PDTFGGHIKF	ALGPKAAHLE	540
GTELKRMGQ	LVGYPIRPH	LAGDVDERGG	YDPPTYIRDL	SIHRTFSRCV	TVHGSNGLLI	600
KDVVGYNL	ECFPTEDGPE	ERNTFDHCLG	LLVKSQTLLP	SDRDSKMCCKM	ITEDSYPGYI	660
PKPRQDCNAV	STFWMANPNN	NLINCAAAGS	EBTGFWFIFH	HVPTGPSVGM	YSPGYSEHIP	720

LGKFYNNRAH	SNYRAGMIID	NGVKITEASA	KDKRPFLSII	SARYSPHQDA	DPLKPREPAI	780
IRHFIAYKNQ	DHGAWLRGGD	VWLDSCHFRG	EAQEGFLLTG	MKAGGILLGG	DEAASGMAQG	840
FSPPCRCLLK	LVTGSPFAH	VSLAHS				866

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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein
5 incorporated by reference as if each individual publication, accession number, or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising detecting a nucleic acid comprising a sequence at least 80%
3 identical to a sequence as described in Tables 2A-80 in a biological sample from said patient,
4 thereby determining the presence or absence of said pathological cell.
- 1 2. The method of Claim 1, wherein:
2 a) said pathology is described in Table 1, including a cancer; and/or
3 b) said biological sample comprises isolated nucleic acids.
- 1 3. The method of Claim 1, wherein said biological sample is tissue from an organ
2 which is affected by said pathology of Table 1, including a cancer.
- 1 4. The method of Claim 2, wherein said nucleic acids are mRNA
- 1 5. The method of Claim 2:
2 a) further comprising a step of amplifying nucleic acids before said step of detecting
3 said nucleic acid; or
4 b) where said detecting is of a protein encoded by said nucleic acid.
- 1 6. The method of Claim 1, wherein said nucleic acid comprises a sequence as
2 described in Tables 2A-80.
- 1 7. The method of Claim 2, wherein:
2 a) said detecting step is carried out by:
3 i) using a labeled nucleic acid probe;
4 ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence
5 as described in Tables 2A-80; or
6 iii) detecting a polypeptide encoded by said nucleic acid; or
7 b) said patient is:
8 i) undergoing a therapeutic regimen to treat said pathology of Table 1; or
9 ii) is suspected of having said pathology or cancer.
- 1 8. An isolated nucleic acid molecule comprising a sequence as described in
2 Tables 2A-80.

- 1 9. The nucleic acid molecule of Claim 8, which is labeled.
- 1 10. An expression vector comprising the nucleic acid of Claim 8.
- 1 11. A host cell comprising the expression vector of Claim 10.
- 1 12. An isolated polypeptide which is encoded by a nucleic acid molecule
2 comprising a sequence as described in Tables 2A-80.
- 1 13. An antibody that specifically binds a polypeptide of Claim 12.
- 1 14. The antibody of Claim 13:
2 a) conjugated to an effector component;
3 b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a
4 cytotoxic chemical;
5 c) which is an antibody fragment; or
6 d) which is a humanized antibody.
- 1 15. A method for specifically targeting a compound to a pathological cell in a
2 patient, said method comprising administering to said patient an antibody of Claim 13,
3 thereby providing said targeting.
- 1 16. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising contacting a biological sample with an antibody of Claim 13.
- 1 17. The method of Claim 16, wherein:
2 a) said antibody is conjugated to:
3 i) an effector component; or
4 ii) a fluorescent label; or
5 b) said biological sample is a blood, serum, urine, or stool sample.
- 1 18. A method for identifying a compound that modulates a pathology-associated
2 polypeptide, said method comprising the steps of:

- 3 a) contacting said compound with a pathology-associated polypeptide, said
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence
5 at least 80% identical to a sequence as described in Tables 2A-80; and
6 b) determining the functional effect of said compound upon said polypeptide.

1 19. A drug screening assay comprising the steps of:

- 2 a) administering a test compound to a mammal having a pathology of Table 1 or a
3 cell isolated therefrom; and
4 b) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as described in
6 Tables 2A-80 in a treated cell or mammal with the level of gene expression of said
7 polynucleotide in a control cell or mammal, wherein a test compound that
8 modulates said level of expression of the polynucleotide is a candidate for the
9 treatment of said pathology.
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